## Schreiber, David

From: Sent: To:

Zhou, Shubo (AU1631) Tuesday, October 08, 2002 4:16 PM Schreiber, David

seq search request

Hi David,

Subject:

This is a Markush search and each SEQ ID is a very short peptide seq. Enjoy!

Joe

Shubo "Joe" Zhou, Ph.D. Patent Examiner (703)-605-1158 CM1/12D06 AU 1631, US PTO

Search Request

\*

Requester's full name: Shubo "Joe" Zhou

**Examiner #:** 78282

Art Unit: 1631

**Phone #:** 703-605-1158

Mailbox #: 12D01/CM1

Results format: pape

New Room #: 12D06

\*

Serial #: 09/422,838

Please search:

Protein databases for

**SEQ ID NOs: 22-32, and 34** 

Including:

1. default search

Please provide 30 alignments for the search.

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October 9, 2002, 08:55:27; Search time 5.32084 Seconds (without alignments) 146.898 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                               US-09-422-838C-22
171
1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                   Run on:
                                                                                                                                                                                                   Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMD.pep:\*
6: /cgn2\_6/ptodata/2/iaa/pcTuS\_COMD.pep:\*

Description	231,	231, 13, 193,	193,	Sequence 193, App Sequence 13, Appl Sequence 193, App	17, 185,	17, 185, 17.		18,	118 122 18 19 19
SUMMARIES	-08-764-640-2 -09-244-298A-	08-764 08-764 08-764	-08-973-225-193 -08-973-225-193 -09-244-298A-13	US-09-244-298A-193 US-09-516-704-13 US-09-516-704-193	-08-764-640-17 -08-764-640-18	US-08-973-225-17 US-08-973-225-185 US-09-244-298A-17	-09-244- -09-516-	-08-764-640-18 -08-764-640-19	-08-973-225-18 -08-973-225-19 -08-973-225-22 -09-244-298A-1
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Score	78.5	73 73 73				73 73	73 73	73	73 73 73 73
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Sequence 232, App Sequence 184, Appl Sequence 194, Appl Sequence 232, App Sequence 195, App Sequence 199, App Sequence 195, App Sequence 195, App Sequence 199, App Sequence 200, App	BIND TO A
16 3 US-09-244-298A-232 16 4 US-09-516-704-18 16 4 US-09-516-704-194 16 2 US-09-516-704-194 14 2 US-09-764-640-195 14 3 US-08-74-610-199 14 3 US-08-73-225-199 14 3 US-09-244-298A-195 14 4 US-09-244-298A-195 14 4 US-09-516-704-199 15 2 US-08-764-640-209 15 2 US-08-764-640-209 15 3 US-08-764-640-215 15 3 US-08-764-640-215	ALIGNMENTS  S/08764640  and J. ald W. en E. tian firstopher R. hard W. ndolph B. urekha TIDES AND COMPOUNDS THAT TIDES AND COMPOUNDS THAT  EPTOR 4  come ive, P.O. Box 13398 le Park atible DOS/MS-DOS lease #1.0, Version #1.30 158, 158, 158, 158, 158, 158, 158, 158,
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RESULT 3
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                                                                                                            Query Match 45.9%; Score 78.5; DB 2; Length 25; Best Local Similarity 46.4%; Pred. No. 0.00027; Matches 13; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schez, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Handren, Richard W.
APPLICANT: Poduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%; Score 78.5; DB 3; Length 25; 46.4%; Pred. No. 0.00027; tive 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
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; OTHER INFORMATION: /product= "Ava"
US-09-244-298A-231
                                       ; OTHER INFORMATION: /product= "Ava"
US-08-764-640-231
                                                                                                                                                                                                       2 EGPTLRQWLAARAGPNGIEGPTLRQWLA 29
                                                                                                                                                                                                                               2 DGPTLREWISFXA-----DGPTLREWIS 24
                                                                                                                                                                                                                                                                                                                                                           Sequence 231, Application US/09244298A Patent No. 6121238
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REGISTRATION NUMBER: 36,392
REFRENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENOTH: 25 amino acids
TYPE: amino acid
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NAME/KEY: Modified-site
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Best Local Similarity 46.4%
Matches 13; Conservative
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MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wel
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                       LOCATION:
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Gaps
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.9%; Score 78.5; DB 4; Length 25; 46.4%; Pred. No. 0.00027;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01 Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HUDAGE, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
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2 DGPTLREWISFXA----DGPTLREWIS 24
                                                                                                                              Sequence 231, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
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; Patent No. 5869451
; Patent No. 5869451 5837683
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEOUENCES: 244
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Matches 13; Conservative
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US-08-764-640-13
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NUMBER OF SEQUENCES:
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                                                                                                                                                                    APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
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                                                               Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                     Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTATION NUMBER: 36,392
REPERENCE/DOCKET NUMBER: PK128
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deprince, Randolph B.
Podduturi, Surekha
Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                         ADDRESSEE:
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US-08-764-640-193
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APPLICANT:
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APPLICANT:
                                                                  APPLICANT:
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                  APPLICANT:
                                APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                             STATE:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.00075; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                 CERAITING SIGHER: PC-LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSES: Glazow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
             ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
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Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                           PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
"has 14; Conserve
                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                         STATE: NC
COUNTRY: USA
27709
                                                                                                     USA
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us-09-422-838c-22.rai

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; Sequence 193, Application US/09244298A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Matches 14; Conserv
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US-08-973-225-193
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                                        Query Match
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                                                                                                                                                                                                                                                                                                                               42.7%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.00075; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Five Moore Drive, P.O. Box 13398
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
                    ATTORNEY/AGENT INFORMATION:
NAME: HIDDLEC, RODERT 1.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
    FILING DATE: 04-Dec-1997
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                            LENGTH: 14 amino acids
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     Length 14;
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Query Match 42.7%; Score 73; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 0.00075; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 73; DB 3; Le
100.0%; Pred. No. 0.00075;
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APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwilla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balsubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Peter J.
APPLICANT: Pedduturi, Surekha
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 13, Application US/09244298A
; Patent No. 6121236
; GENERAL INFORMATION:
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100.0%; Pre
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US-09-516-704-193
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                                                                                                                                                                                                         APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.00075; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                      STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                 Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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Hendren, Richard W.
                                                                                                                                  Wagstrom, Christopher R
Hendren, Richard W.
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Podduturi, Surekha
                                                                                                                                                                      Deprince, Randolph B.
Podduturi, Surekha
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Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, RODETT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-100.
INFORMATION FOR SEQ ID NO: 193:
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                                                                                                                                                                                                                                                                                                    Glaxo Wellcome
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LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
GENERAL INFORMATION:
APPLICANT: Dower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                USA
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APPLICANT:
APPLICANT:
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APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.7%; Score 73; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 0.00075; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
                                                    ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PK3281
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Hendren, Richard W.
                                                                                                 Research Triangle Park
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 244 CORRESPONDENCE ADDRESS:
                                                                                                                                                                       ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                   COUNTRY: USA
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ZIP: 27709
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                           42.7%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Hendren, Christopher R.
APPLICANT: Hendren, Richard W.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 185, Application US/08764640
patent No. 5869451
patent No. 5869451 5837683
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Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                         Query Match
Best Local Similarity 100.C
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 14; Conservative
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                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-17
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                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                  US-08-764-640-185
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Hendren, Richard W.
APPLICANT: Hendren, Richard W.
APPLICANT: Hoduturi, Surekha
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 42.7%; Score 73; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 0.00075; Matches 14; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: HTUDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/POCKET NUMBER: 36,392
REFERENCE/POCKET NUMBER: 98,381
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR EQUID NO: 17:
SECURACTERISTICS:
LENGTH: 15 amino acids
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                                                               ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEFHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
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US-08-764-640-17
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Pal
APPLICANT: Wagstrom, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
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                                                                                       NUMBER OF SEQUENCES: 232
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Five Moore Drive,
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 14; Conservative
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ZIP: 27709
                                                                                                                                                                                                     STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.7%; Score 73; DB 3; Length 15; Best Local Similarity 100.0%; Pred. No. 0.00081; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenful Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec. 1997
ATTONEY/AGENT INFORMATION:
NAME: HILDIGG, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEBHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                             Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                        APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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                                                                           Sequence 17, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                          Schatz, Peter J
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                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-973-225-185
                                                      JS-08-973-225-17
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                                RESULT 14
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CITY: Research Triangle Park
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 14; Conservative
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                   15 amino acids
                                                                                                                                                                                   Best Local Similarity 100.
Matches 14; Conservative
SEQUENCE CHARACTERISTICS
                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-185
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                                      TYPE: amino acid STRANDEDNESS:
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US-09-516-704-17
                     LENGIH:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.7%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.00081; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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APPLICANT: Balasaubzamanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                           APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: HTUDIGC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                             PK3281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research Triangle Park
                                                                                                                                                                  NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
      IBM PC compatible
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
42.7%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.7%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IEM PC compatible
COMPUTER: IEM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: 05/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz, Peter J.
Balasubramanian, Palaniappan
Baystrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-516-704-17
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.7%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              COUNTRY: C. ZIP: 27709

ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
FILING DATE: 11-DEC-1996
                                                                                                                                                                                                             SSEE: Glaxo Wellcome
:: Five Moore Drive, P.O. Box 13398
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: /product= "Beta-ala" US-08-764-640-18
  Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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; Patent No. 5869451
; Patent No. 5869451 5837683
                                                                 Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.7
Best Local Similarity 100.
Matches 14; Conservative
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MOLECULE TYPE: peptide
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TITLE OF INVENTION: PI
TITLE OF INVENTION: RI
NUMBER OF SEQUENCES: :
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                                                                                     APPLICANT:
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                                             APPLICANT:
                                                                   APPLICANT:
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APPLICANT:
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APPLICANT:
                          APPLICANT:
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APPLICANT:
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STATE:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: cDASSIFICATION: cDASSIFICATION: 
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-516-704-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                Sequence 185, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                               APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
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GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Garrett, Royen E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 244
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Best Local Similarity 100.
Matches 14; Conservative
1 IEGPTLROWLAARA 14
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ZIP: 27709
                                                                            US-09-516-704-185
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                                                        RESULT 19
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us-09-422-838c-22.rai

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TOPOLOGY: linear MOLECULE TYPE: peptide
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.7%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                                                                                  COUNTEY: USA

ZIP: 27709

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPatible

OFBRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,640

FILING DATE: 11-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Five Moore Drive, P.O. Box 13398
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                               PK3281
                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION UNDHER: 36,392
REFERENCE/DOCKET UNDHER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 14; Conservative
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US-08-764-640-232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/973,225A
ATTORING DATE: 04-Dec-1997
ATTORING DATE: 04-Dec-1997
ATTORING PATE: NOBER: 36,392
RECTSRATION NUMBER: 36,392
RECTSRATION NUMBER: PK3065USW
TELEPHONE: PW3 1919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16;
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100.0%; Pred. No. 0.00087;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
APPLICATION NUMBER: US/08/764,640
CLASSIPICATION: 514
ATTOCNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTATION NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
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Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 18, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                              LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-764-640-232
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                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
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RESULT 25

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Wrighton, Nicholas C.
TITLE OF INVENTION: PRETIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; ative 0; Mismatches 0; Indels
                                                                                                                                       42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                      LOCATION: 15
OTHER INFORMATION: /product= "Beta-ala"
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: HINDLEC, RODERT T.
REGISTRATION NUMBER: 36, 392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                              Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J.
Barrett, Ronald W.
CWirla, Steven E.
Duffin, David J.
Gates, Christian
                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schatz, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                               14; Conservative
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                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NC
                                                                                                                                                                                                                                                                                                                                             US-08-973-225-194
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-973-225-194
                                                                                               US-08-973-225-18
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                                                                                                                                                                                 Matches
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                       THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Balasubramanian, Palaniappan
                                                                                            Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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REGISTRATION NUMBER: 36,392
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Hendren, Richard W.
                Sequence 220, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 18, Application US/09244298A; Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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                                                                           APPLICANT: Dower, William J.
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NC
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US-08-973-225-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-973-225-220
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APPLICANT:
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APPLICANT:
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COUNTRY: USA
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                  APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COPERATIOG SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/24,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HIUDIGC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 36,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acid
TYPE: amino acid
                                                                                                                              ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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CTHER INFORMATION: /product= "Beta-ala"
US-09-244-298A-18
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APPLICANT: DOWER, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
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Hendren, Richard W.
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; Sequence 194, Application US/09244298A
; Patent No. 6121238
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APPLICANT: Podduturi, Surekha
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Best Local Similarity 100.
Matches 14; Conservative
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MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                               CITY:
STATE:
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-428-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W. APPLICANT: Deptince, Randolph B. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 232, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  16 amino acids
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Best Local Similarity 100.
Matches 14; Conservative
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; MOLECULE TYPE: peptide
US-09-244-298A-194
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STRANDEDNESS:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
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                                         Length 16;
                                                                                     0; Indels
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COMPUTER: IBM PC Compatible
COMPRESATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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RADDRESSER: Glazow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                         42.7%; Score 73; DB 4; L6
100.0%; Pred. No. 0.00087;
tive 0; Mismatches 0;
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Balasubramanian, Palaniappan
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: «UNknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-516-704-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
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Hendren, Richard W.
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                                                                                                                                                                                                                                                                                     Sequence 194, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hrubiec, Robert T.
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 244
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                       Conservative
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                                                                                                                                                                             1 IEGPTLROWLAARA 14
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                                           Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                US-09-516-704-194
  US-09-516-704-18
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Podduturi, Surekha
TITLE OF INVENTION: PRETIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                Query Match
42.7%; Score 73; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                              16 amino acids
                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                    2 IEGPTLRQWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                               TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27709
                                                                                                                                                                                                                         US-09-244-298A-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 29
US-09-516-704-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                              LENGTH:
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Gaps

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(without alignments)
247.023 Million cell updates/sec
                                                                                                                                                   October 9, 2002, 08:50:51; Search time 14.3888 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                 US-09-422-838C-22
                                                                                                                                                                    Run on:
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1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32 747574 segs, 111073796 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Title: Perfect score: Scoring table: Searched: Sequence:

747574 Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:\*
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:\*
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:\*
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997 /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT A\_Geneseq\_032802:\* 9: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ф				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	171	100.0	32	21	AAB17297	TPO-mimetic peptid
10	171	100.0	32	21	AAY96520	Thrombopoietin mim
m	171	100.0	34	21	AAY96527	Thrombopoietin mim
4	156	91.2	32	21	AAB17289	TPO-mimetic peptid
- 51	147.5		31	21	AAB17288	TPO-mimetic peptid
·	147		30	21	AAB17287	TPO-mimetic peptid
7	145.5	85.1	33	21	AAB17290	TPO-mimetic peptid
œ	145		34	21	AAB17291	TPO-mimetic peptid
σ	145		36	21	AAB17306	TPO-mimetic peptid
10	145		36	21	AAY96526	Thrombopoietin mim
:-	144.5	84.5	35	21	AAB17292	TPO-mimetic peptid

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

## ALIGNMENTS

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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin i; cytotoxic real lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:353.
                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                      AAB17297 standard; Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                            99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                     98US-0105371.
99US-0428082.
                                                                             31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                    WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                             Synthetic.
                                                  . AAB17297;
RESULT 1
               AAB17297
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For domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                      The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 171; DB 21; Length 32; 100.0%; Pred. No. 1.8e-17; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note" "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin mimetic peptide compound 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                  Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96520 standard; peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 32; Conservative
                                                                           autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024770-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1 (L_1)_TTMP_2], as new TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x2-x1_0, x2-x1_1, x2-x1_2, x2-x1_1, x2-x1_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                       Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 171; DB 21; 100.0%; Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preα. ν...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin mimetic peptide compound 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96527 standard; peptide; 34 AA.
                                                                                                                                                                                                                                      Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17..20
/label= linker
                                               Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21..34
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3..16
/label= TMP_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0
                                                                                            WPI; 2000-365108/31.
(AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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Matches
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                                                                                                                                                               platelets or platelet precursors (e.g. megakaryocýtes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g.
                                                                                            Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                  aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autolimune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 171; DB 21;
100.0%; Pred. No. 1.9e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17289 standard; Peptide; 32 AA
                                                                                                                                            Claim 16; Page 64; 91pp; English.
                                              Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0428082
98US-0105348
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                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Conservative
                                                                     WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                      34 AA;
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23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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AAB17289
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The present invention describes composition of matter (1) comprising an FC domain, pharmacologically active peptides, and linkers. Where (1) is: (X1)a-F1-(X2)b, where F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-F1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently selected from -(L1)C-F1-(L2)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAAA69526 and AAB10955 to AAB18033 represent uncention acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TMF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vactotoxic; Teall Jymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%; Score 156; DB 21; Length 32; 93.8%; Pred. No. 2.4e-15; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPO-mimetic peptide sequence SEQ ID NO:344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                Boone TC;
                                                                                                                                                                               Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17288 standard; Peptide; 31 AA
              Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371.
99US-0428082.
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Matches 30; Conservative
                                                       WPI; 2000-350702/30.
                                                                                                                                       autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C,
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Matches
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     The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: FI = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-F1-(L1)c-F2.

-(L1)c-F1-(L2)d-F2.

-(L1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNR; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothellal growth factor; matrix metalloproteinase;
                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.3%; Score 147.5; DB 21; Length 31; 93.8%; Pred. No. 3.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLROWLAARAG-GGIEGPTLROWLAARA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                       Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17287 standard; Peptide; 30 AA
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 93.8 Matches 30; Conservative
              WPI; 2000-350702/30.
                                                                                        autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000
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For domain, pharmacologically active peptides, and linkers. Where [1] is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(II)c-P1-(I2)d-P2-(I3)d-P-7; or -(I1)c-P1-(I2)d-P2-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(I3)d-P3-(
                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%; Score 147; DB 21; Length 30; 93.8%; Pred. No. 4.3e-14; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAG--GIEGPTLRQWLAARA 30
                                                                                                                                                                                                                     Example 1; Page 315-316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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99US-0428082.
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                                                                                                                autoimmune diseases -
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es 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17290;
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reforming the composition of the present invention.
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is:
                                                                                   present invention describes composition of matter (I) comprising
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 pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145.5;
Pred. No. 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA-GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                                                Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17291 standard; Peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Conservative
                   autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                33 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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C (Main, pharmacologicalities composition, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3.

(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and as b, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and as t, c, d, e, and f = are each independently linkers; and an extitution, and positions. The compositions are useful for treather functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA89526 and AAB16955 to AAB1803 represent invention.
                                                       The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 145; DB 21;
Pred. No. 9.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARA--GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLROWLAARAGGGGGGIEGPTLROWLAARA 34
               Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17306 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17306;
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(II)C-FI-(II)C-PI-(IZ)d-F2.

(II)C-FI-(IZ)d-F2-(I3)e-P-3, or -(II)C-FI-(IZ)d-F2-(I3)e-F3-(I4)F-P4 where PI, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; IJ, IZ, I3, and I4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently of provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer asthma, thrombosis, or autoimmune diseases. The use of a FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein and possibly placental transfer. AAA69443 to AAAA69526 and AAB16955 to AAB18033 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                          84.8%; Score 145; DB 21; Length 36; 83.3%; Pred. No. 1e-13; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96526 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                            36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96526;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96526
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4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1: cytoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                   DB 21; Length 36;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                   84.8%; Score 145; DB 21
83.3%; Pred. No. 1e-13;
live 0; Mismatches
                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone IC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 317-318; 608pp; English
diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                             AAB17292 standard; Peptide; 35 AA.
                  Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                        30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                  36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                 AAB17292;
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                   AAB17292
                                                                                                                                                                                                                                                                                                                                                                 Db
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us-09-422-838c-22.rag

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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18035 to AAAB180303 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
          The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where FI = an FC domain, X1 and X2 = are each independently selected from -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L3)e-F3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombollytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                     84.5%; Score 144.5; DB 21; Length 35; 85.7%; Pred. No. 1.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARA---GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB16963 standard; Protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                               35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB16963;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
AAB16963
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The present invention describes composition of matter (I) comprising an

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Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2.

(L3)d-P2-(L3)d-P2, (L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3.

(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4

(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4

(L3)d-P3-(L3)d-P3, or -(L3)d-P3, or -(L3)d-P3-(L3)d-P3-(L4)f-P4

(L3)d-P3-(L3)d-P3-(L3)d-P3, or -(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNR; antagonist; mmwp; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 144; DB 21;
Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17293 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%;
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.33
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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where P1, P2, P3, and P4 = are each independently sequences of

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"(L1)c-P1-(L2)d-P2-(L3) = P-73, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a lost consolition and activities. DNAs, vectors and host cells from the present inventions are used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions are used for for comporate functions such as Fc receptor binding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 to AAAA6955 and AAB16955 to AAB1803 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (x.1)a-(x.2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from - (L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)d-P2-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; finuncosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF; antiagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                   84.2%; Score 144; DB 21; Length 36; 83.3%; Pred. No. 1.4e-13; ive 0; Mismatches 2; Indels
  independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17301 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.33
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                          36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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                   pharmacologically active peptides; Li, Li, Li, Li, and Li = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18035 to AAAB180303 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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is:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatio; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetlc; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalioproteinase; asthma; thrombosis; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 144; DB 21;
Pred. No. 1.4e-13;
0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGKGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17303 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18032 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where FI = an FC domain, X1 and X2 = are each independently selected from -(Li)c-PI-(Li)c-PI-(L2)d-P2, -(L1)c-PI-(L2)d-P2, -(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; Li, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or I, provided that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO, TPO, CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vactotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                             84.2%; Score 144; DB 21; Length 36; 83.3%; Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17307 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases
                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                     36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17307;
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17307
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, trombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer. The use of morporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2-x_1_0, X_2-x_1_1, X_2-x_1_2,
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally modified by bromoacetyl or PEG"
                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                               84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoletin mimetic peptide compound 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            AAY96523 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= TMP_1
15 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-2000 (first entry)
                                                                                                                                                                                                                               30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365108/31.
                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024770-A2
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                              RESULT 17
                                                                                                                                                                                                                                                                                                                                                          AAY96523
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                                                                                                                                                                                                                                                                 δλ
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X_2-X_1-3, X_2-X_1-4, X_1-X_1-0, X_1-X_1-1, X_1-X_1-2, X_1-X_1-2, and X_1-X_1-4. X_1=1, X_1=1, X_1, X_2=1, X_1=1, X_1=1, X_2=1, X_3=1, or X_3=1, or X_3=1, or X_1=1, X_2=1, X_3=1, or X_1=1, or X_1=1, X_2=1, X_3=1, X_1=1, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                               84.2%; Score 144; DB 21; Length 36;
83.3%; Pred. No. 1.4e-13;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                              | IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96524 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "optional"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15..22
/label= linker
23..36
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/label* TMP_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                               30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                           36 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                      Query Match
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AAY96524
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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mimetic peptide (TMP) dimer joined by a linker [TMP]-[L]) nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2-X_L0, X_2-X_L1, X_2-X_L2, X_1-X_L2, X_1-X_L2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.2%; Score 144; DB 21; Length 36;
83.3%; Pred. No. 1.4e-13;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin mimetic peptide compound 6.
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/label= linker
19..32
/label= TMP_2
32
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/label= TMP_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 83.38
Matches 30, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
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                 δλ
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A compound which binds to an mpl receptor comprising a thrombopoietin

mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

10 to 14 residues in length comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2,

x_2-x_1-3, x_2-x_1-4, x_1-x_1-0, x_1-x_1-1, x_1-x_1-2, x_1-x_1-3, and

x_1-x_1-4, x_1-1, x_1-1, x_1-x_1-1, x_1-x_1-2, x_1-x_1-3, and

x_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; x_8 = 0, N,

CC X_4 = P; X_5 = T or S; X_1-2 = L, I, V, A, F; M, Or K; X_1-1 = A, I, V,

CC T, V, N, O or G; X_1-4 = A, I, V, L, F; G, S, or G; L, 1 = linker

CC omprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0 or 1. The compounds bind to acid; and n = 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 144; DB 21; Length 36;
Pred. No. 1.4e-13;
0; Mismatches 2; Indels
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diseases which involve thombocytopenia
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                                               Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96528 standard; peptide; 41
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/label= linker
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/label= TMP_1
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/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%
These 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2000 (first entry)
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Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                             is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; famunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropictin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                     Length 41;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                     84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.6e-13;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                 6 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JÇ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                               Claim 16; Page 65; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17281 standard; Peptide; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3°
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                             41 AA;
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17281;
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
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The present invention describes composition of matter (I) comprising an Fr domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a+F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L2)c+P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2. P3, and P4 = are each independently sequences of pharmacologically active peptides: L1, L2, L3, and L4 = are each independently active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently independently linkers; and a, b, c, d, e, and f = are each independently love cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein and mining, complement fixation, and possibly placental transfer. NAA69443 to AAA69526 and AAB16955 to AAB18013 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autofimume disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic Teall Jymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%; Score 144; DB 21; Length 42; 83.3%; Pred. No. 1.7e-13; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPILROWLAARA----GPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 313; 608pp; English.
                 Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17282 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
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Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17282;
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor blading, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
    The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-P1-(X2)b. where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1 -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently on r1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoiethi; thrombopoieth; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%; Score 144; DB 21; Length 42; 83.3%; Pred. No. 1.7e-13; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371.
99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                               42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
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The present invention describes composition of matter (1) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (1) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(1).C-F1-(12)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or provided that at least 1 of a and b 11. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB1803 represent invention.
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42 AA; Sequence

Gaps 4; Length 42; Indels Score 144; DB 21; Pred. No. 1.7e-13; 2; 0; Mismatches 84.2%; 30; Conservative Similarity Query Match Local Matches

1 IEGPTLRQWLAARA ---- GPNGIEGPTLRQWLAARA 32

7 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 42

g ò

RESULT 24 AAY96530

AAY96530 standard; Protein; 42 AA

AAY96530;

(first entry) 04-SEP-2000

Thrombopoietin mimetic peptide.

Immunoglobulin; IgGl; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.

Synthetic

WO200024770-A2.

04-MAY-2000

99WO-US24834 22-OCT-1999;

98US-0105348 23-OCT-1998;

(AMGE-) AMGEN INC

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31. N-PSDB; AAA29225

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Example 2A; Page 48; 91pp; English.

Overlapping oligonucleotides were used to construct a synthetic gene encoding a thrombopoietin mimetic peptide (TMP), which was then fused in-frame to the Pc region of the human IgGl chain (see AAY96529). A compound which binds to an mpl receptor comprising a TMP dimer joined by a linker [TMP\_1 (L\_1), nTMP\_2], is new. TMP\_1 and TMP\_2 are amino acid sequences varying from at least 10 to 14 residues in 

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an
is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising effect domain, pharmacologically active peptides, and linkers. Where (I) i(X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from - (L1)C-F1 - (L1)C-F1-(L2)d-F2, - (L1)C-F1-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antiqen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                        4,
                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                               Score 144; DB 21; Length 42;
Pred. No. 1.7e-13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                         7 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 42
                                                                                                                                                                                                                                             1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                           AAB17311 standard; Peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases
                                                                                                                                                                           42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                      RESULT 25
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where Pl, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently lo or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be useful for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (x,1)_{R+\Gamma}(x,2)_{D}, where: FI = an FC domain; XI and X2 = are each independently selected from -(L1)_C-P1, -(L1)_C-P1-(L2)_d-P2, -(L4)_F-P4 -(L1)_C-P1-(L2)_d-P2-(L3)_E-P3, or -(L1)_C-P1-(L2)_d-P2-(L3)_E-P3-(L4)_F-P4
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                      84.2%; Score 144; DB 21; Length 60;
83.3%; Pred. No. 2.5e-13;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IEGPTLRQWLAARAGGGGGGGGGGGFTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16960 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3 les 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                   60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA69446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1999;
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                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB16960;
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
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where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently loor 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNas, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor blading, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.4e-12;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96531 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG1 Fc TMP fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US24834.
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N-PSDB; AAA29229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P2-(L3)e-P2, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; I1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of the peptides; and a b, c, d, e, and f = are each independently of the composition can or 1, provided that at least 1 of a and b is 1. The composition can
the c-Mpl receptor which mediates the activity of endogenous
                                                                   thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, we have the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                           virus associated ITP, and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 144; DB 21;
Pred. No. 1.4e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:350.
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                                                                                                                                                                                                                                                                                                                                                                                                                         269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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activities DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer

have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FG domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443
                       AAA69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-rP-(X2)b, where F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease, cytostatic; antiastimatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                         .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                sequences used in the exemplification of the present invention.
                                                                                                                                              Length 37;
                                                                                                                                                                                           Indels
                                                                                                                                           Score 143.5; DB 21;
Pred. No. 1.7e-13;
0; Mismatches 2;
                                                                                                                                                                                                                               1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                           AAB17295 standard; Peptide; 38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J,
                                                                                                                                                  83.98;
                                                                                                                                                                     81.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                              Query Match 83.9
Best Local Similarity 81.1
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
                                                                                                         37 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17295;
                                                                                                                                                                                                                                                                                                                                    RESULT 29
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Gaps

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reforming parameters of the composition of the present invention.
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to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; famunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                              9
                                                                                                      Length 38;
                                                                                                                                            Indels
                                                                                                                                            5
                                                                                                  83.6%; Score 143; DB 21;
78.9%; Pred. No. 2.1e-13;
iive 0; Mismatches 2;
                                                                                                                                                                                       1 IEGPTLROWLAARA-----GPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGGGGGGGGGGGGTEGPTLRQWLAARA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                             AAB17304 standard; Peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                Query Match
Best Local Similarity 78.9°
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases
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                                                           38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                      AAB17304;
                                                             Seguence
                                                                                                                                                                                                                                                                                         RESULT 30
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SSXS
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7;
                         DB 21; Length 39;
                                            Indels
                   1 IEGPTLRQWLAARA-----GPNGIEGPTLRQWLAARA 32
                                            0; Mismatches
                                                                                                           Search completed: October 9, 2002, 08:58:54 Job time: 14.3888 secs
                         83.3%;
76.9%;
                                             Conservative
                                    Best Local Similarity
        39 AA;
                                            30;
        Sequence
                          Query Match
                                             Matches
χx
                                                               δλ
                                                                               qq
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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- protein search, using sw model OM protein

(without alignments) 427.397 Million cell updates/sec 9, 2002, 08:54:17; Search time 7.19438 Seconds October Run on:

US-09-422-838C-22 171 Title: Perfect score:

1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 segs, 96089334 residues

Searched:

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* . . . . . . Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## spike glycoprotein disintegrin-like m hypothetical prote UTP--glucose-1-pho hypothetical prote conserved hypothet probable UV damage familial Alzheimer hypothetical prote transport protein SITS-binding prote unknown protein en conserved hypothet nitric-oxide reduc efflux fami conserved hypothet conserved hypothet sorbitol oxidase probable pyruvate probable membrane Description cation F87286 JW0076 D85818 B83471 AG0147 C75350 T35254 S65358 F83487 G72680 D70601 S04987 B95325 T29299 VGVNCV C83221 C75479 DEPSXA AF3634 DB Query Match Length Score Result <u>چ</u>

Cipecies: Caulobacter creacentus
Cipecies: Caulobacter creacentus
Cipecies: Caulobacter creacentus
Cipecies: Caulobacter creacentus
Cipecies: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001
Cincossion: F87286
Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Arritle: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87286
A:Accession: F87286
A:Accession: F87286
A:Accession: F87286
A:Accession: F87286
A:Accession: F87286
Cipecule type: DNA
A:References: GB:AE005673; NID:g13421446; PIDN:AAK22290.1; GSPDB:GN00148

Length 361;

DB 2;

Score 56; DB Pred. No. 8.2;

32.7%; 54.5%;

Best Local Similarity

A; Gene: CC0303 Query Match

prot

probable polA

hypothetical prote

nonooxygenase (imp

transcription acti

probable trna meth photosystem II chl

hypothetical prote

S06469 T20454 C70559 A36925

460 472 904 333

C83365

410

AI3083 H98202

49.5 49.5 49.5

3-methyl-2-oxobuta 2-oxoisovalerate d

cation efflux family protein (imported) - Caulobacter crescentus

hypothetical prote pyruvate dehydroge di-N-acetylchitobi tyrosine-specific probable permease photosystem II chi photosystem II chi photosystem II chi photosystem II chi probable sensor/re collagen alpha 1(x collagen alpha 2 f glutathione S-tran hypothetical prote excisionase - phag excisionase - phag excisionase   phag excisionase   phag excisionase   phag	ALIGNMENTS	RESULT 1  B71325  Conserved hypothetical protein TP0421 - syphilis spirochete C;Species: Treponeme pallidum subsp. pallidum (syphilis spirochete) C;Species: Treponeme pallidum subsp. pallidum (syphilis spirochete) C;Accession: B71325 R;Fraser, C.M.; Nortis, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G C;Accession: B71325 R;Fraser, C.M.; Nortis, S.J.; Weinstock, J.C. Scolence 281, 375-388, 1998 Science 281, 375-388, 1998 A;Attle: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770 A;Accession: B71325 A	
2 T22896 1 DEBSPF 2 AA4140 2 A83032 2 A83032 2 S42647 2 150630 2 A83324 2 A83324 2 A8324 2 A83	ALIC	RESULT 1 B71325 conserved hypothetical protein TP0421 - syphic conserved hypothetical protein TP0421 - syphic Species: Treponema pallidum subsp. pallidum C; Accession: B71325 R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; Son, J.; Khalak, H.; Richardson, D.; Howell, trson, J.; Khalak, H.; Richardson, D.; Howell, trey, L.; Weidman, J.; Smith, H.O.; Venter, J. Science 281, 375-388, 1998 A; Title: Complete genome sequence of Treponema P71216: Complete genome sequence of Treponema P71325 A; Accession: B71325 A; Accession: B71325 A; Accession: B71325 A; Reference number: A71250; MUID: 98332770 A; Residues: 1-683 < COL> A; Genetics: A; Hiller After Aft	
214 369 3869 4859 4859 4859 1024 3108 493 72		RESULT 1 B71325  Conserved hypothetical protein TP0421 C;Species: Treponema pallidum subsp. pr C;Accession: B71325 R;Fraser, C.M.; Norris, S.J.; Weinstool TSON, J.; Khalak, H.; Richardson, D.; Ithalak, H.; Richardson, D.; Ithalak, H.; Richardson, D.; Science 281, 375-388, 1998 A;Title: Complete genome sequence of Transference number: A71250; MUID:98332 A;Accession: B71325 A;Accession: B71325 A;Accession: B71325 A;Coll A;Residues: 1-683 <col a;col<="" a;coll="" td=""/> <td></td>	
288.7 288.7 288.7 288.7 288.7 288.7 288.7 288.7 288.7 288.1 288.1 288.1 288.1		octhetical 1-1990 # se 11-1998 # se 11-1998 # se 11-1950	
44 4444444444444 000000000000000000000		RESULT 1  B71325  Conserved hypothetical pro C.5pecies: Treponema palli C.5chces: Treponema palli C.5chces: Treponema palli C.5chcession: B71325  RF.Fraser, C.M.; Mouris, S., Tron, J.; Khalak, H.; Rich they, L.; Weidman, J.; Smil Science 281, 375-388, 1998 A.7tile: Complete genome s A.8cession: B71325 A.8cession: B7	2
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 B71325 Conserved hypo C;Species: Tre C;Species: 24-Jul C;Accession: B R;Fraser, C.M. R;Fraser, C.M. A;Title: Compla A;Title: Compla A;Title: Compla A;Reference nu	RESULT

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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: A60147
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraqa, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002022; GB:AE000513; NID:g6459590; PIDN:AAF11370.1; PID:g645
A;Experimental source: strain R1
                                                                                                                               A; Molecule type: DNA A; Residues: 1-1095 <5TO> A; Residues: 1-1095 <5TO> A; Cross-references: GB:AE004569; GB:AE004091; NID:g9947339; PIDN:AAG04789.1; GSPDB:GN A; Experimental source: strain PAOl C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable UV damage endonuclease - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Date: 075350
C;Dat
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-296 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC90042.1; PID:915979263; GSPDB:GN00175
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YPO1203 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 2; Length 1095; Pred. No. 46; 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%; Score 53; DB 2; Length 296; 50.0%; Pred. No. 16; Live 1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 IAGVLLFSFLAIR----GHALPTLROWAAASA 76
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No.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.6%;
Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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A;Molecule type: DNA
A;Residues: 1-326 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: AG0147
                                                                                   A; Accession: B83471
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                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Streptomyces Sp.
C; Date: 17-un-1998 #sequence_revision 10-Jul-1998 #text_change 24-Oct-2000
C; Date: 17-un-1998 #sequence_revision 10-Jul-1998 #text_change 24-Oct-2000
C; Accession: JW0076
R; Hirada, K.; Eto, T.; Yoshioka, I.; Oda, K.
Biosci. Biotechnol. Biochem. 62, 347-353, 1998
Biosci. Biotechnol. Biochem 62, 347-353, 1998
A; Title: Molecular cloning and expression of a gene encoding a novel sorbitol oxidase francescent on unber: JW0076
A; Reference number: JW0076
A; Reference number: JW0076
A; Residues: 1-420 cHIRA
A; Residues: 1-420 cHIRA
A; Residues: 1-420 cHIRA
A; Residues: 1-420 cHIRA
C; Comment: This protein oxidizes D-sorbitol to produce hydrogen peroxide and glucose with C; Superfamily: L-gulonolactone oxidase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: D85818
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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                       2; Mismatches
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41.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 GPVGQVWLKQRVGDEGARSVMPAEWLGAR 243
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                                                                                                                                                   10 LAARAGPNGIEGPTLRQWLAAR 31
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                               Conservative
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Best Local Similarity
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A; Residues: 1-346 <STO>
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 18-Aug-2000
C;Accession: T3554
S;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, April 1999
A;Reference number: 221573
A;Reference number: 221573
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocessides: 1-36 < CLI>
A;References: EMBL: AL049587; PIDN: CAB40679.1; GSPDB: GN00070; SCOEDB: SC5F2A.12c
A;Experimental source: strain A3(2)
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A;Reference number: A82950; MUID:20437337
A;Accession: F83487
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C;Superfamily: Streptomyces coelicolor conserved hypothetical protein SC5F2A.12c
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R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, .: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 25-Apr-1997
C;Accession: $6538 Farstmoto, R.; Fujiwara, Y.
Eur. J. Blochem. 230, 337-343, 1995
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                                                                                                                                                                                            conserved hypothetical protein SC5F2A.12c - Streptomyces coelicolor
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29;
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1; Mismatches
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Pred. No.
                                           374 GPDLRSALAGRVGPIGF----PFSAARA 397
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             1 IEGPTLRQWLAARAGPNGIEGPTLRQWLA 29
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46.7%;
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34.48;
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Best Local Similarity 46.,°,
Best Local 14; Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-440 <MAT>
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A;Molecule type: DNA
A;Residues: 1-371 <STO>
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C.Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
C.Superfamil: This protein is a membrane bound protein and involved in cell/cell and c.Superfamil: howology
C.Keywords: hydrolase; metalloproteinase; zinc
C.Keywords: hydrolase; metalloproteinase; zinc
E.3420-503/Domain: disintegrin homology <DIS>
E.348,352,388/Binding site: zinc (His) #status predicted
F:349/Active site: Glu #status predicted
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A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM
                                                                                                                                                                                                                                                                                                            C, Accession: A33443
R; Masters, P.S.; Bella, R.S.; Butcher, M.; Patel, B.; Ghosh, H.P.; Banerjee, A.K. Viology 171, 285-290, 1989
A; Title: Structure and expression of the glycoprotein gene of Chandipura virus. A; Reference number: A32443; MUID: 89299473
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                                                                                                                                                                                                                                     spike glycoprotein G precursor - Chandipura virus
C;Species: Chandipura virus
C;Date: 30-Sep_1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Speciës: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: G. Superfamily: rhabdovirus spike glycoprotein G. Superfamily: rhabdovirus spike glycoprotein; transmembrane protein; C;Superfamily: signal sequence #status predicted <SiG> F:1-27/Domain: signal sequence #status predicted <SiG> F:28-524/Product: spike glycoprotein G #status predicted <SiG> F:472-491/Domain: transmembrane #status predicted <TMN> F:184,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:J04350; NID:g323376; PIDN:AAA42916.1; PID:g323377 C;Genetics:
          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
        9
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                                                                                    A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                         ----PNGIEGPTLRQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Herren, B.; Raines, E.W.; Ross, R. submitted to the EMBL Data Library, January 1996 A;Reference number: H01157 A;Accession: G02390
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-461 <MCK>
A; Experimental source: articular chondrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: PC4263; MUID:97168971
A; Accession: PC4263
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1359 IDGPVLKEPKGKRESPSGISSDIWTQW 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGPNGIEGPTLRQW 27
        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%;
37.0%;
                                                   2 EGPTLRQW-LAARAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: G02390; PC4263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-524 <MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-814 <HER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A32443
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
  Matches
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C; Genetics:

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Ciral-binding protein sp105 - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
R;Jentsch, T.J.; Garcia, A.M.; Lodish, H.F.
Biochem. J. 261, 155-166, 1989
A;Title: Primary structure of a novel 4-acetamido-4'-isothiocyanostilbene-2,2'-disulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: C83221
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Actover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecoule type: DNA
Residues: 1-600 <SYO>
A;Cross_references: GB:AE004761; GB:AE004091; NID:99949533; PIDN:AAG06794.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome seguence of Pseudomonas aeruginosa PAO1, an opportunistic pa A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: hasD; PA3406
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 12/2
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transport protein HasD PA3406 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                             C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; Length 600;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-589 <JOH>
A;Cross-references: EMBL:U41557; PIDN:AAA83307.1; CESP:C50F7.2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 2; Length 589;
Pred. No. 60;
3; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                              C,Accession: T29299
(C,Accession: T29299
(R,Johnson, D.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C50F7.
A;Reference number: Z20601
                                                                                                                                                                               hypothetical protein C50F7.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EGPTLROWLAARAGPNGIEGP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%;
ilarity 52.9%;
Conservative
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   Query Match
Best Local Similarity
9, Conserva
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:C50F7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T29299
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                                                                                                                                  RESULT 15
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                                   qq
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C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
R; Kawarsbayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kamazaki, Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:Ap000060; NID:g5104188; PIDN:BAA79847.1; PID:d1043633; PID:g510
A;Experimental source: strain Kl
A;Genetics:
A;Gene: APE0867
C;Superfamily: Aeropyrum pernix hypothetical protein APE0867
A;Cross-references: GB:AE004556; GB:AE004091; NID:g9947194; PIDN:AAG04656.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A; Experimental source: strain H37Rv
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C;Superfamily: Escherichia coli UTP--glucose-1-phosphate uridylyltransferase
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                13;
                                                                                                                                                                  DB 2; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 34.4%; Pred. No. 28;
Matches 11; Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%; Score 51; DB 2; Length 306;
69.2%; Pred. No. 30;
Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein APE0867 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                               | :|| :||| :||| :||| | 145 PNAARWLLDQAGPRLRLYAEVSEVDGSRLRLADGRWLSAEA 186
                                                                                                                                                                                                                                                                                              4 PTLRQWLAARAGP----NGIEGPTLR----QWLAARA 32
                                                                                                                                                               30.1%; Score 51.5; D
31.0%; Pred. No. 32;
ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 TLRQWLAARAGPN----GIEGPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SLRQWMRS---PNRYDIPGVDSPEVGWWLESR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.89
Best Local Similarity 69.29
Matches 9; Conservative
                                                                                                                                                                  Query Match 30.1
Best Local Similarity 31.0
Matches 13; Conservative
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A; Title: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
A; Accession: AF3634
A; Accession: AF3634
A; Accession: AF3634
A; Molecule type: DNA
A; Residues: 1-150 < KUR>
A; Cross references: GB: AE008918; PIDN: AAL54241.1; PID:g17985213; GSPDB:GN00191
A; Experimental source: strain 16M
A; Experimental source: strain 16M
A; Map position: II
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A;Experimental source: strain R1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-410 <BURN
Cross-references: EMBL:X13004
R;Madhusudhan, K.T.; Huang, G.; Burns, G.; Sokatch, J.R.
J. Bacteriol. 172, 5655-5663, 1990
A;Title: Transcriptional analysis of the promoter region of the Pseudomonas putida br
A;Reference number: A36133; MUID:91008935
A;Accession: B36133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Decies: Deinococcus radiodurans
C;Decies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: C75479
K;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
K;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S;Smith, H.O.; Venter, J.C.; Fraser, C.M.
S;Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Reference number: A75250; MUID:20036896
A;Accession: C75479
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 20;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 TLKAWMAAQ -- PSGIEG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.8
Matches 10; Conservative
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein SMa0937 [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizoblum meliloti
C;Species: Sinorhizoblum meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B95225
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe A; Rarnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Cross-references: GBs. AE006469; PIDN: AAK65164.1; PID: 914523607; GSPDB: GN00165
A.Experimental source: strain 1021, megaplasmid psymA
R.Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A.Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidher, S.; Wells, D.H.; Wong, R.; Yeh, K.A; Fitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A.Reference number: A96039; MUID: 21368234; PMID: 11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitric-oxide reductase cytochrome c chain (EC 1.7.99.7) [imported] - Brucella melitensis C; Species: Brucella melitensis C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                    A.Molecule type: protein
A.Residues: 2-11.435-449, X',451-452, X',454-459;634-649 <JEN2>
C.Superfamily: SITS-149, X',451-452, X',454-459;634-649 <JEN2>
C.Superfamily: SITS-140ding protein sp105
C.Superfamily: SITS-binding protein #status experimental <MAT>
F;2-697/Product: SITS-binding protein #status predicted <TMI>
F;30-507/Domain: transmembrane #status predicted <TMI>F;503-521/Domain: transmembrane #status predicted <TM2>
F;542-562/Domain: transmembrane #status predicted <TM3>
F;542-562/Domain: transmembrane #status predicted <TM3>
F;25.112,134,162,386,405,405,406,58/Binding site: carbohydrate (Asn) (covalent) #status predicted <TM3>
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                                                                                A;Molecule type: mRNA
A;Residues: 1-697 <JEN1>
A;Cross-references: EMBL:X16078; NID:g64403; PIDN:CAA34209.1; PID:g64404
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Pred. No.
        A; Reference number: S04987; MUID: 89374082
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36.4%;
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Matches 12; Conservative
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Hes 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-719 <KUR>
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                                              A; Accession: S04987
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R; Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.
R; Hester, X.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.
R; Hester, X.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.
R; Hester, X.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.
R; Title: Purification of active El-alpha(2)-beta(2) of Pseudomonas putida branched-chain
A; Reference number: S63475; MUID: 96085147
A; Accession: S63475
A; Reference number: S63475
A; Recession: S63475
A; Rocession: S63475
A;
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A; Status: preliminary
A; Molecule type: DA
A; Residues: 1-410 <STO>
A; Cross-references: GB: AE004650; GB: AE004091; NID: 99948267; PIDN: AAG05635.1; GSPDB: GN001
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C;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bid
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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Pred. No. 55;
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R)Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, September 1997
A; Reference number: 221733
A; Accession: T38324
A; Accession; Type: DNA
A; Company and Company and Company
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55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: strain PAO1 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.3.
Best Aconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.3 ses 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 GPSLIEWVTYRAGPH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 GPSLIEWVTYRAGPH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTLRQWLAARAGPN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GPTLRQWLAARAGPN 17
                                                   A; Molecule type: DNA
A; Residues: 1-17 <MAD>
preliminary
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photosystem II chlorophyll a-binding protein psbC - Synechocystis sp. (strain PCC 680 N;Alternate names: chlorophyll-binding protein, 43K; photosynthetic reaction center 4 C;Species: Synechocystis sp. A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-7 <CAR>
A; Note: the authors definitely establish that the Met-1 GTG is the initiation codon a
R; D2e1zkalns, V.A.: Bogorad, L.
EMBO J. 7, 333-338, 1988
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A; Residues: 'MKTLSSLRRFSPV', 2-54,'N',56-149,'I',151-288 <D2E>
A; Cross-references: EMBL:X07018; NID:948064; PIDN:CAA30071.1; PID:948066
A; Oross-references: EMBL:X07018; NID:948064; PIDN:CAA30071.1; PID:948066
A; Note: the authors translated the codon CAT for residue 131 as Phe; this sequence us
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 'MKTLSSLERERSPV', 2-41,'A', 43-460 <KAN>
A; Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BAA17799.1; PID:g165
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A; Note: this sequence uses an incorrect initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 07-Jun-1990 #sequence_revision 19-Jan-1996 #text_change 20-Jun-2000 C;Accession: S06469; S07497; S02380; S74838 R;Chisholm, D.; Williams, J.G.K. Plant Mol. Biol. 10, 293-301, 1988 A;Title: Nucleotide sequence of psbC, the gene encoding the CP-43 chlorophyll a-bindi A;Reference number: S06469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: photosystem II chlorophyll a-binding protein psbC
C;Reywords: chlorophyll; membrane-associated complex; photosynthesis; photosystem II;
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A;Cross-references: EMBL:298977; PIDN:CAB11659.1; GSPDB:GN00066; SPDB:SPAC23H4.04
A;Experimental source: strain 972h-; cosmid c23H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosiduas: 'MRTLSSLRREPV',2-460 < CHI>
A;Cross-references: GB:M21538; NID:340699; PIDN:AAA85378.1; PID:91161272
A;Note: this sequence uses an incorrect initiation codon
B;Carpenter, S.D.; Charite, J.; Eggers, B.; Vermaas, W.F.J.
A;Rolectr. 260, 135-137, 1990
A;Title: The psbC start codon in Synechocystis sp. PCC 6803.
A;Reference number: S07496; MUID:90127396
A;Accession: S07497
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                                                                                                                                                                                                                                                                                                              DB 2; Length 415;
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62;
                                                                                                                                                                                                                                                                                                      Score 50; DB;
Pred. No. 56;
4; Mismatches
                                                                                                                                                                                             A;Introns: 34/1; 54/3
C;Superfamily: probable membrane protein YDL033c
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGPNGIEGPTLRQW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 VEGVEMRNWLDEDSAPSGC - - PAERDW 82
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35.0%;
                                                                                                                                                                                                                                                                                                      29.2%;
ilarity 37.0%;
Conservative
                                                                                 C; Genetics:
A; Gene: SPDB:SPAC23H4.04
                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 10; Conserv
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                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                  Query Match
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A; Cross-references: EMBL:222705; NID:9297851; PIDN:CAA80406.1; PID:9581832
R; Meijer, W.G.; Arnberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuiz
Mol. Gen. Genet. 225, 320-330, 1991
A;Title: Identification and organization of carbon dioxide fixation genes in Xanthoba
A; Reference number: S13573; MUID:91172133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monooxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Decies: IJ-Jan-2002
S;Accession: Al3083
R;Wood, D.W.: Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
science 294, 2317-2333, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H98202
hypothetical protein AGR_L_1143 [imported] - Agrobacterium tumefaciens (strain C58, C
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: H98202
                                                                                                                              is required for expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193
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A;Cross-references: GB:AE008689: PIDN:AAL45087.1; PID:917742754; GSPDB:GN00187
        C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 24-Sep-1999 C;Accession: A36525; S13.78; S35408
E;Naccession: A36525; S13.78; S35408
J. Bacteriol. 175, 6097-6104, 1993
A;Title: CDBR, a LysR type transcriptional activator, is required for expres A;Reference number: A36925; MUID:94012468
A;Reference number: A36925; MUID:94012468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.5; DB 2;
Pred. No. 52;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :|:|| 111:| 11:| 212 QGQQSPEWIAANMEGREVYPNGLERLAAQARDWTAAR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EGPTLRQWLAAR----AGPNGIE--GPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: transcription activator LysR-type C;Keywords: DNA binding; transcription regulation
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Best Local Similarity 35.1%; Pred. No. 53;
Matches 13; Conservative 4; Mismatches
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66.7%;
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Matches 10; Conservative
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264 VEGLPVVRQWLAVRA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEG-PTLROWLAARA 14
                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-150 <MEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable polA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: C70559
C;Accession: C70559
R;Obe, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID: 98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: DNA
A;Residues: 1-904 <COL>
A;Cross-references: GB:Z95554; GB:AL123456; NID:g3261771; PIDN:CAB08882.1; PID:g2113913
A;Cross-references: strain H37Rv
C;Genetics:
A;Gene: polA
C;Superfamily: DNA-directed DNA polymerase I
              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281054; PIDN:CAB02881.1; GSPDB:GN00022; CESP:F01D4.4
A;Experimental source: clone F01D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                       hypothetical protein F01D4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20454
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
        10;
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           Indels
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        13;
                                                                                              29.2%; Score 50; DB 2; Let 42.4%; Pred. No. 1.2e+02; Wiematches 8;
                                                             3 GPTLR-----OWLAARAGPNGIEGPTLRQ----WLAARA 32
                                                                                                                                                                                                                                                                                                                                                                 Riwild, A. submitted to the EMBL Data Library, October 1996 A: Reference number: 219278 A: Reference number: 219278 A: Accession: T20454 A: Status: preliminary: translated from GB/EMBL/DDBJ A: Molecule type: DNA A: Residues: 1-472 <WILL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LAARAGPNGIEG-----PTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 59/3; 127/3; 334/3; 455/3
C;Superfamily: human carboxypeptidase H
     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 PAQRQWLTGRSNINGVD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PTLRQWLAARAGPNGIE 20
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: F01D4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C70559
14;
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  Matches
                                                                                                                                                                                                  RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
A;Accession: H98202
A;Accession: H98202
A;Accession: H98202
A;Residues: preliminary
A;Wolecule type: DNA
A;Residues: 1-355 <KUR>
A;Cross: Treferences: GB:AE007870; PIDN:AAK89146.1; PID:g15158956; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_1143
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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R; Harris, B.
submitted to the EMBL Data Library, May 1996
A; Reference number: 219633
A; Accession: T22896
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-214 <WILL>
A; Cross references: EMBL:273427; PIDN:CAA97801.1; GSPDB:GN00022; CESP:F58B3.3
A; Experimental source: clone F58B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Introns: 68/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F58B3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.9%; Score 49.5; DB 2; Length 355; Best Local Similarity 35.1%; Pred. No. 55; Matches 13; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.7%; Score 49; DB 2; Length 214; Best Local Similarity 50.0%; Pred. No. 38; Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EGPTLRQWLAAR----AGPNGIE--GPTLRQWLAAR 31
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|| 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 191 || 
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A;Gene: CESP:F58B3.3
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Search completed: October 9, 2002, 09:05:00 Job time : 10.1944 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:51:41; Search time 3.82201 Seconds (without alignments) 324.181 Million cell updates/sec Run on:

Title: Perfect score:

US-09-422-838C-22 171 1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	noines omod 013810	0 chand		torpe	_		_									mns	P11683 bacteriopha	P03699 bacteriopha					<u>.</u>		_	P41643 pinus thunb	O15067 homo sapien	mus m	bser		٠.	homo sa	mycob
SUMMAKIES	ID	SCO2 HITMAN	VGLG_CHAV	AD15_HUMAN	SP15_TORCA	DEFM_HUMAN	TONB_PASHA	ODBA_PSEPU	TRMU_SCHPO	PSBC_SYNY3	DPO1_MYCTU	CBBR_XANFL	ODPA_BACST	DIAC_HUMAN	CNG1_CHICK	CA1B_BOVIN	UROC_MOUSE	VXIS_BP434	VXIS_LAMBD	YL76_VIBCH	XERC_MYCLE	ODPA_BACSU	CA21_HUMAN	SYK_AERPE	FRT2_HUMAN	PYRD_MYCTU	PSBC_PINTH	PUR4_HUMAN	CA21_MOUSE	IE18_PRVKA	IE18_PRVIF	PTPO_RAT	CA1B_HUMAN	XERC_MYCTU
	DB	: -	7	7	П	~	-	-	٦	Н	7	Н		Н	Н	П	_		_												~	-	Н	П
	Length	266	524	814	969	243	246	410	415	472	904	333	368	385	735	911	122	72	72	270	297	370	1366	562	113	357	473	1338	1372	1446	1461	1711	1806	298
æ	$^{ry}_{ch}$	31.3	31.0	30.7	29.8	29.5	29.5	29.5	29.5	29.5	29.5	28.9	28.7	28.7	28.7	28.7	28.4	28.1	28.1	28.1	28.1	28.1	28.1	27.8	27.5	27.5	27.5	27.5	27.5	27.5	27.5	27.5	27.5	26.9
	Score	53.5	53	52.5	51	20	20	20	20	20		49.5	9	49	49	49	48.5	48	84.	8 4	84.	48	- 1	5.7	4.7	47	47	47	47	47	47	47	47	46
	Result No.		7	m	♥ (	2	9	7	∞ (	5,	01.	11	12	13	14	15	16	17	81.	19	20	$\frac{21}{21}$	22	23	74	25	2 <sub>0</sub>	/7	58	29	30	31	32	93

O06399 mycobacteri	P02460 gallus gall	P49471 odontella s	P54234 clarkia arc	P54236 clarkia fra	P54239 clarkia wil	P54240 clarkia xan	P54243 oenothera m	P54235 clarkia con	P34796 clarkia lew	P54238 clarkia ros	P23608 a poly-beta
FABH_MYCTU	CA12_CHICK	PSBB_ODOSI	G6P1_CLAAR	G6P1_CLAFR	G6P1_CLAWI	G6P1_CLAXA	G6PI_OENME	G6P1_CLACO	G6P1_CLALE	G6P1_CLARO	PHBC_ALCEU
	-	<del>, ,</del>	-	Н	٦	<del>, -</del>	٦	<del></del>	Н	П	٦
335	369	509	268	268	268	268	268	569	569	570	589
26.9	76.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	56.9
46	40	46	46	46	46	46	46	46	46	46	46
34	ري د د	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

		Last sequence update) Last annotation update) mitochondrial precursor.	Craniata; Vertebrata; Euteleostomi;	Catarrhini; Hominidae; Homo.		I./GenBank/DDR.I databases	S FIC LXS-140 AND PHE-225.	52; vidson M.M., Tanji K., Nishino I.,	Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Van Coster R., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S.,	and	ly gene.";	ROLE IN EITHER MITOCHONDRIAL COPPER	OPPER INTO THE ACTIVE SITE OF COX. hondrial (By similarity).	FOUS. E THE CAUSE OF FATAL INFANTILE	CARDIOENCEPHALOMYOPATHY WITH COX DEFICIENCY. THIS DISEASE IS CHARACTERIZED BY HYPERTROPHIC CARDIOMYOPATHY. LACTIC ACTORS: AND			SCOI/Z FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformation and the Burn contestion	citute. There are no restrictions on its	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial	eement (See http://www.isb-sib.ch/announce/	SID.CII).				Transit peptide; Disease mutation; Polymorphism.
SULT 1 02_HUMAN STANDARD: SCO2_HUMAN STANDARD:	043819; Q9UK87; 30-MAY-2000 (Rel. 39, 30-MAY-2000 (Pol. 39,	16-OCT-2001 (Rel. 40, SCO2 protein homolog, SCO3	Homo sapiens (Human) Eukaryota; Metazoa; Chordata;	<pre>Mammaila; Eutheria; Primates; // NCBI_TaxID=9606;</pre>	– oo ⊨						mutations in SCO2, a COX assembly gene."; Nat. Genet. 23:333-337/1999.						_							EMBL; AF17738 EMBL; AL02168 MIM: 604373:	MIM;	InterPro; IPR	Mitochondrion;
SC ID	AC	DE	800	288	A A A	RA	RN	K A	RA RA	RA	RL	88	38	35	88	88	55	3 8	000	88	38	ပ္ပ ပ္ပ	38	DR DR	2 2 2	DR	KW

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                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VITOLOGY 171:285-290(1989).

-i-FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.

-i-FUNCTION: THIS PROTEIN FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL. THE INTERACTION BETWEEN THE INTERACTORNEWTS OF THE VIRION AND THE PORTION OF THE GIXCOPROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBUNIT: TRIMERS IN THE ENDOPLASMIC RETICULUM.
-i- PTM: THIS PROTEIN IS MODIFIED BY THE COVALENT ADDITION OF PALMITIC ACID VIA A THIOETHER LINKAGE TO A CYSTEINE. IT COULD BE EITHER ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A34443; VGVNCV.
Interpro; IPR001903; Rhabd_glycop.
Pfam; PP00974; Rhabd_glycop; 2.
Transmembrane; Envelope protein; Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and expression of the glycoprotein gene of Chandipura virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P., Banerjee A.K.;
                                                                                                                                                            31.3%; Score 53.5; DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandipura virus (strain 1653514).
Viruses; ssRNA negative strand viruses; Mononegavirales;
Rhabdoviridae; Vesiculovirus.
NCBL_TaxID=11273;
                                                                                                                                                                                                                          6 LROWLAARAGP-----QMLAARA 32
                                                                                                                                                                                                                                                       33 LRSWLLSROGPAETGGGGGPQGPGLRTRLLITGLFGAGLGGAWLALRA 80
                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
MITOCHONDRION (POTENTIAL).
SCOZ PROTEIN HOMOLOG.
R -> P (IN DBSNP:140523).
/FTIG-VAR_011738.
E -> K (IN FIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION 479 OR 484.
SIMILARITY: 39% IDENTITY TO THE G PROTEINS OF VSV.
                                                                                                                             BC2F40E057329BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPIKE GLYCOPROTEIN.
                                                                            /FTId=VAR_008874.
S -> F (IN FIC).
/FTId=VAR_008875.
                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                             4.8;
                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                    Spike glycoprotein precursor.
                                                                                                                              29810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J04350; AAA42916.1; -
                                                                                                                                                                               33.3%;
                                                                                                                                                                             Best Local Similarity 33.33
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
472
472
496
524
184
                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A32443; VGVNCV
                                                                                                                              266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRUS BUDDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
22
22
473
497
184
                                                             140
                                                                                               225
                                                                                                                                                                                                                                                                                                                                        VGLG_CHAV
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                SEQUENCE
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
   TRANSIT
                                   VARIANT
                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                    CHAIN
                                                                                                                                                                                                                                                                                                         RESULT 2
VGLG_CHAV
                                                                                                                                                                                                                                                                                                                                                       FT FT FT SO
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INTERACTION WITH INTEGRIN ALPHAV-BETA3.

**MEDLINE=98184837; PubbMed=9516430; Achang X.P., Kanata T., Vokoyama K., Puzon-McLaughlin W., Takada Y.; Achang X.P., Kanata T., Vokoyama K., Puzon-McLaughlin W., Takada Y.; Tahang X.P., Kanata T., Vokoyama K., Puzon-McLaughlin W., Takada Y.; Tahang X.P., Kanata T., Vokoyama K., Puzon-McLaughlin W., Takada Y.; Tahang X.P., Tahang Y.P., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                013444; 013493; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 01-MRT-2002 (Rel. 41, Last annotation update) 40-MRT-2002 (Rel. 41, Last annotation update) 40-MRT-2002 (Rel. 41, A. 24, -24, -24) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteinerich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Breast carcinoma;
MEDLINE-96214870; PubMed-8617717;
Kraetzschmar J., Lum L., Blobel C.P.;
"Metargidin, a membrane-anchored metalloprotease-disintegrin protein with an RGD integrin binding sequence.";
J. Biol. Chem. 271:4593-4596(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Umbilical vein;
MEDLINE-97192141; Pubmed-9039960;
MEDLINE-97192141; Pubmed-9039960;
MERTER B., Raines E.W., Ross R.,
"Expression of a disintegrin-like protein in cultured human vascular
                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
344 N-LINKED (GLCNAC. ..) (POTENTIAL).
179 PALMITATE (POTENTIAL).
184 PALMITATE (POTENTIAL).
58826 MW; A84APOASFFPB73CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SORTING NEXIN 9 (BY SIMILARITY).
--- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHAV-BETA3.
--- PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
                                                                                                                                   DB 1; Length 524;
                                                                                                                                                         Pred. No. 11;
4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i-SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i-SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  814 AA.
                                                                                                                                     Score 53;
                                                                                                                                                                                                                                                                                               359 IDGPVLKEPKGKRESPSGISSDIWTQW 385
                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGPNGIEGPTLRQW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                     31.0%;
37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells and in vivo.";
FASEB J. 11:173-180(1997).
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
     344
479
484
                                                                                524 AA;
                                                                                                                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAM15 OR MDC15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Metargidin)
                                                                                                                                                                                             10:
                                                                                                                                                                                                                                                                                                                                                                                                                                       AD15_HUMAN
        CARBOHYD
                                                                                      SEQUENCE
                                                                                                                                        Query Match
                                 LIPID
                                                                                                                                                                                                                                                                                                                                                                                                           AD15_HUMAN
                                                             LIPID
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
        FT
FT
SO
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728 LKGPTC-QYRAAQSGPSERPGPPQRALLA 755

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                                                                                                                                                                                                                                                                                               P Fram; PF01421; Reprolysin; 1.

R Probom; PD000664; Disintegrin; 1.

R PART; SM00180; DISIN, 1.

R PROSITE; PS00215; ADAM_MEPRO; 1.

R PROSITE; PS00127; DISINTEGRIN_1; FALSE_NEG.

R PROSITE; PS00124; DISINTEGRIN_2; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS00146; CINC_PROTEASE; 1.

R PROSITE; PS00146; CYSTELNE, SWITCH; FALSE_NEG.

R PROSITE; PS00146; CYSTELNE_SWITCH; FALSE_NEG.

R PROSITE; PS00146; CYSTELNE_SWITCH; FALSE_NEG.

H Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;

Transmembrane; EGF-like domain; SH3-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
POTEWITAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.7%; Score 52.5; DB 1; Length 814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD2EC26CB1314576 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3-BINDING (POTENTIAL). SH3-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> S (IN REF. 2)
-> P (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISINTEGRIN-LIKE.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYSTEINE SWITCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
ADAM 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                 InterPro; IPR001818; Matrixin.
InterPro; IPR002870; Pep_M12B_propep.
                                                                                                                                                                                                                                              InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00200; disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
                                                                                                                                                                                      InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87686 MW;
                                                                                                                       EMBL; U41767; AAC51112.1; -.
                                                                                                                                                                                                       InterPro; IPR000561;
                                                                                                                                                HSSP; P18619; 1FVL.
MEROPS; M12.215; -.
MIM; 605548; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714
791
814 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323
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DISULFID
DISULFID
DISULFID
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TRANSMEM
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METAL
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE CHLORIDE CHANNEL.
-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-!- TISSUE SPECIFICITY: ELECTROPLAX TISSUE, BRAIN (200-FOLD LESS), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEART (500-FOLD LESS).
-1- MISCELLANEOUS: BINDS 4-ACETAMIDO-4'-ISOTHIOCYANOSTILBENE-2,2'-DIS ULPHONIC ACID (SITS), AN INHIBITOR OF A VARIETY OF ANION TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SITS)-binding membrane protein highly expressed in Torpedo californica electroplax.";
Biochem. J. 261:155-166(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2011 (Rel. 40, Last annotation update)
17-CT-2011 (Rel. 40, Last annotation update)
18-CT-2011 (Rel. 40, Last annotati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89374082: PubMed=2775201;
Methsch T.J., Garcia A.M., Lodish H.F.;
"Primary structure of a novel
"Primary structure of a novel
4-acetamido-4'-isothiocyanostilbene-2,2'-disulphonic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 1; Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50C4BE98AFAFBEB4 CRC64;
                                                                                                                                                                                                                                                                Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X16078; CAA34209.1; -.
PIR; S04987, S04987.
InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567 N-
78325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein.
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                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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28
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                                                                                                                                                                                                                                                                                         NCBI_TaxID=7787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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SP15_TORCA
ID SP15_TORCA
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DOMAIN
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CARBOHYD
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                                                      ΩĬ
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Gaps

1;

Indels

6

Pred. No. 20; 6; Mismatches

44.88;

13; Conservative

Best Local Similarity

Matches

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1 IEGPTLRQWLAARAGPNGIEGPTLRQWLA 29

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Wed Oct

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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                            Mannheimia
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                                                                                                                                                                                                                                                                                                                                                                                              pfan; PF01327; Pep_deformylase; 1.
ProDom; PD003844; Pep_deformylase; 1.
Protein blosynthesis; Hydrolase; Iron; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                              01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Peptide deformylase, mitochondrial precursor (EC 3.5.1.88) (PDF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                 Giglione C., Serero A., Pierre M., Boisson B., Meinnel T.; "Identification of eukaryotic peptide deformylases reveals universality of N-terminal protein processing mechanisms."; EMBO J. 19:5916-5929(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 1; Length 243; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (POTENTIAL). PEPTIDE DEFORMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON (BY SIMILARITY)
B15A3456F0F8D689 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000181; Pep_deformylase.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-20514156; Pubmed-11060042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF239156; AAG33968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27013 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                            (Polypeptide deformylase). PDF1A OR PDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AARAGPNGIEGPTLRQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 SSTAAPDGVEGPALRR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella haemolytica.
                                                                                                                                                   Homo sapiens (Human).
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214
215
215
218
243 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=9606;
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8
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METAL
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              09HBH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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                                                                                    Graham M.R., Lo R.Y.C.;

Graham M.R., Lo R.Y.C.;

Graham M.R., Lo R.Y.C.;

Graham M.R., Lo R.Y.C.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

L. Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

CARRY OUT HIGH-APPINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE BENERGY PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELAKING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELAKING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELAKING PROTEINS OF LIGANDS BOUND BY THESE OUTER MEMBRANE PROTEINS (BY SIMILARITY).

C.: SUBCELLULAR LOCATION: ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE PRIPLASM (BY SIMILARITY).

C.: SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burns G., Brown T., Hatter K., Idriss J., Sokatch J.R.; "Similarity of the El subunits of branched-chain-oxoacid dehydrogenase from Pseudomonas putida to the corresponding subunits of mammalian branched-chain-oxoacid and pyruvate dehydrogenases."; Eur. J. Blochem. 176:311-317(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4) (Branched-chain alpha-keto acid dehydrogenase component alpha chain (El))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM 8 28 SIGNAL-ANCHOR (POTENTIAL).

DOMAIN 29 246 PERIPLASMIC (POTENTIAL).

SEQUENCE 246 AA; 27785 MW; C9582F619FCBA5B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=91008935; PubMed=2211503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U62565; AAB09530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 GPEIKQGIVAKAIPNAAEG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
'Local 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas putida.
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                                                                SEQUENCE FROM N.A.
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NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                            Architecture of 2-oxo acid dehydrogenase multienzyme complexes.";
Nat. Struct. Biol. 6:785-792(1999).

-!- FUNCTION: THE BRANCHED-CHAIN ALPHA-KETO DEHYDROGENASE COMPLEX
CATALYZES THE OVERALL CONVERSION OF ALPHA-KETO ACIDS TO ACYL-COA
AND CO(2). IT CONTAINS MULTIPLE COPIES OF 3 ENZYMATIC COMPONENTS:
BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE (E1), LIPOAMIDE
ACYLTRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E3).

-!- CATALYTIC ACTIVITY: 3-methyl-2-oxobutanoate + lipoamide = S-(2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown D., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC_2.1.1.61).
Madhusudhan K.T., Huang G., Burns G., Sokatch J.R.; Transcriptional analysis of the promoter region of the Pseudomonas putida branched-chain keto acid dehydrogenase operon."; J. Bacteriol. 172:5655-5663(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00676; El_dehydrog; 1.
Oxidoreductase; Flavoprotein; Thiamine pyrophosphate; 3D-structure.
SEQUENCE 410 AA; 45268 MW; 0C998460CCFB9CF4 CRC64;
                                                                                                                                          Aevarsson A., Seger K., Turley S., Sokatch J.R., Hol W.G.J., "Crystal structure of 2-oxoisovalerate and dehydrogenase and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                  methylpropanoyl)dihydrolipoamide + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=99356017; Pubmed=10426958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No
                                                                                                                                                                                                                                                                                                                                                                          THIAMINE PYROPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M57613; AAA65614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001017; El_dh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.2
Best Local Similarity 53.3
Matches , 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:||:||:||||:
| 198 GPSLIEWVTYRAGPH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GPTLRQWLAARAGPN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1QS0; 18-AUG-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thiouridylate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                          COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S01317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EC 2.1.1.6
SPAC23H4.04
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013947;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chisholm D., Williams J.G.K.; "Nucleotide sequence of psbC, the gene encoding the CP-43 chlorophyll a-binding protein of photosystem II, in the cyanobacterium Synechowstis 6803 ":
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evolution and isolation of a complementing clone by a novel screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97061201; PubMed-8905231; Raneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Suquirra M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Vamada S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S.; Sapada M., Tabata S.; Sapada M., Tabata S.; Sapada M., Tabata S.; Seguence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSBC_SYNY3 STANDARD; PRT; 472 AA.
P09193; P73749;
01-MAR-11999 (Rel. 10, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kba reaction center protein (P6 protein) (CP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: THE 43 kDa PROTEIN (P6) IS A COMPONENT OF THE CORE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88211542; PubMed-3130247;
Dzelzkalns V.A., Bogorad L.;
"Molecular analysis of a mutant defective in photosynthetic oxygen
                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOTOSYSTEM II. IT IS A CHLORÒPHYLL BINDING PROTEIN.
                                                                                                                                                                                                                                              DB 1; Length 415; 21;
                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                        Interpro; IPR004135; tRNA_Me_trans.
Pfam; PF03054; tRNA_Me_trans; 1.
Transferase; Methyltransferase; tRNA processing.
SEQUENCE 415 AA; 47626 MW; D2B604335B7A935F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSBC OR SIL0851.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE PSBB / PSBC FAMILY.
                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      Score 50;
Pred. No. ;
                                                                                                                                                                                                                                                                                                                                                            :|| :| || : | :| | 58 VEGVFMRNWLDEDSAPSGC--PAERDW 82
                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGPNGIEGPTLRQW 27
                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 10:293-301(1988).
                                                                                                                         EMBL; Z98977; CAB11659.1; -.
                                                                                                                                                                                                                                                      29.28;
                                                                                                                                                                                                                                                                        37.0%;
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                                                                                                                                                                                                                                                                   Best Local Similarity 37.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 7:333-338(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THYLAKOID MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis 6803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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us-09-422-838c-22.rsp

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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Petersch J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H37RV;
MDDLINE-9829987; PubMed-9634230;
MDDLINE-9829987987; PubMed-9634230;
MDDLINE-9829987987; PubMed-9634230;
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Chilingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Shiston J.E., Taylor K., Whitehead S., Barrell B.G.;
Pocciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Mature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetais; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94124016; PubMed=8294019;
Mizrahi V., Huberts P., Dawes S.S., Dudding L.R.;
A PCR method for the sequence analysis of the gyrA, polA and rnhA
gene segments from mycobacteria.";
Gene 136:287-290(1993).
                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                        Score 50; DB 1; Length 472; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                       3; Mismatches 13; Indels
                                                                                                                    Photosynthesis; Photosystem II; Thylakoid; Chlorophyll;
                                                                                                                                                                                                                                                    R -> A (IN REF. 2).
T -> N (IN REF. 3).
Y -> I (IN REF. 3).
D94D9FE73F66192D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   352 GETMREWDFRGPWLEPLRGPNGLDLDKLRNDIQPWQVRRA 391
                                                                                                                                                                                                                                                                                                                                                                                       3 GPTLR-----QWLAARAGPNGIEGPTLRQ----WLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DOLA polymerase I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                POTENTIAL.
                                                                                                                                                                POTENTIAL
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                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                  51760 MW;
                                                                                                                                                                                                                                                                                                                              29.2%;
          EMBL; M21538; AAA85378.1; -. EMBL; D90909; BAA17799.1; -.
                                          CAA30071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                        PIR; S06469; S06469.
PIR; S02380; S02380.
InterPro; IPR000932; PSII.
Pfam; PF00421; PSII; 1.
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 35.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                            182
224
259
291
445
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67
162
472 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
                                                                                                                                     Transmembrane;
                                           X07018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPO1_MYCTU
007700;
                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                  SEQUENCE
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DPO1_MYCTU
                                           EMBL;
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                                                                                    -!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthobacter flavus.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.2%; Score 50; DB 1; Length 904;
                                                                                                                                                        -:- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-:- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                       laboratory strains."; Submitted (APR-2001) to the {\tt EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 904 AA; 98471 MW; 1C8E560FE5F74323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) RuBisCO operon transcriptional regulator. CBBR OR CFXO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002562; 3_5_exonuclease.
InterPro; IPR002421; 5_3_exonuclease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003584; HHH_2.
Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94012468; PubMed=8407781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002298; DNA_poll..
Interpro; IPR001098; DNA_pol_A.
Interpro; IPR00513; Exo_N_I.
Interpro; IPR003583; HHH_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007030; AAK45935.1; -. HSSP; P19821; 1BGX.
                                                                                                                                                                                                                                                                                                                                              EMBL; L11920; AAB46393.1; -. EMBL; Z95554; CAB08882.1; -.
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SMART; SW00474; 35EXOC; 1.
SMART; SW00475; 53EXOC; 1.
SMART; SW00278; HhH1; 1.
SWART; SW00279; HhH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00482; POLAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Puberculist; Rv1629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              est Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=281;
                                                                                                                                               + {DNA}(N).
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P25545;
                       Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASTALINEWA 1935;
MEDLINE-90345939;
PubMed=2200674;
Hawkins C.F., Borges A., Perham R.N.;
"Cloning and sequence analysis of the genes encoding the alpha and beta subunits of the El component of the pyruvate dehydrogenase multienzyme complex of Bacillus stearothermophilus.";
Eur. J. Biochem. 191:337-346(1990).
-!- FUNCTION: THE PRIVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL.-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (El).
DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE (E1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE CBB OPERON (CBBLSXFP) FOR ROBLISCO AND OTHER CALVIN CYCLE GENES. BINDS SPECIFICALLY TO TWO BINDING SITES IN THE CBBR-CBBL INTERGENIC REGION.
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                       Meijer W.G., Arnberg A.C., Enequist H.G., Terpstra P., Lidstrom M.E.,
                                                                                                                                                                                                                                                                                                                                                    Dijkhuizen L.; "Identification and organization of carbon dioxide fixation genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
van den Bergh E., Dijkhuizen L., Meijer W.G.;
"CbbR, a LysR-type transcriptional activator, is required for
expression of the autotrophic CO2 fixation enzymes of Xanthobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Pyruvate dehydrogenase El component, alpha subunit (EC 1.2.4.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator; DNA-binding.

22 41

H-T-H MOTIF (BY SIMILARITY).

SEQUENCE 333 AA; 36003 MW; 9B375B4FB2D1EE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49.5; D
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00126; HTH_1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthobacter flavus H4-14.";
Mol. Gen: Genet. 225:320-330(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X17252; -; NOT_ANNOTATED_CDS.
PIR; S13578; S13578.
InterPro; IPR000847; HTH_LYSR.
                                                                                                                                Bacteriol. 175:6097-6104(1993).
                                                                                                                                                                                                                                                                                MEDLINE=91172133; PubMed=1900916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.9%;
66.7%;
                                                                                                                                                                                                            SEQUENCE OF 1-150 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 222705; CAA80406.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| | :|||| | 1|
264 VEGLPVVRQWLAVRA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEG-PTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NCA 1503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODPA_BACST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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ODPA_BACST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
       RAT RELEASED BY BEING SECOND S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.

Liu B., Aronson N.N. Jr.;

Structure of the human gene for lysosomal di-N-acetylchitobiase.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: INVOLVED IN THE DECRADATION OF ASPRAGINE-LINKED

GIYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCOSAMINE

(1-4)N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END

OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.

-!- SUBCELLULAR LOCATION: Lysosomal.

-!- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fisher K.J., Aronson N.N. Jr., "Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase di-N-acetylchitcbiase."; J. Biol. Chem. 267:19607-19616(1992).
                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001017; E1_dh.
Pfam; PF00676; E1_dehydrog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%; Score 49; DB 1; Length 368; 50.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                              SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 AA; 41338 MW; 46199FEF69EE4662 CRC64;
-!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Di-N-acetylchitobiase precursor (EC 3.2.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 25;
3; Mismatches
                     acetyldihydrolipoamide + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 EGPTLIETLCFRYGPHTMSGDDPT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92406917; PubMed=1527079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EGPTLRQWLAARAGPNGIEG--PT 23
                                                                                                                                                                                                                                                                                                 EMBL; X53560; CAA37628.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                           PIR; S10798; DEBSPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                              HSSP; P09060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTBS OR CTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAC_HUMAN
Q01459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INIT_MET
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIAC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: VISUAL STONAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cyclic nucleotide gated channel, cone photoreceptor, alpha subunit (CNG channel 1) (CNG-1).
                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels.";
Neuron 10:865-877(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93264082: PubMed-7684234;
Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
Molday R.S., Kaupp U.B.;
                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                           0A9D14C8B26B52EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                         EMBL; M95767; AAA35684.1; -.
EMBL; AF085706; AAC35852.1; -.
EMBL; AF085701; AAC35852.1; JOINED.
EMBL; AF085701; AAC35852.1; JOINED.
EMBL; AF085702; AAC35852.1; JOINED.
EMBL; AF085703; AAC3582.1; JOINED.
EMBL; AF085704; AAC3582.1; JOINED.
EMBL; AF085705; AAC35822.1; JOINED.
                                                                                                                                                                                                                                                                                                                                             43759 MW;
                                                                                                                                                                                                                                                                                                                                                                          28.7%;
37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
                                                                                                                                                PIR; A44102, A44102.
PIR; S27959; S27959.
MIM; 600873; -.
                                                                                                                                                                                                                                                                                               228
262
299
299
385 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOTORECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNG1_CHICK
Q90805;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNG1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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A REDILINE-92078200; Pubmed=1744123;

Brown K.E., Lawrence R., Sonenshein G.E.;

Brown K.E., Lawrence R., Sonenshein G.E.;

Concreted modulation of alpha 1(XI) and alpha 2(V) collagen mRNAs in borine vascular smooth muscle cells.;

J. Biol. Chem. 266:23268-23273(1991).

-! FURLILOGENESIS BY

CONTROLLING LATERAL GROWTH OF COLLAGEN IN FIBRILLOGENESIS BY

ALPHA 2(XI), AND ALPHA 3(XI). ALPHA 1(V) CAN ALSO BE FOUND INSTEAD

CONTROLLING ALPHA 3(XI). ALPHA 1(V) CAN ALSO BE FOUND INSTEAD

OF ALPHA 3(XI)-1(I) (BY SIMILARITY).

CONTROLLINGS AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING

OUT IT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

CONTROLLINGS TO THE FIBRILLAR CLASS OF COLLAGENS.

CONTROLLINGS TO THE FIBRILLAR CLASS OF COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                 Ionic channel; Ion transport; cAMP-binding; Transmembrane; Vision; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 1; Length 735;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
H5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
H6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CAMP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                006 CAMP (POTENTIAL).
149 N-LINKED (GLCNAC. .) (PC 85031 MW, A67ADFDD942CEFCE CRC64;
                                                                                                                                                                                                                                                                                                                                                    H1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
H2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTL-----RQWLAARAGPNGIEGPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Collagen alpha 1(XI) chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 911 AA.
EMBL; X89598; CAA61757.1; -.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR000595; CNMP_binding.
                                                                                                                                                SMART; SM00100; CNMP; 1.
PROSTIF; PS00889; CNMP_BINDING_1; 1.
PROSTIE; PS00899; CNMP_BINDING_2; 1.
PROSTIE; PS50042; CNMP_BINDING_3; 1.
                                                                              Pfam; PF00520; cNMP_binding; 1. Pfam; PF00520; ion_trans; 1.
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34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   735 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAIB_BOVIN
Q28083;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 50:23-33(1998).

-!- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF ADRENOCOPTICOPTORPIC HORMODE (ACTH). BINDS WITH HIGH AFFINITY TO CRF RECEPTOR TYPES 1, 2-ALPHA, AND 2-BETA.

-!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
                                                                                                                                                                                                                  AMINO-TERMINAL PROPEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                COLLAGEN ALPHA 1(XI) CHAIN.
NONHELICAL REGION.
TRIPLE-HELICAL REGION (INTERRUPTED).
                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                  Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98292491; PubMed-9628819; Zhao L., Donaldson C.J., Smith G.W., Vale W.W.; "The structures of the mouse and human urocortin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                 C05C4B3350749CFC CRC64;
                                                                                                                                                                                                                                                                                SHORT NONHELICAL SEGMENT
                                                                                                                                                                                                                                                                                                                   TRIPLE-HELICAL REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UROC_MOUSE STANDARD; PRT; 122 AA. P81615; 088390; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                  CROSSLINKING.
                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                   TELOPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000187; CRF.
InterPro; IPR003620; Urocortin_CRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00473; CRF; 1.
ProDom; PD005970; Urocortin_CRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 IEGPPGPAGPAGLMGPPGLQGPT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGPNGIEGPT 23
                                                                                                                                 InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 11.
                                                                                                                                                                                                                                                                                                                                                                 89259 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                  28.7%;
47.8%;
                                                                                                                 EMBL; M82977; AAA30369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                              Glycoprotein; Collagen.
NON_TER 1 1
PROPEP <1 278
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>911
186
275
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                                                                                                                                                                                                                                                                                276
279
296 >9
379
911
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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SMART; SM00039; CRF; 1,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Phage HK022;
SPECIES-Phage HK022;
MEDLINE-89342-95; PubMed=2547971;
MEDLINE-89342-95; PubMed=2547971;
Yaqil E., Dolev S., Oberto J., Kislev N., Ramaiah N., Weisberg R.A.;
"Determinants of site-specific recombination in the lambdoid coliphage HK022. An evolutionary change in specificity.";
J. Mol. Biol. 207:695-717(1989).
I- FUNCTION: EXCISIONASE AND INTEGRASE ARE NECESSARY FOR THE EXCISION OF PROHABGE FROM THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION AT
                                                               UROCORTIN. AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Limberger R.J., Campbell A.M.;
*Functional elements of DNA upstream from the integrase operon that
are conserved in bacteriophages 434 and lambda.";
Gene 61:135-144(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker J., Limberger R., Schneider S.J., Campbell A.; "Recombination and modular exchange in the genesis of new lambdoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda phage group.
                                                                                                                                                                                1;
                Cleavage on pair of basic residues; Signal.
                                                                                                                                             28.4%; Score 48.5; DB 1; Length 122;
                                                                                                                                                                           11; Indels
                                                                                                              D2969756F36F5DEA CRC64;
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DNA recombination; DNA-binding.

DESA4843503344AA CRC64;
                                                                                                                                                                                                                                                                                                               D11683; P16408; PRT; 72 AA. P11683; P16408; P10-0CT-1989 (Rel. 12, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update)
                                                  BY SIMILARITY.
                                                                                                                                                           Pred. No. 9.6;
2; Mismatches
                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88167849; PubMed=2965063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Phage 434;
MEDLINE=91346141; PubMed=1715186;
                                                                                                                                                                                                         4 PTLRQWLAARAGPNGIEGPTLRQW 27
                                                                                                                                                                                                                                         21 PESSOWSPAAAAATGVODPNLR-W 43
                                                                                                              122 AA; 13557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60848; AAA67901.1; -. EMBL; X51962; CAA36222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-64 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Biol. 3:297-308(1991).
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambda phage group.
NCBI_TaxID=10712, 10742;
                                 25
80
120
120
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage 434, and
PS00511; CF
Amidation;
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PIR; S06533; S06533.
                                                                                                                                                       Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=Phage 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                26
81
120
                                                                                                                                                                                                                                                                                                                                                                                                    Excisionase.
                                                                                                              SEQUENCE
 PROSITE;
                                                               PEPTIDE
MOD_RES
                                                                                                                                             Query Match
                  Hormone;
                                 SIGNAL
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                                                   PROPEP
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-1- FUNCTION: EXCISIONASE AND INTEGRASE ARE NECESSARY FOR THE EXCISION OF PROPHAGE FROM THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-80234646; PubMed-6446713; Hoess R.H., Foeller C., Bidwell K., Landy A.; Seller crecombination functions of bacteriophage lambda: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of regulatory regions and overlapping structural genes for
                                                                                                                                                                                                                                                                                                                                                                                              'DNA sequence of the int-xis-Pi region of the bacteriophage lambda;
                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10710;
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                                    .,
                                                                                                                                                                                                                                                                                                          Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.,
"Nucleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1; Length 72;
Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
         Score 48; DB 1; Length 72;
Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA recombination; DNA-binding.
SEQUENCE 72 AA; 8605 MW; 0E6A4843502200AA CRC64;
                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 AA.
         Ouery Match 28.1%; Score 48; DB Best Local Similarity 37.5%; Pred. No. 6.5; Matches 9; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          overlap of the int and xis genes."; Nucleic Acids Res. 8:1765-1782(1980).
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                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                    MEDLINE-83189071; Pubmed-6221115;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-81053845; Pubmed-6253947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TLRQWLAARAGPNGIEGPTLRQWL 28
                                                          5 TLROWLAARAGPNGIEGPTLROWL 28
                                                                                 4 TLQEWNARQRRPRSLE--TVRRWV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.1%;
37.5%;
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Best Local Similarity 37.59
Matches 9; Conservative
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                              Bacteriophage lambda.
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                    Davies R.W.;
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ID YL76_VIBCH
                                                                                                                                                                                                       Excisionase
                                                                                                                                             VXIS_LAMBD
P03699;
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                                                                                                                                   VXIS_LAMBD
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                                                                                                                     RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20406833; PubMed=10952301; Medline-20406833; PubMed=10952301; Medline-20406833; PubMed=10952301; Medline-20406833; PubMed=10952301; Medline-2040687; E.K., Melson W.C., Clayton R.A., Umayam L.A., Goll S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Gill S.R., Nelson K.E., Pass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
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Cole S.T., Edjameier K., Parkhill J., James K.D., Thomson N.R.,
Muheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Ouail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels 10; Gaps
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                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 48; DB 1; Length 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 protein; Complete proteome.
270 AA; 30984 MW; 1EC54ACDEED8AB92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE UPF0162 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
11-OCT-2001 (Rel. 41, Last annotation update)
Probable integrase/recombinase xerC.
16-0cr-2001 (Rel. 40, created)
16-0cr-2001 (Rel. 40, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
Hypothetical protein VC2176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 TLQAWLVGHKGPLAKLKPQHLQSVDNPTIIGRWLA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 TLRQWLAARAGP-----NGIEGPT-LRQWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 25;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004289; AAF95321.1; -. TIGR; VC2176; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XERC OR ML1600 OR MLCB250.62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity 31.4 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                            Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09CBU0; 033037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XERC_MYCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholerae
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                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                    Incerrio, invocation phage_integrase; 1.

Pfam: PF00589; Phage_integrase; 1.

PDNA recombination; DNA integration; Complete proteome.

ACT_SITE 278 278 TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                       -!- FUNCTION: Participates in site-specific recombination. Acts by catalyzing the cutting and rejoining of the recombining DNA molecules. Acts jointly with XerD (By similarity).
-!- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P21881; 059227;
0-1MAY-1999 (Rel. 18, Created)
15-JUL-1999 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyruvate dehydrogenase El component, alpha subunit (EC 1.2.4.1) (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the mobA-ampS region of the Bacillus subtillis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hemila H., Palva A., Paulin L., Arvidson S., Palva I.; "Secretory S complex of Bacillus subtilis: sequence analysis and identity to pyruvate dehydrogenase."; J. Bacteriol. 172:5052-5063(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Winters P., Caldwell R., Enfledd L., Ferrari E.,
"The ampS-nprE (124 degrees-127 degrees) region of the Bacillus
subtilis 168 chromosome: sequencing of a 27 kb segment and
identification of several genes in the area.";
Microbiology 142:3033-3037(1996).
                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 E70FA43F15286053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
 "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 28;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Score 48;
                                                                                                                                                                                                                                 Leproma; ML1600; -.
InterPro; IPR002104; Phage_integrase.
                                                                                                                                                                                                                                                                                                                                                                                                                4 PTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                           49 PVLRSWLATAAGAGAARTTLARRISAVKA 77
                                                                                                                                                                                                    EMBL; Z97369; CAB10656.1; ALT_INIT.
EMBL; AL583922; CAC30551.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90368558; PubMed=1697575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97124187; PubMed=8969500;
                                                                                                                                                                                                                                                                                                                                  297 AA; 32180 MW;
                                                                                                                                                                                                                                                                                                                                                            28.18;
37.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caldwell R.M., Ferrari E.;
                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDHA OR ACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
ODPA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                      Matches
δ
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                                                                                                                                                                                  FUNCTION: THE PYRUVATE DEHYDRÓGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
                                                                                                                                                                                                                                                                                                             FUNCTION: THE B.SUBTILIS PDH COMPLEX POSSESSES ALSO BRANCHED-CHAIN
                                                                                                             "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
                                                                                                                                                                                                                                                               DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Wet W.J., Bernard M.P., Benson-Chanda V., Chu M.-L., Dickson L.A.,
Weil D., Ramirez F.;
"Organization of the human pro-alpha 2(1) collagen gene.";
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00676; El_dehydrog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                     Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                             2-OXOACID DEHYDROGENASE (BCDH) ACTIVITY.
CATALYTIC ACTIVITY: Pyruvate + lipoamide - S-acetyldihydrolipoamide + Co(2).
COFACTOR: THIAMINE PYROPHOSPHATE.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3183EB8881E1BD6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A -> R (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA21_HUMAN STANDARD; PRT; 1366 AA. P08123; P003464; Q9UEB6; Q9UPH0; 01-AUG-1988 (Rel. 08, Created) CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen alpha 2(I) chain precursor.
                                        MEDLINE=97443988; PubMed=9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 EGPTLIETLTFRYGPHTMAGDDPT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88058962; PubMed=2824475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EGPTLRQWLAARAGPNGIEG--PT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF012285; AAC24932.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 AA; 41417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z99111; CAB13331.1;
PIR; B36718; DEBSPA.
HSSP; P09060; 1QS0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M57435; AAA62681.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subtilist; BG10207; pdhA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001017;
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SEQUENCE OF 1-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178
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                                                                                                                                                                                        -! - FUNCTION:
                                                                                            Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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ij

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SEQUENCE FROM N.A.

Korkko J.M., Earley J.J., Ala-Kokko L., Prockop D.J.;

Kankko J.M., Earley J.J., Ala-Kokko L., Prockop D.J.;

Analysis of the COLIA1 and COLIA2 genes by CSGE and DNA sequencing in analysis with mild OI (Type I). Identification of common sequences if patients with milations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuivaniemi H., Sabol C., Tromp G., Sippola-Thiele M., Prockop D.J.; "A 19-base pair deletion in the pro-alpha 2(I) gene of type I procollagen that causes in-frame RNA splicing from exon 10 to exon 12 in a proband with atypical osteogenesis imperfecta and in his asymptomatic mother.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVIEW ON VARIANTS.
MEDILNE-9725599; PubMed-9101290;
Kulyaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of a cDNA for the pro alpha 2 chain of human type I procollagen. Comparison with chick cDNA for pro alpha 2(I) identifies structurally conserved features of the protein and the gene."; Biochemistry 22:1139-1145(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterization of the cyanogen bromide peptides from the alpha 1 and alpha 2 chains of human skin collagen."; Blochemistry 9:4699-4706(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fietzek P.P., Furthmayr H., Kuehn K.;
"Comparative sequence studies on alpha2-CB2 from calf, human, rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maekelae J.K., Vuorio T., Vuorio E.;
KTOVATh-dependent modulation of type I collagen production and mRNA
levels in cultured human skin fibroblasts.";
Biochim. Biophys. Acta 1049:171-176(1990).
                                                                                                                                                                                        Kuivaniemi H., Tromp G., Chu M.-L., Prockop D.J.;
"Structure of a full-length cDNA clone for the prepro alpha 2(I)
chain of human type I procollagen. Comparison with the chicken gene
confirms unusual patterns of gene conservation.";
Blochem. J. 252:633-640(1988).
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 623-1366 FROM N.A.
MEDLINE-83178919; PubMed-6687691;
Bernard M.P., Myers J.C., Chu M.-L., Ramirez F., Eikenberry E.F.,
                                                                                                Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  Kallcki J., Wamsley P., Gibson A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91184577; Pubmed-2010058;
Kuivaniemi H., Tromp G., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 263:11407-11413(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 47:257-261(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 145-198 FROM N.A.
MEDLINE-88298792; Pubmed=3403536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=71038625; PubMed=5529814; Click E.M., Bornstein P.;
                                                                                                                                                              TISSUE=Placenta;
MEDLINE=88339824; PubMed=3421913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-75008198; PubMed-4412529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90304220; PubMed=2364107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 960-1351 FROM N.A.
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 181-1366 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FASEB J. 5:2052-2060(1991).
                                                                                                                                        SEQUENCE OF 1-765 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pig-skin collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 417-447.
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Weil D., D'Alessio M., Ramirez F., Eyre D.R.; "Structural and functional characterization of a splicing mutation in the pro-alpha 2(I) collagen gene of an Ehlers-Danlos type VII Bateman J.F., Hannagan M., Chan D., Cole W.G.; "Characterization of a type I collagen alpha 2(I) glycine-586 to valine substitution in osteogenesis imperfecta type IV. Detection of the mutation and prenatal diagnosis by a chemical cleavage method."; Biochem. J. 276:765-770(1991). Fertala A., Westerhausen A., Morris G.M., Rooney J.E., Prockop D.J.; "Two cysteine substitutions in the type I procollagen genes (CoLiAl and CoLiA2) that cause lethal osteogenesis imperfecta. The location of glycine substitutions does not in any simple way predict their effets on protein function or phenotype."; Am. J. Hum. Genet. 47:A216-A216(1990). MEDLINE=88227975; PubMed=2897363; Menstrup R.J., Cohn D.H., Cohen T., Byers P.H.; Menstrup R.J., Cohn D.H., Cohen T., Byers P.H.; triple-helical domain of the products of one alpha 2(I) collagen allele (COLIA2) produces the products of one alpha 2(I) collagen allele (COLIA2) produces the progressis imperfecta type IV phenotype."; J. Biol. Chem. 263:7734-7740(1988). MEDLINE=89123407; PubMed=2914942;
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carboxyl terminus destabilizes the whole triple helix.";
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comprissing the N-telopeptide region of a pro-alpha 2(I) chain.";
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Pred. No. 14;
                                                                                                                                                                                                                                                                             InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002904; tRNA-synt_lys_1.
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MEDLINE=98297355; PubMed=9635432;
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Best Local Similarity 35.79
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                    Byers P.H., Cohn D.H., "The effects of different cysteine for glycine substitutions within alpha 2(1) chains. Evidence of distinct structural domains within the Irype I collagen triple helix.", J. Biol. Chem. 266:2590-2594(1991).
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DNA Res. 6:83-101(1999).
-!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93244832; PubMed-1284475; Bateman J.E., Meeller I., Hannagan M., Chan D., Cole W.G.; Lethal perinatal osteogenesis imperfecta due to a type I collagen alpha 2(I) Gly to Arg substitution detected by chemical cleavage of mrnna:cDNA sequence mismatch."; Mutat. 1:55-62(1992).
                                                                                                                                                                       MEDLINE-91340689; PubMed=1874719;
Tsuneyoshi T., Westerhausen A., Constantinou C.D., Prockop D.J.;
Tsuneyoshi T., Westerhausen A., Constantinou C.D., Prockop D.J.;
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type I procollagen in lethal osteogenesis imperfecta. The
conformational strain on the triple helix introduced by a glycine
substitution can be transmitted along the helix.";
J. Biol. Chem. 266:15608-15613(1991).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lysyl-trna synthetase (EC 6.1.1.6) (Lysine--trna ligase) (LYSRS).
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Wenstrup R.J., Shrago-Howe A.W., Lever L.W., Phillips C.L.,
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Pred. No. 1.3e+02;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01921; tRNA-synt_1f; 1. PROSTE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
AMAINGACY1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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PHOSPHORYLATION. MAY BE IMPLICATED IN TUMOR PROGRESSION.
-:- SIMILARITY: BELONGS TO THE GSK-3-BINDING PROTEIN FAMILY.
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; 753664E2937FBF27 CRC64;
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CCEC4EE7746694AC CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GSK 3 binding protein FRAT2 (Fragment).
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9825987; PubMed-9634230; Carnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Edilmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares T., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Squares J., Squares G., Squares R., Butter S., Seeger K., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
-i- SUBDNIT: HOMODIMER (BY SIMILARIY).
-i- SUBCELLULAR LOCATION: INNER SIDE OF THE MEMBRANE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE DIHYDROOROTATE DEHYDROGENASE FAMILY.
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1773;
                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)
 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S)-dihydroorotate + 0(2) = orotate +
   5; Indels
                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   2; Mismatches
                                                                                                                                                                                                                                       (DHOdehase) (DHODase) (DHOD).
PYRD OR RV2139 OR MT2197 OR MTCY270.29C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- COFACTOR: FMN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001295; DHO_dh.
InterPro; IPR001309; FNN_enzyme.
InterPro; IPR0013009; FNN_enzyme.
PROBITE: PS00911; DHODEHASE_1; 1.
PROSITE; PS00912; DHODEHASE_2; 1.
                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z95388; CAB08654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE007067; AAK46481.1;
                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 393:537-544(1998).
   8; Conservative
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv2139; -.
                                  14 AGPNGIEGPTLROWL 28
                                                               15 AGPSALPGPCRRGWL 29
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MT2197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H(2)0(2)
                                                                                                                                           PYRD_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bishai W.;
                                                                                                                                                               006236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                              PYRD_MYCTU
      Matches
                                                                                                             RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photosynthesis; Photosystem II; Thylakoid; Chlorophyll; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
U-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kba reaction center protein (P6 protein) (CP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-95024047; PubMed-7937893;
Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus. NCBI_TaxID=3350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.5%; Score 47; DB 1; Length 473; 32.5%; Pred. No. 59; Live 5; Mismatches 12; Indels
Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
                                                                                                   Score 47; DB 1; Length 357;
Pred. No. 45;
                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 AA; 51826 MW; 0E05E8FC7268465C CRC64;
                                           FMN (POTENTIAL).
3D9D107DD9B4FCB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus thunbergii (Green pine) (Japanese black pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 GETMRFWDLRAPWLEPLRGPNGLDLSKLRKDIQPWQERRS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLR-----QWLAARAGPNGIEGPTLRQ----WLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                  473 AA.
                                                                                                                             Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                            37998 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D17510; BAA04424.1; -. Mendel; 10000; PINth;psbC;1. InterPro; IPR000932; PSII. Pfam; PF00421; PSII; 1.
                                                                                                       27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                             Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                              256 RLGPGGISGPPLAQ 269
                                                                                                                                                                                       13 RAGPNGIEGPTLRQ 26
                                             294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserv
                                                              357 AA;
                         Complete proteome.
                                                 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUR4_HUMAN
015067;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                  PSBC_PINTH
P41643:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                   SEQUENCE
                                                                                                            Query Match
                                                 NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUR4_HUMAN
                                                                                                                                                                                                                                                                                                                   PSBC_PINTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 27
                                                                                                                                                                                                                                                                                               RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO TYPE-1 GLUTAMINE AMIDOTRANSFERASES.
                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-2010111; bubmed=10548741;
MEDLINE-20101111; bubmed=10548741;
Patterson D., Bleskan J., Gardiner K., Bowersox J.;
"Human phosphoribosylformylglycinamide amidotransferase (FCARAT):
regional mapping, complete coding sequence, isolation of a functional genomic clone, and DNA sequence analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                Migase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new CDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).

-!- CATALYTIC ACTIVITY: APP + 5'-phosphoribosylformylglycinamide + L-glutamine + H(2)0 = ADP + phosphate + 5'-phosphoribosylformylglycinamidine + L-glutamine + H(2)0 = ADP + phosphate + 1-glutamine + H(2)0 = ADP + phosphate + 1-glutamine + H(2)0 = ADP + phosphate + 1-glutamine + 1-glutamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) (FGAM synthase) (FGAMS) (Formylglycinamide ribotide amidotransferase) (FGRARAT) (Formylglycinamide ribotide synthetase).
PRAS OR KIAA0361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.5%; Score 47; DB 1; Length 1338; 35.7%; Pred. No. 1.7e+02; Live 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1205 RWASVRVGPGPALMLRGMEGAVLPVWSA 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB002359; BAA20816.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 OWLAARAGP----NGIEGPTLROWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen alpha 2(I) chain precursor. COLIA2 OR COLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000728; AIRS_related.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97349984; PubMed-9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 35.7 nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 602133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA21_MOUSE
ID CA21_MOUSE
AC Q01149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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   OF DIA
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                                                                                                                                                                                                                                                         Phillips C.L., Morgan A.L., Lever L.W., Wenstrup R.J.; "Sequence analysis of a full-length cDNA for the murine pro alpha 2(1) collagen chain: comparison of the derived primary structure with human pro alpha 2(1) collagen."; Genomics 13:1345-1346(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Construction of a full-length murine pro alpha 2(I) collagen cDNA by the polymerase chain reaction.";
J. Invest. Dermatol. 97:980-984(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONVERTED TO AN ALDEHYDE GROUP THAT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-23 FROM N.A.

MEDLINE-87289565; pubmed=3039494;

Rossi P., de Crombrugghe B.; percific transcriptional enhancer in the first intron of a call-specific transcriptional enhancer in the first intron of the mouse alpha 2 (type I) collagen gene."; proc. Natl. Acad. Sci. U.S.A. 84:5590-5594(1987).

-!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN (FIBRILLAR FORMING COLLAGEN).

-!- SUBGUIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.

-!- SIBGUIT: TRIEST FORMS THE FIBRILS OF TENDON, LIGAMENTS AND BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01110; COLET; 1.
Pfam; PF01391; Collagen; 18.
Probom; PB002078; Fib_collagen_C; 1.
SMART; SM00038; COLET; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN ALPHA 2(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINO-TERMINAL PROPEPTIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phillips C.L., Lever L.W., Pinnell S.R., Quarles L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
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MGD; MGI:88468; Colla2.
InterPro; IPR000087; Collagen.
InterPro; IPR008885; Fib_collagen_C.
                                                                                                                                                                                                                              MEDLINE=92372043; PubMed=1505972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92084969; PubMed=1748823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X58251; CAA41205.1; -. EMBL; BC007158; AAH07158.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K01832; AAA37331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-110 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROXYAPATITE.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Calvaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wenstrup R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
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                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91021039; PubMed=2171211; Vlcek C., Kormik Z., Paces V., Schirm S., Schwyzer M.; Vlcek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.; Pseudorables virus immediate-early gene overlaps with an oppositely oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: THIS IS PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREQUATING ITS OWN SYNTHESIS.
-i- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-i- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                  . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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                                                                                                                                                                                                                            Score 47; DB 1; Length 1372;
Pred. No. 1.7e+02;
1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.5%; Score 47; DB 1; Length 1446; 44.0%; Pred. No. 1.8e+02; tive 2; Mismatches 10; Indels
INVOLVED IN CROSS-LINKING
(BY SIMILARITY).
N-LINKED (GLCNAC, ..) (POT.
V -> A (IN REF. 4).
R -> TT (IN REF. 1).
7 MM; ODI7DF5D6C1452D1 CRC64;
                                                                                                -> A (IN REF. 4).
-> TT (IN REF. 1).
0D17DF5D6C1452D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1446 AA; 148640 MW; 81F43A3DE3DDA068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION.
-!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudorabies virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Phosphorylation; Nuclear protein.
DOMAIN 347 354 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY - SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GPTL--RQWLAARAGPNGIEGPTLR 25
                                                                                                                                                                                                                                                                                                                                                                                                                          758 IVGPTGSVGAAGPSGPNGPPGP 779
                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGPNGIEGP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immediate-early protein IE180.
                                                                                                                                                                                                                               27.5%;
50.0%;
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                                                                                                                                                                1372 AA; 129557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 179:365-377(1990)
                                                                                                                                                                                                                                                                                              Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
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15
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                                                                                                                                                                                                                                                             Local Similarity
mes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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ID IE18_PRVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IE18_PRVKA P33479;
                                                                                                    CONFLICT
                                                                                                                                                                SEQUENCE
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                                                                      CARBOHYD
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DT 01-FEB
ON NCHL
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RN MEDLIN
RY PSEUC
RT 07-FEB
CC 1- P
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      FTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                          "DNA nucleotide sequence analysis of the immediate-early gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                       Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV). Viruses; dSDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=31523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

390 405 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1; Length 1461;
Pred. No. 1.9e+02;
2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7F31E7ABE403B208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION.
-!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
           01-OCT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                  pseudorabies virus.";
Nucleic Acids Res. 17:4637-4646(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 GPSAAPRRWSPARGDPVGEPGPAAR 214
                                                                                                                                                                                    MEDLINE=89315207; PubMed=2546124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTL--RQWLAARAGPNGIEGPTLR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1461 AA; 149833 MW;
                                                          Immediate-early protein IE180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X15120; CAA33214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%;
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nes 11; Conservative
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                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                     Cheung A.K.
                                                                                                                                                                                                                                                                             REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1,

Search completed: October 9, 2002, 09:00:07

Job time : 4.90535 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 9, 2002, 08:52:16; Search time 11.466 Seconds

(without alignments)
482.803 Million cell updates/sec

Title: US-09-422-838C-22

Perfect score: 171 Sequence: 1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 562222

562222 seqs, 172994929 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

imum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL\_19:\*
1: Sp\_archea:\*

1: \*\*\*Sp\_archea:\*
2: \*\*\*Sp\_bacteria:\*
3: \*\*\*Sp\_fung:\*\*
4: \*\*\*Sp\_fung:\*\*
5: \*\*\*Sp\_invertebrate:\*\*
6: \*\*\*Sp\_mammal:\*\*
7: \*\*\*Sp\_mhc:\*\*
7: \*\*\*Sp\_nhc:\*\*
9: \*\*\*Sp\_nhge:\*\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

escription 203436 treponema p 91804 polyangium	Q9s5e5 streptomyce	Q9Vz8z grosophila O9abc7 caulobacter	094192 paracoccidi	P97011 streptomyce	Q9i3u4 pseudomonas	29s0m9 deinococcus	Q9rte6 deinococcus	296c78 homo sapien	Q9x7n5 streptomyce	6161 mytilus edu	19kzd5 streptomyce	291096 streptomyce	091477 pseudomonas
Description 083436 tre 091864 poly						_		Ö	õ	0	60	60	ö
OMMAKIES 1D 083436 Q9L8D4	Q9S5E5	Q9V28Z Q9ABC7	094192	P97011	Q913U4	6M0S60	Q9RTE6	Q96C78	Q9X7N5	016161	Q9KZD5	O9L096	091477
DB 16	7	16	٣	7	16	7	16	4	7	2	7	7	16
% Query Query Match Length DB 36.8 683 16 36.7 2	509	361	1744	420	1095	305	326	814	386	902	196	1349	371
% Query Match 36.8	35.1	32.7	32.5	32.2	31.6	31.0	31.0	30.7	30.4	30.4	30.4	30.4	30.1
Score 63 62	09	56	55.5	55	54	53	53	52.5	52	52	52	52	51.5
Result No.	m <del>-</del>	4 ւՆ	9	7	80	6	10	11	12	13	14	15	16

	Q9hyj8 pseudomonas Q92zh9 rhizobium m Q91907 pagrus majo Q981n1 rhizobium l Q9gy79 leishmania	0931y8 streptomyce 0981g1 rhizobium 1 09rwb0 deinococcus 09f2f9 streptomyce	Oyfobo mycobacteri O9f5b8 agrobacteri O911m2 pseudomonas O17754 caenorhabdi O98pl0 rhizobium 1 O9uqh1 homo sapien	Q9bxa9 homo sapien Q941x0 perilla fru Q9w74 mus musculu Q9aqh5 achromobact Q20968 caenorhabdi	Q913A3 rhizobium 1 Q9as26 oryza sativ Q43416 cenchrus ci Q9rkm5 streptomyce
000	16 Q9HYJ8 16 Q92ZH9 13 Q9I907 16 Q98INI 5 Q9GY79	99	9 9	1 Q9BXA9 10 Q94LX0 11 Q9WV74 2 Q9AQH5 5 Q20968	Q9L3H3 0 Q9AS26 0 Q43416 Q9RKM5
			400 2 403 2 410 1 472 5 604 1 1272 4	•	249 2 250 1 307 1 319 2
$\sigma\sigma\sigma\sigma\sigma\sigma$	29.8 29.8 29.5 29.5	00000	<i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>		$\infty$ $\infty$ $\infty$
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17 18 19 20 21	22 23 24 25 26	22 29 30 30	32 33 34 35	37 38 39 40 41	444 444 5

#### ALIGNMENTS

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SEQUENCE FROM N.A.
STRAIN-NICHOLS;
STRAIN-NICHOLS;
STRAIN-NICHOLS;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
Venter J.C.,
Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 683 AA; 74518 MW; F91407FA7094AAD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 281:375-388(1998).
EMBL, AE001220, AAC65409.1;
TIGR; TP0421; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001258; NHL.
InterPro; IPR001440; TPR.
Pfam; PF01436; NHL; 4.
Pfam; PF00515; TPR; 1.
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spirochete.";
                                                                               083436
RESULT 1
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MEDLINE=97000351; PubMed=8843436;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CTT-2000 (TrEMBLrel. 15, Last annotation update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
0RF1, ORF2, ORF3, ORF4, ORF5 GENES, COMPLETE CDS (PUTATIVE DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molnar I., Schupp T., Ono M., Zirkle R.E., Milnamow M.,
Nowak-Thompson B., Engel N., Toupet C., Stratmann A., Cyr D.D.,
Nowak-Thompson B., Engel N., Toupet C., Stratmann A., Cyr D.D.,
"The blosynthetic gene cluster for the microtubule-stabilizing agents
epothilones A and B from Sorangium cellulosum So ce90.";
Chem. Biol. 7:97-109(2000).
Hypothetical protein.
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%; Score 62; DB 2; Length 607; 34.8%; Pred. No. 5.5; 7; Indels tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Uneyama T., Ping Chin L., Horinouchi S.;
"Multicopy suppressor gene of afsR mutant.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seeger K.J., Harris D.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607 AA; 66326 MW; F113CA299B25048E CRC64;
                                                                                                                                                                                                                                                                                                                          Myxococcales; Sorangineae; Polyangiaceae; Polyangium NCBI_TaxID=56;
                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 66.3 KDA PROTEIN (FRAGMENT).
Polyangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 AA.
                                                                                                                                                                  607 AA
                                            74 PLILEWLGNAYYRSGIEGAALHOWGAAR 101
  4 PTLROWLAARAGPNGIEGPTLROWLAAR 31
                                                                                                                                                                  PRT;
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MEDLINE=20130945; PubMed=10662695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 34.8 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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RA MEDLINE=ZOLYOUGE; PURDEGI-LU/J132;

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Radmas M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y. H.C., Blazej R.G., Champpe M., Pfeififer B.D.,

RA Brandon R.C., Radrer S.E., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basud A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basud A., Buller B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Basam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Boyones M., Dugan-Rocha S., Dunkov B.C.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Brad Cablos B., Carell J.H., Gu Z., Guan P., Harris M.,

RA Bortislan A.E., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Katchum K.A.,

Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum K.A.,

Jalail M., Mattel B., Morntosh T.C., Morris J., Liang Y., Lin X.,

Liu X., Mattel B., Morntosh T.C., Morris J., Wopherson D.,

RA Mount S.M., Nelson K.A., Whobarry C., Morris J., Wopherson D.,

Ra Alazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Snele B.,

Rabiscol M., Nelson K.A., Wanskern D.R., Paceleb J.M.,

Rabiscol M., Nelson K.A., Wanskern D.R., Smith T.,

Syirskas R., Tector C., Turner R., Venter E., Wang S., Pao O., Zaho D.,

Hang S., Yeng S., Zhan M., Zhong W., Zhon G., Zhao O., Zhao O., Zhan G., Zhao O., Zhao O.,
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
MMOI. Microbiol. 21:77-96 [1996].
EMBL; AB017438; BAA82701.1;
EMBL; A1356592; CAB92204.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.1%; Score 60; DB 2; Length 509; 44.1%; Pred. No. 8.2; ive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                           DNA-binding.
SEOUTENCE 509 AA; 54398 MW; 7BB074DAAEOF1867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
CG7479 PROTEIN.
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MEDLINE=20196006; PubMed=10731132;
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Matches 15; Conservative
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CHITIN SYNTHASE.
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STRAIN-ATCC 19089 / CB15,
MEDLINE-21173698; ubbade-11259647;
MEDLINE-21173698; ubbade-11259647;
Miterman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. US.S. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                            Pram: PF00133; TRNA-Synt_1; 1.
PRINTS; PR00985; TRNASYNTHLEU.
PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
SEQUENCE 869 AA; 99299 MW; E87AlECBEBB27B67 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL; AE003482; AAF47043.1;
FlyBase; FBgn0035576; CG7479.
InterPro; IPR002300; tRNA-synt_1.
InterPro; IPR001412; tRNA-synt_1.
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Last annotation update)
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8
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Pred. No. 22;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002524; Cation_efflux.
InterPro; IPR002395; Kininogen.
Pfam: PF01545; Cation_efflux; 1.
PRINTS; PR00334; KININOGEN.
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                                                                                                                                                                                                                                                                                                   34.28;
                                                                                                                                                                                                                                                                                                                           40.6%;
                                                                                                                                                                                                                                                                                                                                                13; Conservative
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les 12; Conservative
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=69394;
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SEGUENCE 361 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"Cloning of a gene encoding a sorbitol oxidase from Streptomyces sp.
H-7 775.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces sp.
Bacteria; Firm.cutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Paracoccidioides brasiliensis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00242; MYSC; 1.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
SROUENCE 1744 AA; 193777 MW; DB7622D0A69F0705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF107624; AAD19613.2; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                Nino-Vega G.A., San-Blas G.; "Sequence analysis of the CHS4 gene of Paracoccidioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases EMBL, AB000519; BAA19135.1; InterPro; IPR001575; Oxid_FAD_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01565; FAD_binding_4; 1.
SEQUENCE 420 AA; 45181 MW; EF3189045CAF0649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 55.5; DB 3; 51.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TLROWL-AARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 GPVGQVWLKQRVGDEGARSVMPAEWLGAR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002923; Chitin_synth.
InterPro; IPR00117; Cu-oxidase.
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR001109; myosin_head.
Pfam; PF03142; Chitin_synth_2; 1.
Pfam; PF00063; myosin_head; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQWLAARAGPNGIEGPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                            MEDLINE=20210320; PubMed=10746225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 51.7
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 37.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                            NCBI_TaxID=121759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SORBITOL OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-H-7775
                                                                                                                                                                                                                                                                                                                                                                                     brasiliensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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P97011;
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STRAIN-R1;
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                               SEQUENCE
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                                                                                                                                                                                               O9RTE6
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                                                                                                                                                                        STRAIN=ATCC 15692 / PAO1:
STRAIN=ATCC 15692 / PAO1:
MEDIINE=20437337; PubMed=10984043;
MEDIINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-O.F. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.N., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 54; DB 16; Length 10
45.5%; Pred. No. 1.1e+02;
tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34370FB8BEC201AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                          (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00188; BIOTIN: 1.
PROSITE: PS00188; BIOTIN: 1.
PROSITE: PS00867; CPSASE 2; UNKNOWN_1.
PROSITE: PS00205; CRYSTALLIN_BETACAMMA; UNKNOWN_1.
BIOTIN: COMPLETE PTOTEOME; PSYLVATE.
SEQUENCE 1095 AA: 116876 WW; 34370FB8BEC201AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 AA.
                                                                                                                                                                                                                                                                                                    opportunistic pathogen.";
Nature 466:595-964 (2000)
-1. COFACTOR: BIOTIN (BY SIMILARITY).
EMBL: AE004569; AAG04789.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001249; Accoa_biotincC.
InterPro; IPR001882; Biotin.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR000901; CSaboxyl_trans.
InterPro; IPR000901; CPsase.
InterPro; IPR001064; Crystallin.
                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02785; Biotin_carb_C: 1.
Pfam; PF0364; biotin_lipoyl: 1.
Pfam; PF01039; Carboxy_trans; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGPNGIEGP 22
                                                                                   PROBABLE PYRUVATE CARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, UV-ENDONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 45.59
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus radiodurans
                                                                                                               Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         HSSP; P24182; 1BNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1299;
                                                                                                                                                  NCBI_TaxID=287;
                                                           01-MAR-2001
01-DEC-2001
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                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                     091304;
                         Q913U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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RESULT 8
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             0913U4
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12; Gaps
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
A DISTUTECRIN AND METALLOPROTEINASE DOMAIN 15 (METARGIDIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.0%; Score 53; DB 16; Length 326; 40.5%; Pred. No. 40;
                                                                                                                                          Score 53; DB 2; Length 305;
Pred. No. 37;
4; Mismatches 6; Indels
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014566; AAH14566.1; -.
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases EMBL, AB033747; BAA85759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 286:1571-1577(1999).

EMBL; AE002022; AAF11370.1; -.
TIGR; DR1819; -.
Endonuclease; Complete proteome.

SEQUENCE 326 AA; 35693 MW; C4EA0D0AD2C38988 CRC64;
                                                                                    B94D333243E2FEA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 EDPSVREWVLRARATWQPPEWQVVHLSNGIEGPQDRR 285
                                                                                                                                                                                                                                                                                                      228 EDPSVREWVLRARATWQPPEWQVVHLSNGIEGPQDRR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EGPTLRQW-LAARAG-----PNGIEGPTLRQ 26
                                                                                                                                                                                                                                                               2 EGPTLRQW-LAARAG------PNGIEGPTLRQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 814 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last and
01 DARA-201 (TrEMBLrel. 16, Last and
01 DARAGE ENDONUCLEASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20036896; PubMed=10567266;
                                                                                             305 AA; 33592 MW;
                                                                                                                                             31.0%;
Best Local Similarity 40.5%;
Matches 15; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.5<sup>3</sup>
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deinococcus radiodurans
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                                                                  Endonuclease.
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Streptomyces coelicolor.
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902 AA;
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Saunders D.C.,
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                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KZD5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KZD5
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Q9L096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                          Length 814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 2; Length 396;
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
87717 MW; 683A8368AD30996B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                 30.7%; Score 52.5; DB 4;
44.8%; Pred. No. 1.2e+02;
ative 6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                  396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   902 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 66;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 PPARRWLSGRLAPG -- EGPSAERRAKSWFSVR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLRQWLAARAGPNGIEGPT----LRQWLAAR 31
                                                                                                                                                                                                 128 LKGPTC-QYRAAQSGPSERPGPPQRALLA 755
                                                                                                                                                                    1 IEGPTLRQWLAARAGPNGIEGPTLRQWLA 29
                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%;
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Best Local Similarity 34.4°,
These 11; Conservative
                                                                                                               13; Conservative
                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
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  814 AA;
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1902;
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  SEQUENCE
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                                                                                                         Matches
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Q9X7N5
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
-! - CATAINTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-! - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL, A15389015.1;
InterPro: IPR001750; Oxidored_q1.
Ffam; PP00361; oxidored_q1.
Ffam; PP00361; oxidored_q1.
NAD: Oxidoreductase; Transmembrane.
SEQUENCE 967 AA; 101770 MW; A727564D3EEE05AC CRC64;
                                                                                                                                                                                                                                                                                                                                                 Gaps
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Coyne K.J., Qin X.X., Waite J.H.;
"Extensible collagen in mussel byssus: A natural block copolymer.";
Science 277:1830-1832(1997).
EMBL. AF015539; AAB807191; -.
InterPro; IPR000087; Collagen.
Pfam; PF01391, Collagen.
Signal; Collagen. 7.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
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                                                                                                                                                                                                                                                                                           Length 902;
                                                                                                                                                                                                                                                                  30.4%; Score 52; DB 5; Length 902 52.4%; Pred; No. 1.66+02; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.4%; Score 52; DB 2; Length 96/
53.6%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                          DIEF09DEA2BD9EF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE NADH DEHYDROGENASE I COMPLEX, SUBGNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                967 AA
                                                                                                                                                                                                                  COLLAGEN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 WLAAR---AG-PNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                 20 PO'
902 CO
78526 MW;
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                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.4
Matches 11; Conservative
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Hypothetical protein; Complete proteome. SEQUENCE 371 AA; 39174 MW; 016D60440BAD50D7 CRC64;
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                STRAIN=K1;
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                             09YD00;
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                                                                                                                                                                    RESULT 17
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  SQ SQ
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EMBL; AL163003; CAB86115.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MINELSINE-20437337; PubMed-10984043;
Minelse R.L., Goller, E.L., Hufnayle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goller, L., Tolentino E., Westbrock Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Nature 406:559-964(2000).
                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1349;
                                                                                                                                                                                                                      Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR00719; Euk_pkinase.
InterPro: IPR000209; Peptidase_S8.
InterPro: IPR000209; Peptidase_S8.
Pfam: PF00069; pkinase: 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN.1.
ATP-binding: Hypothetical protein; Transferase.
SEQUENCE 1349 AA: 145671 MW; F0902A235D694B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                            STRAIN=A3(2);
Brown S.P., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN PA1267.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 145.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.4%; Score 52; DB 2; I 51.6%; Pred. No. 2.4e+02; tive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                         STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                   Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 16; Conserva
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                               SEQUENCE FROM N.A.
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A KAWATABAYASI Y., HINDERGY, HOLIKAWA H., YAMAZAKI A., KOSUGI H.,
AN JIN-NO K., TAKAHASHI M., SEKINE M., BABA S.-I., ANKAI A., KOSUGI H.,
HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJİMA K., NAKAZAWA H.,
A TAKAMIYA M., MASUGA S., FUNAHASHI T., TANAKA T., KUGOH Y.,
AN YAMAZAKI J., KUSHİGA N., OQUCHİ A., AOKİ K.-I., KUBOTA K.,
AN RAĞMULYA Y., NOMULYA N., SAKO Y., KİKUCHİ H.;
COMDLELE GENOME SEQUENCE ÖĞ AN AERODYLUM PERINIK KI.";
DINA RES. 6:83-101(1999).
BENBL, AROUONGO; BAA79847.1; -.
BENBL, AROUONGO; BAA79847.1; -.
BENBL, AROUONGO; BAA79847.1; -.
ROSTIFE; PSOULLY ZINC_PROTEASE;
RYPOCHÈLICAL PLOCLENI; COMPLELE PROTEAGE.
SON HYDOCHÈLICAL DIOLEANS, OQROSHEĞE92CB4IE CRC64;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
30.1%; Score 51.5; DB 16; Length 371; 31.0%; Pred. No. 72; Live 7; Mismatches 9; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 51; DB 17; Length 281; 34.4%; Pred. No. 62; ive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TIEMBLEEL. 12, Last sequence update) 01-JUN-2001 (TIEMBLEEL. 17, Last annotation update) HYPOTHETICAL 32.1 KDA PROTEIN APE0867.
                                                                                                                                                                       | :|| :|| | :||| | 14:|| | 145 PNAARWLLDQAGPRLRLYAEVSEVDGSRLRLADGRWLSAEA 186
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                                                                                                                                     4 PTLRQWLAARAGP-----NGIEGPTLR----QWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                      281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 SLRQWMRS---PNRYDIPGVDSPEVGWWLESR 40
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01-NOV-1999 (TrEMBLrel. 12, Last seq
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                                     Best_Local Similarity 31.0
Matches 13; Conservative
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Plasmid
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Q18756
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Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the blology of Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOI. Microbiol. 21:77-96(1996).
EMBL; A1177669; CAB56131.1; -.
Hypothetical protein.
SEQUENCE 322 AA; 35339 MW; DD55BB0480090638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                  Score 51; DB 16; Length 306;
Pred. No. 68;
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Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.,
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         3; Indels
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                              306 AA; 32378 MW; 24C2387443B0A3E8 CRC64;
                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                  322 AA
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                                                                                                                                                                                      1; Mismatches
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                                                                                                              InterPro, IPR01825; NTP_transferase. Pfam; PF00483; NTP_transferase; 1. Complete proteome.
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                    29.8%;
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 RAGPDRLDTPELREW 47
                                                                                                      Tuberculist; Rv0993; -
                                                                                                                                                                                                                       3 GPTLRQWLAARAG 15
                                                                                                                                                                             Best Local Similarity
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09RK51
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Q9X757
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WEDLINE-94150718; PubMed-7906398; Wilson R., Baynes C., Berks M., Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Caraton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Rifken L., Roopra A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R. Smaldon N., Smith A., Sonhammer E., Staden R., Sullston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91158299; PubMed-1963529; Papariotlaou G.A., Medeiros A.A., Jacoby G.A.; Medeiros A.B., Medeiros A.B., Novel plasmid mediated beta-lactamase (MIR-1) conferring resistance to oxyimino- and alpha-methoxy-beta-lactams in clinical isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Jacoby G.A., Tran J.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M37839; AAD22636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE . 381 AA; 41171 MW; DD5B1D789C03142E CRC64;
                                    Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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InterPro; IPR001586; Beta_lactam_C.
Pfam; PF00144; beta_lactamase; 1.
PROSITE; PS00336; BETA_LACTAMASE_C; 1.
         Created)
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250 MASWLIANMKPDSLQAPSLKQGIA 273
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01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, DETA-LACITAMASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.8 Best Local Similarity 33.3 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella pneumoniae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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                                                                                                                                                                 Klebsiella pneumoniae.
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                                                                                                                                                                                            Plasmid pMG230
                                                                                                                                                                                                                                                              Klebsiella.
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STRAIN-ATCC 15692, PAO1;
MEDIANG-ATCC 15692, PLOME-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Nature 406:959-964(2000).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
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Pred. No. 1.4e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                   29.8%; Score 51; DB 5; Length 589; 42.9%; Pred. No. 1.4e+02; tive 3; Mismatches 9; Indels
"The sequence of C. elegans cosmid CSOF7.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U41557; AAA83307.1; -.
InterPro; IPRO00087; Collagen.
SEQUENCE 589 AA: 55491 MW; 038508B5221A5EB9 CRC64;
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SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Complete proteome; Transport.
ATP-binding; Complete proteome; Transport.
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Last annotation update)
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InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR001140; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
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52.9%;
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Best Local Similarity 42.5%
Conservative
Processing
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Best Local Similarity 52.9
Matches 9; Conservative
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                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                Waterston R.
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MEDINE=21240220; PubMed=11342118;

MEDINE=21240220; PubMed=11342118;

MEDINE=21240220; PubMed=11342118;

Touhata K., Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;

Touhata K., Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;

Tohain of red seabream.";

Tohain of red seabream.";

LI Blochhin. Blophys. Acta 1517:323-326(2001).

REMBL, AB045975; BAB03287.1;

REMBL, AB045975; BAB03287.1;

RICEPPO; IPR000087; Collagen...

RICEPPO; IPR001230; Prid.collagen...

RICEPPO; IPR001230; Prenyltn.

RICEPPO; IPR001230; Prenyltn.

RICEPPO; IPR001230; Prenyltn.

RICEPPO; IPR001230; Prenyltn.

RICEPPO; IPR001230; Prenyltn.

RICEPPO; IPR001200; Prenyltn.

RICEPPO; IPR0012078; Fib_collagen...

RICEPPO; PR002078; Fib_collagen...

RICEPPO; PR002078; Fib_collagen...
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Barloy-Hubler F., Bowser L., Capela D., Gallbert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti psyma megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9888(2001).
EMBL, ARSIGA11.
Plasmid: Hypothetical protein: Complete proteome.
SEQUENCE 719 AA, 77245 MW; 045DDBCCB1691789 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                     Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _{\rm V} Match 29.8%; Score 51; DB 16; Length 719; Local Similarity 36.4%; Pred. No. 1.7e+02; hes 12; Conservative 5; Mismatches 12; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PRO-ALPHA 1 TYPE V/XI COLLAGEN.
COLV/XIA1.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN SMA0937.
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                                                                                                                                                                                          Rhizobium meliloti (Sinorhizobium meliloti).
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Collagen.
SEQUENCE 1820 AA; 181678 MW; 46E45EBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=1021;
MEDLINE=21396509; PubMed=11481432;
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SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
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MEDLINE-21083930; PubMed=11214968;
MEDLINE-21083930; PubMed=11214968;
MEDLINE-21083930; PubMed=11214968;
MARAINE T., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL: AP003015; BAB54678 1;
Plasmid; Complete proteome.
SEQUENCE 526 AA; 57216 MW; A20E4A4F13C98BD7 CRC64;
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                               Gaps
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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Oliver K.;
                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBL_TaxID=381;
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29.8%; Score 51; DB 13; Length 1820; 52.6%; Pred. No. 4.5e+02; tive 2; Mismatches 7; Indels (
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                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TEMBLrel. 18, Last annotation update)
REPLICATION PRIMASES.
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01-CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE HYPOTHETICAL 21.3 KDA PROTEIN.
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                                                                                                                                                                                                                                                          Rhizobium loti (Mesorhizobium loti).
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                                                                     EMBL, AL390114; CAC01975.2;
InterPro; IPR001313; PUM.
Pfam; PF00806; PUF; 6.
SMART; SM00025; Pumilio; 7.
SEQUENCE 1460 AA; 153236
                                                        3 GPTLRQWLAARAGPNGIEG 21
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Local Similarity 50.09
hes 15; Conservative
                             Conservative
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              Local Similarity
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  Query Match
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Q981N1;
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Length 1460;

DB 5;

Score 50.5;

29.5%;

Query Match

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                      Gaps
                                                                                                                                                                                                                                                                                                                                Streptomyces sp. PGA64.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=161235;
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STRAIN-MAFF303099;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metsa-Ketela M., Kantola J., Ylihonko K.;
"Cloning and Characterization of a Silent Angucycline-type Gene
"Cluster from a Rubronycin B Producing Streptomyces sp. PGA64.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY034378, AAK5721.1;
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SE00ENCE 250 AA, 26031 MW; 597EE6581FFFRC97 CRC64;
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37.9%; Pred. No. 4.1e+02;
tive 6; Mismatches 7; Indels
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SEQUENCE 268 AA; 27788 MW; 86698FFD04036653 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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Last annotation update)
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                                                                                 4 PILRQWLAARAGP----NGIEGPILRQW 27
                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19; Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE SHORT CHAIN DEHYDROGENASE
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002198; ADH_short.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP002996; BAB48502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 38.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=PGA64;
                                                                                                                                                                                                                                                                                            PGAK (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98LG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLL1036
                                                                                                                                                                                                               Q93LY8;
                                                                                                                                                                                              Q93LY8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           098LG1
                                                                                                                                                      RESULT 27
Q93LY8
                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             098LG
                                                                                               qq
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-RI;
MEDLINE-20036896; PubMed=10567266;
White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; FirmLoutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBL_TaxID=47716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blanco G., Patallo E.P., Brana A.F., Trefzer A., Bechthold A., Rohr J., Mendez C., Salas J.A.;
"Identification of a sugar flexible glycosyltransferase from Streptomyces olivaceus, the producer of the antintumor polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBI_TaxID=1299;
                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus
/ Match 29.2%; Score 50; DB 16; Length 268; Local Similarity 40.0%; Pred. No. 79; les 14; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 29.2%; Score 50; DB 16; Length 35 Local Similarity 34.2%; Pred. No. 1.1e+02; les 13; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 AA; 38454 MW; 31B01305A7B28694 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ELLORAMYCIN GLYCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| | || : |: || || || || 206 QGIADRFGPHRIDGPDYRQRGTEPAQPLSEAEFAAWLA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QWLAARAGPNGIEGPTLRQ-------WLA 29
                                                                                                                                                                           351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 AA
                                                                                                                                      8 QWLAARAGPNG------IEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571-1577(1999).
EMBL; AE001931; AAF10338.1; -.
TIGR; DR0759; -.
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           O9RWBO;
                                                                                                                                                                                                                                                                                                                                                                     Q9RWB0
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Matches
                                                                 Matches
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Q9RWB0
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Search completed: October 9, 2002, 09:03:02 Job time: 13.5494 secs

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            "Deoxysugar methylation during biosynthesis of the antitumor polyketide elloramycin by Strepomyces olivaceus: characterization of three methyltransferase genes."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                      "Identification of a sugar flexible glycosyltransferase from Streptomyces olivaceus, the producer of the antitumor polyketide elloramycin.";
                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                Length 384;
                                                                                                                                                                                                                                                                                                                              29.2%; Score 50; DB 2; Length 384
52.2%; Pred. No. 1.2e+02;
tive 2; Mismatches 9; Indels
                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ300305; CAC16413.1; -. EMBL; AJ309821; CAC32467.1; -. InterPro; IRR008905, Acetate_kin. PROSITE; PS01076; ACETATE_KINASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                384 AA; 39674 MW; A254F56B6ED12F2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    152 VRÓLLAERLGPAGSEPPPERYFL 174
                                                                                                                                                                                                                                                                                                                                                                                                     6 LRQWLAARAGPNGIEGPTLRQWL 28
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 52.29 nes 12; Conservative
                                                                                                      SEQUENCE FROM N.A.
Patallo E.P.;
                                                                                                                                                                                                                                                                              Transferase
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                  Matches
οy
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:50:51; Run on:

US-09-422-838C-23 Perfect score:

1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database :

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981. A\_Geneseq\_032802:\*

. DAT: \* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.

/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:\*
/SIDSI/gcddata/hold-rownong. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:\* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA2000.DAT /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999 12: 13: 14: 16: 16: 17: 19: 19: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:\*

TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid
TPO-mimetic peptid Thrombopoietin mim Thrombopoietin mim TPO-mimetic peptid Description SUMMARIES AAB17287 AAB17290 AAY96526 AAB17292 AAB17289 AAB17297 AAB17288 AAY96527 AAB17306 AAB17291 a 21 21 21 21 21 21 21 21 21 21 Query Match Length DB 100.0 100.0 100.0 91.2 86.3 86.0 85.1 84.8 84.8 Score 156 147.5 147.5 145.5 145 145 145 Result

-mimetic -mimetic	TPO-mimetic peptid TPO-mimetic peptid	o '	Thrombopoietin mim	1 .				Σ	Thrombopojetin mim	Synthetic TMP-TMP-	TMP-TMP-Fc protein	, E	ָ מַלְי	0	ic penti	pent i	c pepti			Ω	C		0	c pepti	nimetic	mimetic pepti	nimptio penti	io penti	ic penti	yclic or linear
296	AAB17301 AAB17303	AAB17307	AAY96524	52		AAB17281	CA	m	AAY96530	AAB17311	AAB16960	AAY96531	AAB17294	AAB17295	AAB17304	AAB17305	AAB17302	AAB17296	AAB17286	AAB16959	AAB17285	AAB16970	AAB16973	AAB16974	AAB16971	AAB16975	AAB16976	AAB17298	29	55
21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
36	36	36	300	36	41	42	42	42	43	w	569	$\omega$	37	38	39	39	40	42	29	268	78	53	31	31	29	58	53	36	36	36
84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	83.9	83.6	83.3	83.3	83.0	82.5	82.2	81.9	78.4	78.1	78.1	78.1	74.6	70.5	70.5	0.69	0.69	0.69
144	144	4 4		4	144	144	4	4.	4	144	Ţ.	14	•	14	•	42.	4	14	140.5	140	Ξ3	33.	ش	33.	27.		20.	$\vdash$	118	_
13	124	16 17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	б М	40	41	42	43	44	45

#### ALIGNMENTS

AAB17297 standard; Peptide; 32 AA. RESULT 1 AAB17297

AAB17297; 

(first entry) 31-OCT-2000 TPO-mimetic peptide sequence SEQ ID NO:353.

Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;

Synthetic.

asthma; thrombosis; pharmaceutical.

WO200024782-A2.

04-MAY-2000.

99WO-US25044. 25-OCT-1999;

23-OCT-1998;

98US-0105371. 99US-0428082. 22-OCT-1999;

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

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ine piesent invention describes composition of indeced (1) is:

Ex domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where F1 = an FC domain; X1 and X2 = are each
independently selected from -(L1)c-F1, -(L1)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
cc independently linkers; and a, b, c, d, e, and f = are each independently
cc or 1, provided that at least 1 of a and b is 1. The composition can
cartivities. DNAs, vectors and host cells from the present invention can
cc be used for producing pharmaceutical compositions. The compositions are
cc useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an FC domain (rather than a Fab domain) can provide a longer
cc half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443
cc sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                   The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 171; DB 21; Length 32;
Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 171; I Best Local Similarity 100.0%; Pred. No. 1.6 Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLROWLAARACPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                   Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..14
/label= TMP_1
15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96520 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19..32
/label= TMP_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96520
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A compound which binds to an mpl receptor comprising a thrombopoietin commetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], and the set amino acid sequences varying from at least constant of the set and the sequences varying from at least constant of the set and the sequences varying from at least constant of the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and the set and set and the set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and set and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                              Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 171; DB 21; 100.0%; Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin mimetic peptide compound 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96527 standard; peptide; 34 AA.
                                                                                                                                                                                                                                 Claim 16; Page 61; 91pp; English.
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/label= linker
21..34
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/label= TMP_2
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                                                 Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0
Best Local Similarity 100.0
Matches 32; Conservative
                                                                                           WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AA;
(AMGE-) AMGEN INC
                                                 Feige U,
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                 Liu C,
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Boone TC;

Cheetham J,

Liu C,

Feige U,

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production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                              Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO: TPO; CTLA4; minetic; IL-1: TNF: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                Length 34;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                       virus associated ITP, and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                              100.0%; Score 171; DB 21;
100.0%; Pred. No. 1.9e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:345.
                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                 3 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
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                                                                                                                     Claim 16; Page 64; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17289 standard; Peptide; 32
                                       Feige U, Cheetham J;
98US-0105348
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 32; Conservative
                                                          WPI; 2000-365108/31.
                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                            34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
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23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                            Sequence
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                                       Liu C,
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(1)-C-F1-(L1)c-F2-(L3)e-F3.

-(L1)-P1-L2)d-P2-(L3)e-F^3, or -(L1)c-F1-(L2)d-P2-(L3)e-F3-(L4)f-F4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB1803 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 156; DB 21;
Pred. No. 2.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
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                                                                                                                                                                        Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17288 standard; Peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                   WPI; 2000-350702/30.
                                                                                                                                   autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
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AAB17288
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RESULT 7
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                                                                                                            The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(L1)C-F1-(L2)d-P2.

(L1)C-P1-(L2)d-P2-(L3)e-P^3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2. P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or producing pharmaceutical from the present invention can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are be used for producing pharmaceutical composition. The compositions are useful for treating cancer asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein to AAA69556 and AAB16955 to AAB1803 represent uncelectide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        86.3%; Score 147.5; DB 2 93.8%; Pred. No. 3.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:343.
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAG-GGIEGPTLRQWLAARA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                        Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17287 standard; Peptide; 30 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                30; Conservative
                                                                 autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30
            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                               31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17287
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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c. (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b-F2-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-(X3)b-F3-
                                                                                                                                                                                                                                                                                                              The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease; cytostalic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoiethi; thrombopoieth; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 147; DB 21;
Pred. No. 4.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAG--GIEGPTLRQWLAARA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone TC;
                                                                                                                                                                                                           Example 1; Page 315-316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17290 standard; Peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.0%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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The present invention describes composition of matter (I) comprising an (X1)a-P1-(X2)b, where F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

(X1)a-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (MPC-P1-(L3)e-P3-(L3)e-P3-(L4)f-P4 (MPC-P1-(L3)e-P3-(L3)e-P3-(L4)f-P4 (MPC-P1-(L3)e-P3-(L3)e-P3-(L4)f-P4 (MPC-P1-(L3)e-P3-(L3)e-P3-(L4)f-P4 (MPC-P1-(L3)e-P3-(L3)e-P3-(L4)f-P4 (MPC-P1-(L3)e-P3-(L4)f-P4 (MPC-P3-(L3)e-P3-(L4)f-P4 (MPC-P3-(L3)e-P3-(L4)f-P4 (MPC-P3-(L3)e-P3-(L4)f-P4 (MPC-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4 (MPC-P3-(L3)e-P3-(L4)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autofimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor: erythropoietin; thrombopoietin; interleukin 1; vactotoxic; T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 145.5; DB 21; Length 33;
Pred. No. 7.9e-14;
0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.96
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLROWLAARA-GPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Cheetham J, Boone TC;
                                                                          Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17291 standard; Peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.1%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune diseases -
                              autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: FC domain, where FI = an FC domain, XI and X2 = are each independently selected from -(L1)C-PI-(L1)G-P2, (L3)G-P2, (L4)F-P4, (L1)C-PI-(L2)G-P2, (L3)G-P3, or -(L1)C-PI-(L2)G-P2-(L3)G-P3-(L4)F-P4, where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a and b is 1. The composition can have eytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an FC domain (rather than a Fab domain) can provide a longer can incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443

to AAA69526 and AAB16955 to AAB180303 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%; Score 145; DB 21; Length 34;
88.2%; Pred. No. 9.6e-14;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARA--GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLROWLAARAGGGGGGGIEGPTLROWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                  Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 324; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17306 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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The formation, pharmacologically active peptides, and linkers. Where II is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
(L1)c-F1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                     The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.8%; Score 145; DB 21; Length 36; 83.3%; Pred. No. 1e-13; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTIRQWIAARAGGGGGGGGGGTGPTIRQWIAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin mimetic peptide compound 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96526 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..14
/label= TMP_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                   4 ;
                                                                                                                                                                                                                              Score 145; DB 21; Length 36;
Pred. No. 1e-13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      1 IEGPTLROWLAARA----GPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                1 IEGPTLROWLAARAGGGNGSGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                        AAB17292 standard; Peptide; 35 AA.
                   Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Cheetham J,
                                                                                                                                                                                                                                84.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105371, 99US-0428082.
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases
                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
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                                                                                                                                                                                                                                                  30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                          AAB17292;
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                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                     Matches
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Example 1; Page 317-318; 608pp; English.

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The present invention describes composition of matter (1) comprising an Fc domain, planmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1,C-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3, or -(L1)C-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4 where P1; P2, P3, and P4 = are each independently sequences of planmacologically active peptides; L1, L2, L3, and L4 = are each independently (0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive contivities. DNAs, vectors and host cells from the present invention can be usef for producing pharmaceutical compositions. The compositions are usef for producing pharmaceutical compositions. The compositions are usef for producing pharmaceutical compositions. The compositions are usef for producing pharmaceutical compositions. The compositions are usef for producing pharmaceutical compositions. The compositions are usef for producing pharmaceutical transfer. AAA69443

The use of an Fc domain (rather than a Fab domain) can provide a longer complement fixation, and possibly placental transfer. AAA69443

TO AAA69526 and AAB16955 to AAB18003 represent uncleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              .5;
1.2e-13;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 144.5; D
Pred. No. 1.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARA---GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGIEGPTLRQWLAARA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB16963 standard; Protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       84.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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The present invention describes composition of matter (I) comprising an

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Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2.

(L3)e-P3. and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
independently linkers; and a, b, c, d, e, and f = are each independently
independently linkers; and a, b, c, d, e, and f = are each independently
be used for provided that at least 1 of a and b is 1. The composition can
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Feb domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443
                                                                                                                                                                                                                                                                                          A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.4e-13;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17293 standard; Peptide; 36 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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        Qγ
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us-09-422-838c-23.rag

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independently selected from -(LI)c-Pl. -(LI)c-Pl-(L2)d-P2.

-(LI)c-Pl-(L2)d-P2-(L3)e-P-3, or -(LI)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

-(L1)c-Pl-(L2)d-P2-(L3)e-P-3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

-(L1)c-Pl-(L2)d-P2-(L3)e-P-3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

-(L2)d-P2-(L3)e-P3-(L3)d-P3-(L3)d-P3-(L4)f-P4

-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L4)f-P4

-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L4)f-P4

-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EFO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoieth; thrombopoieth; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%; Score 144; DB 21; Length 36; 83.3%; Pred. No. 1.4e-13; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17301 standard; Peptide; 36 AA
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can useful for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAAA69526 and AAB16955 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L1)c-F1-(L2)d-F2. (-1)a-F1-(L2)d-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F2-(L3)a-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 144; DB 21; Length 36; Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17303 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
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independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18903 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc domain, pharmacologically active peptides, and linkers. Where [T] is:

(X1)a-Fl-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each independently selected from -(L1)C-Pl-(L1)G-P2, -(L3)G-P2, -(L3)G-P2, -(L3)G-P2, -(L3)G-P2, -(L3)G-P2, -(L3)G-P2, -(L3)G-P2, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(L3)G-P3, -(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer and fall-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin, mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2-x_{-1}, x_2-x_{-1},
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                               Length 36;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                             2;
                                                                                                                                                                                               DB 21;
                                                                                                                                                                                              84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.4e-13;
                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin mimetic peptide compound 4.
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⁄label≖ linker
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X_2-x_1_3, X_2-x_1_4, X_1-x_1_0, X_1-x_1_1, X_1-x_1_2, X_1-x_1_3, and X_1-x_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; or E; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = G, N, Or E; X_9 = W, Y or F; X_1_0 = L, I, V, A, F, W, or K; X_1_1 = A, I, V, L, F, G, S, or Q; X_1_1 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, Comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the C-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. applacttc anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
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                                                                                                                                                                                                                                                         84.2%; Score 144; DB 21; Length 36;
83.3%; Pred. No. 1.4e-13;
Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound 5.
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/label= TMP_1
9..31
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/label= linker
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/label= TMP_2
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Matches 30; Conservative
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                                                                                                                                                                                                                                36 AA;
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Modified-site
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mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2, x_2-x_1_1, x_2-x_1_2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-2, x_1-x_1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "optionally linked to an Fc molecule"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 144; DB 21;
Pred. No. 1.4e-13;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin mimetic peptide compound 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96525 standard; peptide; 36 AA.
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/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 84.2%;
Best Local Similarity 83.3%;
Matches 30; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024770-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Thrombopoietic peptides which activate mpl receptors and increase the

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Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                     2; Indels
                                                                                                                                                      virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                     Score 144; DB 21;
Pred. No. 1.4e-13;
                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGGGGGFTLRQWLAARA 36
                                                                                                                                                                                                                    1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound 9.
diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                         AAY96528 standard; peptide; 41 AA
               Claim 16; Page 62; 91pp; English
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/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                        28..41
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                  /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Cheetham J;
                                                                                                                                                                                      84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105348
                                                                                                                                                                                                                                                                                                        04-SEP-2000 (first entry)
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365108/31.
                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMGE-) AMGEN INC.
                                                                                                                                                                      36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                         AAY96528;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                           RESULT 20
                                                                                                                                                                                                                                                                   AAY96528
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 - X_1 = 0, X_2 - X_1 = 0, X_2 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                 production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin i; cytotoxic real lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.2%; Score 144; DB 21; Length 41; 83.3%; Pred. No. 1.6e-13; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 IECPTLROWLAARAGGGGGGGGGTEGPTLROWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17281 standard; Peptide; 42 AA
                                                                                                     Claim 16; Paqe 65; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.35
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where: FI = an FC domain; Al and X2 = are each independently selected from -(L1)C-F1-(L2)C-F2-(L3)C-F3-(L3)C-F3, or -(L1)C-F1-(L2)d-F2-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)C-F3-(L3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF: antagonist; MMF; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloprofeinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 144; DB 21; Length 42; Pred. No. 1.7e-13; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17282 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          84.28;
83.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.2
Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                       42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
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22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 22
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
of or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an FC domain (rather than a Fab domain) can provide a longer
naif-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443
cto AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; mMP: inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%; Score 144; DB 21;
83.3%; Pred. No. 1.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17308 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044.
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99US-0428082.
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Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 AA;
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us-09-422-838c-23.rag

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The formation, pharmacologically active peptides, and linkers. Where It is command, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-FI-(XX)b, where: FI = an Fc domain; XI and X2 = are each independently selected from -(LI)c-PI-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3
The present invention describes composition of matter (I) comprising an
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42 AA; Sednence

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Gaps
                            4 ;
84.2%; Score 144; DB 21; Length 42; 83.3%; Pred. No. 1.7e-13;
                          Indels
                          5;
                                                                 1 IEGPTLROWLAARA----GPNGIEGPTLROWLAARA 32
                         0; Mismatches
                          30; Conservative
              Best Local Similarity
 Query Match
                         Matches
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AAY96530 RESULT

Ą AAY96530 standard; Protein; 42

AAY96530;

04-SEP-2000 (first entry)

Thrombopoietin mimetic peptide.

Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.

Synthetic.

WO200024770-A2.

04-MAY-2000.

99WO-US24834. 22-OCT-1999;

98US-0105348 23-OCT-1998;

(AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31. N-PSDB; AAA29225.

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Example 2A; Page 48; 91pp; English.

gene encoding a thrombopoietin mimetic peptide (TMP), which was then fused in-frame to the Fc region of the human IgGl chain (see AAY96529). A compound which binds to an mpl receptor comprising a TMP dimer joined by a linker [TMP\_1 (L\_1)\_nTMP\_2], is new. TMP\_1 and TMP\_2 are amino acid sequences varying from at least 10 to 14 residues in Overlapping oligonucleotides were used to construct a synthetic 

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length comprising X.2-X.1_0, X.2-X.1_1, X.2-X.1_2, X.2-X.1_3, X.2-X.1_4, X.1-X.1_2, X.1-X.1_3, and X.1-X.1_4, X.1=1, A, X.1-X.1_2, X.1-X.1_3, and X.1-X.1_4, X.1=1, A, X.2-X.1_5, and X.1-X.1_4, X.1=1, A, X.2-X.1_5, and X.1-X.1_4, X.1=1, A, X.2-X.1_5, and X.1-X.1_4, X.1=1, A, X.4=P; X.2=T or S; X.6=L, I, V, A, F; M, Or F; X.2=0, N, or E; X.9=W, Y or F; X.1_0=L, I, V, A, F; M, or K; X.1_1=A, I, V, L, F, S, T, K, H, or E; X.1_2=A, I, V, L, F, S, T, K, H, or E; X.1_2=A, I, V, L, F, T, R, E, or G; L.1=1inker comprising 1 to 20 amino acids; and n=0 or 1. The compounds bind to and activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoietin. The precursors (e.g. megakaryocytes) in a mammal, which is useful for thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (x1)a\cdot F(1-(x2)b), where: F1 = an Fc domain; x1 and x2 = are each independently selected from - (L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autofimmune disease; cytostatic; antiasthmatic; thrombolytic; WBCF; immunosuppressive; BPO; CTLA4; minetic; IL-1; TWF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic TMP-TmP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                                                                                                                                                              Score 144; DB 21; Length 42;
Pred. No. 1.7e-13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                7 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 331; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17311 standard; Peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                  84.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                              42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17311;
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ношо
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where Pl, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently of or l, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (x,1)a+\Gamma(x,2)b, where: FI = an FC domain; XI and X2 = are each independently selected from - (Li)c-Pi, -(Li)c-Pi-(L2)d-P2, -(L3)d-P2-(L3)e-P3, or -(Li)c-Pi-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease; cytostalic; antiathmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; thrombolytic; VEGF; wMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                         Length 60;
                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                      84.2%; Score 144; DB 21;
83.3%; Pred. No. 2.5e-13;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                         2 IEGPTLRQWLAARAGGGGGGGGGGFTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMP-TMP-Fc protein sequence SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB16960 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                    Query Match 84.2
Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                  60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/
N-PSDB; AAA69446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                    Seguence
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where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma. Hrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18035 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A compound which binds to an mpl receptor comprising a thrombopoletin mimetic peptide (TMP) dimer joined by a linker [TMP]-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2^-X_1^-0, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-1, X_2^-X_1^-2, X_2^-X_1^-3, and X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-X_1^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3, X_2^-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 84.2%; Score 144; DB 21; Length 269; Local Similarity 83.3%; Pred. No. 1.4e-12; les 30; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IEGPILRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of platelets or platelet prediseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IgG1 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96531 standard; Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA29229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024770-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96531
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                thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b. where F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1. (L2)c-P2. (L3)c-P2. (L3)c-P2. (L3)c-P3, or -(L1)c-P1. (L2)d-P2-(L3)e-P3. (L3)c-P1. (L2)d-P2-(L3)e-P3. (L3)c-P1. (L2)d-P2-(L3)e-P3. (L3)c-P1. (L2)d-P2-(L3)e-P3-(L4)f-P4. There is an each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
activate the c-Mpl receptor which mediates the activity of endogenous
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                           Length 269;
                                                                                                                                                                                                                        Indels
                                                                                             virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                        Score 144; DB 21; I
Pred. No. 1.4e-12;
. --+-hos 2;
                                                                                                                                                                                                                                                                                   234 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 269
                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boone TC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                        AAB17294 standard; Peptide; 37
                                                                                                                                                                           84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044
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99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000 (first entry)
                                                                                                                                                                                                                        30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                       269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
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                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17294;
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                    RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                  AAB17294
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer

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The present invention describes composition of matter (1) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a<sup>-</sup>F1<sup>-</sup>(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2.

(L1)C-P1-(L2)d-P2.

(L3)d-P2-(L3)d-P3, or -(L1)C-P1, -(L2)d-P2-(L3)e-P3-(L4)F-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inters; and a, b, c, d, e, and f = are each independently contingent in the composition can be explosited, antiasthmatic, thrombolytic and immunosuppressive cortivities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO: TPO; CTLA4; mimetic; IL-1; NF; antagonist; MMP; inhibitor; erythropoicatin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                            5,
                                                                                                                                        83.9%; Score 143.5; DB 21; Length 37;
                                                                                                                                                                                Indels
                                                                                                                                        ,7e-13;
2;
                                                                                                                                                                                                                      1 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                1 IEGPTLROWLAARAGGGGGGGGGGIEGPTLROWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                0; Mismatches
                                                                                                                                                              Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                 AAB17295 standard; Peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                           81.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases
                                                                                                                                                       Local Similarity
nes 30; Conserv
                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
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                                                                                                37
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                                                                                                                                                                                                                                                                                                                                                                                                         AAB17295;
                                                                                                   Sequence
                                                                                                                                        Query Match
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                              AAB17295
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re domain, pharmacologically active peptides, and linkers. Where II is:

(X1)a-F1-(X3)b, where: F1 = an Fc domain; X1 and X2 = are each

(X1)a-F1-(X3)b, where: F1 = an Fc domain; X1 and X2 = are each

(L1)c-P1-(L2)d-P2-(L3)e-P-3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

where P1, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently

of or provided that at least 1 of a and b is 1. The composition can

have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

activities. DNAs, vectors and host cells from the present invention can

be used for producing pharmaceutical compositions. The compositions are

useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer

half-life or incorporate functions such as Fc receptor binding, protein

A binding, complement fixation, and possibly placental transfer. AAA69443

to AAA69526 and AAB18955 to AAB1803 represent invention amino acid

sequences used in the exemplification of the present invention.
to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an .Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                9;
                                                                                                         Length 38;
                                                                                                                                                  2; Indels
                                                                                                     Score 143; DB 21;
Pred. No. 2.1e-13;
0; Mismatches 2;
                                                                                                                                                                                       1 IEGPTLROWLAARA-----GPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                   AAB17304 standard; Peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J,
                                                                                                     83.6%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                     Query Match 83.6
Best Local Similarity 78.9
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                          AAB17304;
                                                                Sequence
                                                                                                                                                                                                                                                                                          RESULT 30
AAB17304
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Gaps
                                                             7;
                                    DB 21; Length 39;
                                                             Indels
                                  Score 142.5; DB 21;
Pred. No. 2.5e-13;
0; Mismatches 2;
                                                                                     1 IEGPTLRQWLAARA-----GPNGIEGPTLRQWLAARA 32
                                                                                                     1 IEGPTLRQWLAARAGGGKPEGGGGIEGPTLRQWLAARA 39
                                    83.3%;
76.9%;
                                              Local Similarity 76.9 tes 30; Conservative
            39 AA;
            Sequence
                                     Query Match
                                                             Matches
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Search completed: October 9, 2002, 08:58:55 Job time: 15.3888 secs

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Sequence 231, App
Sequence 231, App
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Sequence 131, App
Sequence 193, App
Sequence 193, App
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Sequence 193, App
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17, Appl
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185, App
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186, Appl
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                                                                                                          9, 2002, 08:55:27; Search time 5.32084 Seconds (without alignments) 146.898 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
Sequence
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Copyright (c) 1993 - 2002 Compugen Ltd.
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1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32
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US-09-244-298A-231
US-08-754-640-133
US-08-754-640-133
US-08-973-225-133
US-08-973-225-193
US-09-244-298A-133
US-09-244-298A-193
US-09-244-298A-193
US-09-244-298A-193
US-09-244-298A-193
US-09-516-704-193
US-08-764-640-175
US-08-973-225-185
US-08-973-225-185
US-09-244-298A-17
US-08-973-225-185
US-08-973-225-185
US-09-244-298A-17
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S-08-973-225-194
S-08-973-225-220
S-09-244-298A-18
S-09-244-298A-194
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US-09-516-704-17
US-09-516-704-185
US-08-764-640-18
                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                  231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
Sequence:
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Sequence 232, Sequence 194, A Sequence 195, Sequence 195, Sequence 195, Sequence 199, Sequence 199, Sequence 199, Sequence 199, Sequence 200, Sequence 200, Sequence 200, Sequence 215, Sequence 200, Sequence 215, Sequence 200, Sequence 215, Sequence 200, Sequence 215, Sequence 200, Sequence 215,	BIND TO A
3 US-09-244-298A-232 4 US-09-516-704-18 4 US-09-516-704-194 US-09-516-704-194 2 US-08-764-640-195 2 US-08-764-640-195 3 US-08-973-225-195 3 US-08-973-225-195 3 US-09-244-298A-195 4 US-09-216-704-195 4 US-09-516-704-195 5 US-08-764-640-200 5 US-08-764-640-200 5 US-08-764-640-200 7 US-08-764-640-200 7 US-08-764-640-200 8 US-08-764-640-200 9 US-08-764-640-200 9 US-08-764-640-200 9 US-08-764-640-200 9 US-08-764-640-200 9 US-08-973-225-196	IGNMENTS  Oriappan R.  COMPOUNDS THAT  Box 13398  3, Version #1.30  140
4 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 6 4 2 2 . 7 1 1 7 1 1 7 1 1 1 1 1 1 1 1 1 1 1 1	pplication 151 583768 WIDN: Dower, Will Sarrett, Will Will Sarrett, Will Will Sarrett, Will Will Sarrett, Will Will Sarrett, Will Will Sarrett, Will Will Sarrett, Will Will Will Sarrett, Will Will Will Will Will Will Will Wil
28 30 31 31 31 31 31 31 31 31 31 44 40 60 60 60 60 60 60 60 60 60 60 60 60 60	SEGULT 1 US-08-764-640-231 Sequence 231, Applic Patent No. 5869451 5 GENERAL INFORMATION APPLICANT: DOWER APPLICANT: Gates APPLICANT: Gates APPLICANT: Gates APPLICANT: Gates APPLICANT: Gates APPLICANT: Gates APPLICANT: Balas APPLICANT: Balas APPLICANT: Wagst APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: Belas APPLICANT: ALD COUNTRY: NG COUNTRY: NG COUNTRY: LIN COUNTRY: LIN APPLICATION NUM FILING DATE: 1 CLASSIFICATION NUM APPLICATION NUM APPLICATION NUM FILING DATE: 1 CLASSIFICATION NUM APPLICATION PLICANT APPL

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                           45.9%; Score 78.5; DB 2; Length 25;
46.4%; Pred. No. 0.00027;
tive 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING STEEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 13
OTHER INFORMATION: /product= "Ava"
                                    ; OTHER INFORMATION: /product= "Ava"
US-08-764-640-231
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REGISTRATION: NUMBER: 36,392
REFRENCE/COCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEHONDE: 919-48-1000
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       2 EGPTLRQWLAARAGPNGIEGPTLRQWLA 29
                                                                                                                                                                                                2 DGPTLREWISFXA-----DGPTLREWIS 24
                                                                                                                                                                                                                                                                                                         Sequence 231, Application US/09244298A Patent No. 6121238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                  Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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N: 514
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LOCATION: 13
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amino acid
Modified-site
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                                                                                                 Query Match
Best Local Similarity 46.4%
Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-09-244-298A-231
  NAME/KEY:
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APPLICANT:
                      LOCATION:
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Podduturi, Surekha
TITLE OF INVENTION: PEFTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPFATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: /product= "Ava"; US-09-516-704-231
                                                                                                                                                                                                                                                                                         Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EGPTLRQWLAARAGPNGIEGPTLRQWLA 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
:||||||:|:: | :|||||:|::
2 DGPTLREWISFXA----DGPTLREWIS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
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Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
                                                                                                                                ; Sequence 231, Application US/09516704; Patent No. 6251864
; GENERAL INFORMATION:
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                                                                                                                                                                                              APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.9%
Best Local Similarity 46.4%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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P.O. Box 13398
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APPLICATION NUMBER: US/08/973,225A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 13, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                           Research Triangle Park
                                                                                                                                                                                                                                                                                            FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUBIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                            Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 27709
COMPUTER READABLE FORM:
    NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 amino acids
                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                      COUNTRY: US
                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-764-640-193
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                                                                               CITY: F
                                                               STREET:
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                                                                                                                                                                                              APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
42.7%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION WIBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                            E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                         Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                Wagstrom, Christopher R. Hendren, Richard W.
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Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                       Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HTUDIGC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                   CITY: Research Triangle Park
Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                         Gates, Christian
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ADDRESSEE: Glaxo Wel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-764-640-13
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                     STATE:
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Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.7%; Score 73; DB 2; Length 14; Best Local Similarity 100.0%; Pred. No. 0.00075; Matches 14; Conservative 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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; Sequence 193, Application US/09244298A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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US-09-244-298A-193
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  US-08-973-225-193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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Wrighton, Nicholas C.
INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                             Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                      0; · Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMFUTER: FROM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                        Ouery Match 42.7%; Score 73; DB 3; Lk Best Local Similarity 100.0%; Pred. No. 0.00075; Matches 14; Conservative 0; Mismatches 0;
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HINDLEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HINDIEC, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/OCCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Stewen E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 193, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
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  Length 14;
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APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
Score 73; DB 3; Le;
Pred. No. 0.00075;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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APPLICANT: Barrett, Ronald W.
APPLICANT: CWirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W. APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun TITLE OF INVENTION: RECEPTOR TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           Sequence 13, Application US/09244298A patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Triangle Park
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
  Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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LENGTH: 14 amino acids
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US-09-516-704-193
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                          APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.00075; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
                                                                                          Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-48-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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Patent No. 6251864
GENERAL INFORMATION:
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Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                   Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                      Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           USA
Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       27709
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.7%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.00075; tive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                        ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PK3281 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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Hendren, Richard W.
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 193, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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NUMBER OF SEOUENCES: 244
                                                                                                                                 COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
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                     CORRESPONDENCE ADDRESS:
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ULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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NUMBER OF SEQUENCES: 244
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LENGTH: 15 amino acids
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                    Query Match
Best Local Similarity 100.
Matches 14; Conservative
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                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                       Yin, Qun
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    TYPE: amino acid
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                    STRANDEDNESS
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ZIP: 27709
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US-08-764-640-185
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APPLICANT:
APPLICANT:
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US-08-764-640-17
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                          42.7%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.00075; tive 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Peter J.
APPLICANT: Ragstrom, Christopher R.
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CITY: Research Triangle Park
                                                       ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-516-704-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08764640 Patent No. 5869451 Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: HIUDIEC, ROBERT T.
REGISTATION UNBER: 36,392
REERENCE/DOCKET MUMBER: PK32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glaxo Wellcome
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 244
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Best Local Similarity 100.
Matches 14; Conservative
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APPLICANT:
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                                            Gaps
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42.7%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.00081;
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                            0; Mismatches
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Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REPERENCE/DOCKET NUMBER: P83281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            . Sequence 185, Application US/08764640
patent No. 5869451
Patent No. 5869451 5837683
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Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                              Barrett, Ronald W. Cwirla, Steven E. Gates, Christian
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Dower, William J.
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MEDIUM TYPE: Floppy disk
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LENGTH: 15 amino acids
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CITY: Research Triangle Park
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
                                           NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                           Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOLETIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: #Unblec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECHMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA

APPLICATION NUMBER: 05/08/973,225A

FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                 Sequence 17, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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                                                                                                                                                                                    Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                  Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                        SEOUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                        NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-973-225-185
                 US-08-973-225-17
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RESULT 14
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Gaps
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                                             TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.00081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
                                                                                                                                                           P.O. Box 13398
                                                                     THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                      STREET: Five Moore Drive, P.(CITY: Research Triangle Park
                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 17, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
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Podduturi, Surekha
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Hendren, Richard W.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEGGENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.7%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.00081; Live 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATINE SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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APPLICATION NUMBER: US/09/244,298A
FILLING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 185, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                               NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: HIUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 14; Conservative
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
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COUNTRY: US,
ZIP: 27709
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COMPUTER:
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPFIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.7%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                                                    Length 15;
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 27709
COMPUTER: PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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0.00081;
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100.0%; Pred. No. v.
... Q; Mismatches
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-516-704-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 17:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 244
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Best Local Similarity 100.(
Matches 14; Conservative
                                                                                                                                                                       Local Similarity 100.
Les 14; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                           ; MOLECULE TYPE: peptide US-09-244-298A-185
                                                                                                                                                                                                                                                      2 IEGPTLRQWLAARA 15
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                                                                                                                                                                                                                                  1 IEGPTLRQWLAARA 14
                LENGTH: 15 amino TYPE: amino acid STRANDEDNESS:
                                                                             linear
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                                                                                                                                                          Query Match
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: PECEPTOR
NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.7%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 1.DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    SEE: Glaxo Wellcome
: Five Moore Drive, P.O. Box 13398
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: /product= "Beta-ala" US-08-764-640-18
        Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 194, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
                                                                  Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 amino acids
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                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                          APPLICANT:
APPLICANT:
                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                              COUNTRY:
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APPLICANT:
                                                                  APPLICANT:
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                                                                                                                                                                                                                                                            STATE:
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()
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                      Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGIC: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                      Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                        Sequence 185, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                 APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 27709
COMPUTER READABLE FORM:
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Matches 14; Conservative
1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 27709
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                                                                        US-09-516-704-185
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APPLICANT:
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APPLICANT:
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Gaps ; 0

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.00087;
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                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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Five Moore Drive, P.O. Box 13398
                                  STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Podduturi, Surekha
Yin, Qun
                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIGG., RODERT 7.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
                  Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.7%
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 16 amino acids
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                                                                                                                      COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
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ZIP: 27709
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                                                                                              COUNTRY: U
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US-08-764-640-232
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                  ADDRESSEE:
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                                                                      STATE:
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Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 42.7%; Score 73; DB 2; Le Best Local Similarity 100.0%; Pred. No. 0.00087; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Research Triangle Park
APPLICATION NUMBER: US/08/764,640 FILLING DATE: 11-DEC-1996 CLASSIFICATION: 514
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Haselden, Sherril S.
Mattheakis, Larry C.
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 18, Application US/08973225A; Patent No. 6083913; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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                                                                                                                                      REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 232
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                                                                                                                                                                                                                                                                                         TYPE: amino acid
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US-08-973-225-18
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RESULT 26
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Mattheakis, Larry C.
Schatz, Peter J.
Wagstron, Christopher R.
Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                          Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.7%; Score 73; DB 3; Length 16; Best Local Similarity 100.0%; Pred. No. 0.00087; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSER: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                          OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                Query Match
42.7%; Score 73; DB 3; Lk
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3065USW TELECOMBNIACATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                       Sequence 194, Application US/08973225A
Patent No. 6083933
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                  NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duffin, David J. Gates, Christian
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                                                                                                                                                                                                                                        1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 27709
                                                                                                                                                                                                                                                                                                                  RESULT 24
US-08-973-225-194
FEATURE:
                                                                                               US-08-973-225-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09244298A
Patent No. 612138
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/973,225A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HIUDIGC, ROBERT T,
REGISTRATION NUMBER: 36,392
                     Sequence 220, Application US/08973225A; Patent No. 6083913; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagstrom, Christopher R. Hendren, Richard W.
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Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                      Wrighton, Nicholas C
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                          APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 27709
US-08-973-225-220
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APPLICANT:
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RESULT 28
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                                                                                                                             ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ); NAME/KEY: Modified-site
); LOCATION: 15
); OTHER INFORMATION: /product= "Beta-ala"
US-09-244-298A-18
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W. APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha
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                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
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APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARA 14
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; tive 0; Mismatches 0; Indels
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OCHERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Barrett, Ronald W.

Cwirla, Steven E.

Gates, Christian

Schatz, Peter J.

Balasubramanian, Palaniappan
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APPLICATION NUMBER: US/09/244,298A
FILLING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 232, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-09-244-298A-194
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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COUNTRY: USA
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                     27709
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                           Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.00087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                    42.7%; Score 73; DB 4; L
100.0%; Pred. No. 0.00087;
tive 0; Mismatches 0;
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Balasubramanian, Palaniappan
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APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 9, 2002, 09:06:29
                                                                                                                                                                                                                                    RESULT 30
US-09-516-704-194
: Sequence 194, Application US/09516704
: Patent No. 6251864
: GENERAL INFORMATION:
: APPLICANT: Dower, William J.
Barrett, Ronald W.
CWAITIA, Steven E.
Gates, Christian
'''' Pater J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-Mar-2000
CLASSIFICATION: <UDANOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                    Query Match 42.7
Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.0
Matches 14, Conservative
                                                                                                                                                          1 IEGPTLRQWLAARA 14
                                                                                                                                     1 IEGPTLROWLAARA 14
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              US-09-516-704-18
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                                                                                                                                                                                                                                             42.7%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.00087; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSES: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deprince, Randolph B.
Podduturi, Surekha
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-516-704-18
Sequence 18, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
Barrett, Ronald W.
CWIRla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 244
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                   LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                         STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-233
                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 29
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:54:17; Search time 7.19438 Seconds Run on:

(without alignments)
427.397 Million cell updates/sec

US-09-422-838C-23 171 1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32 score: Sednence: Perfect

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 segs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

PIR\_71:\* Database

pir1:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

•	Description	conserved hypothet	cation efflux fami	sorbitol oxidase	o.	probable pyruvate	probable membrane	probable UV damage	spike glycoprotein	disintegrin-like m	conserved hypothet	familial Alzheime	hypothetical prote	hypothetical prote	- 1	hypothetical prote	transport protein	SITS-binding prote	conserved hypothet	nitric-oxide reduc	conserved hypothet	3-methyl-2-oxobuta	2-oxoisovalerate d	probable trna meth	photosystem II chl	hypothetical prote		transcription acti	O)	hypothetical prote
SUMMAKIES	QI	B71325	F87286	JW0076	D85818	B83471	AG0147	C75350	VGVNCV	602390	T35254	S65358	F83487	G72680	D70601	T29299	C83221	S04987	B95325	AF3634	C75479	DEPSXA	C83365	T38324	S06469	T20454	C70559	A36925	308	н98202
	DB	7	7	7	7	N	7	7	-	7	7	7	7	7	~	7	7		7	7	~	<del>, -</del>	7	7	7	7	7	7	7	7
	Length	683	361	420	346	1095	296	326	524	814	396	440	371	281	306	589	009	697	719	150	351	410	410	415	460	472	904	333	341	355
æ	Query Match	36.8	32.7	2	31.6	31.6	31.0	31.0	31.0	30.7	30.4	30.4	30.1	29.8	29.8	29.8	29.8	29.8	29.8	29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.5	28.9	28.9	28.9
	Score	63	99	55	54	54	53	53	'n	52.5	52	52	51.5	51	51	51	51	51	. 51	20	20	20	20	20	20	20	20	6	49.5	
	Result No.	-	2	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	pyruvate dehydroge	<pre>di-N-acetylchitobi</pre>	tyrosine-specific	probable permease	photosystem II chl	photosystem II CP4	alpha subunit of c	probable sensor/re	collagen alpha 1(X	collagen alpha 2 f	glutathione S-tran	hypothetical prote	excisionase - phag	excisionase - phag	excisionase [impor
T22896	DEBSPF	A44102	AD0748	A83032	S42647	AD2342	150630	A83324	S18251	A43426	C87617	T48219	RSBPXL	506533	A90729
7	٦	C	7	7	7	7	7	7	7	7	~	7	Ţ	~	7
214	369	382	403	425	459	459	735	992	1024	3198	209	493	72	72	72
28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.4	28.4	28.1	28.1	28.1
49	49	49	49	49	49	49	49	49	49	49	48.5	48.5	48	48	48

## ALIGNMENTS

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C) Species: Treponema pallidum subsp. pallidum (syphilis spirochete C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999 C; Accession. B71325 R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998 A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Reference number: A71250; MUID:98332770 A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-683 <COL>
A; Cross-references: GB:AE001220; GB:AE000520; NID:93322705; PIDN:AAC65409.1; PID:9332 A; Chenetics: A; Chenetics: A; Chenetics: A; Chenetics: A; Chenetics: A; Chenetics: A; Chenetics: A; Chenetics: A; Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenetics: Chenet
RESULT 1
B71325
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0; 36.8%; Score 63; DB 2; Length 683; ilarity 46.4%; Pred. No. 2; Conservative 3; Mismatches 12; Indels Local Similarity nes 13; Conserva Query Match Best Loc Matches

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Gaps

4 PTLRQWLAARAGPNGIEGPTLRQWLAAR 31 δŏ

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RESULT 2 F87286

cation efflux family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001
C;Accession: F87286
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.;Laub, M.T.; DeBsoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Teference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87286

A; Status: preliminary A; Molecule type: DNA A; Residues: 1-361 <STO>

A; Cross-references: GB: AE005673; NID: 913421446; PIDN: AAK22290.1; GSPDB: GN00148 C; Genetics:

A; Gene: CC0303

Score 56; DB 2; Length 361; Pred. No. 8.2; 32.7%; 54.5%; Query Match Best Local Similarity

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C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Accession: AGO147
R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Ohillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. Nature 413, 523-527, 2001
A; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Artitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: ABO001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                     GB:AE004091; NID:99947339; PIDN:AAG04789.1; GSPDB:GN
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   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337 A;Accession: B83471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.D.; Dodson,
T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable UV damage endonuclease - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: C75350
R;White. O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC90042.1; PID:g15979263; GSPDB:GN00175
C;Genetics:
A;Gene: YP01203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein YPO1203 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                    ore 54; DB 2; Length 1095;
ed. No. 46;
Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 2; Length 296;
Pred. No. 16;
1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 326;
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 IAGVLLESFLAIR----GHALPTLROWAAASA 76
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGPNGIEGP 22
                                                                                                          A Status: preliminary
A Molecule type: DNA
A Residues: 1-1095 <STO>
A Cross-references: GB:AE004569; GE
A Experimental source: strain PAO1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%;
45.5%;
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Best Local Similarity 50.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:AE002022;
A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.65
Best Local Similarity 45.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-326 <WHI>
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                                                                                                                                                                                                                                                                                                                                                A; Gene: PA1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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                                                                                                                                                                                                                                                                                                                            Sorbitol oxidase (EC 1.-.-.) - Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Streptomyces sp.

C;Species: Julian Blook Stression 10-Jul-1998 #text_change 24-Oct-2000

R;Hiraga, K; Eto, T.; Yoshioka, I.; Oda, K.

By Shiring Streptom Streptom Stression of a gene encoding a novel sorbitol oxidase fracestion: JW0076

A;Reference number: JW0076

A;Reference number: JW0076

A;Residues: 1-420 AHIRA

A;Residues: 1-420 AHIRA

A;Cross-references: DBJ:AB000519; NID:g1856966; PIDN:BAA19135.1; PID:g1856967

C;Comment: This protein oxidizes D-sorbitol to produce hydrogen peroxide and glucose with C;Superfamily: L-gulonolactone oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Escherichia coli (Strain of Species: Escherichia coli (Strain of Species: Escherichia coli (Strain of Species: Escherichia coli (Strain of Species: Escherichia coli (Strain of Species: Escherichia coli (Strain of Species: Escherichia coli (Species: Escherichia coli of Species: Escherichia coli of Species: Perana, N. T.; Plunket III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Article: Genome sequence of enterohemorrhagic Escherichia coli ol57:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Residues: I-346 <STO>
A; Residues: I-346 <STO>
A; Residues: I-346 <STO>
A; Cross-references: GB:AE005174; NID:g12516109; PIDN:AAG57008.1; GSPDB:GN00145; UWGP:Z3G C; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Generics: Gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
D85818
unknown protein encoded within prophage CP-933U [imported] - Escherichia coli (strain Ol
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       Gaps
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   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.6%; Score 54; DB 2; Length 346; 41.9%; Pred. No. 14; 1:1ve 3; Mismatches 9; Indels
   8; Indels
   Mismatches
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                                                                           LAARAGPNGIEGPTLRQWLAAR 31
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Matches 11; Conservative
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Matches 13; Conservative
   Conservative
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; R;Stover, C.K.; Pham, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A,Reference number: A82950; MUID:20437337
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R; Matsumoto, A.; Matsumoto, R.; Fujiwara, Y.
Eur. J. Biochem. 230, 337-343, 1995
A; Title: Molecular cloning of human cDNA with a sequence highly similar to that of th A; Reference number: $65358; MUID:95324544
                                                                                                                                                                                                                                                                                                                                                                                                                 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, April 1999
A;Reference number: Z21573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-396 <OLI>
A;Cross-references: EMBL:AL049587; PIDN:CAB40679.1; GSPDB:GN00070; SCOEDB:SC5F2A.12c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Streptomyces coelicolor conserved hypothetical protein SC5F2A.12c
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 25-Apr-1997
                                                                                                                                                                                                                                                                                                                  C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.4%; Score 52; DB 2; Length 396; 34.4%; Pred. No. 29; tive 5; Mismatches 10; Indels
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 PPARRWLSGRLAPG--EGPSAERRAKSWFSVR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PTLRQWLAARAGPNGIEGPT----LRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 GPDLRSALAGRVGPTGF-----PFSAARA 397
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                                                            1 IEGPTLRQWLAARAGPNGIEGPTLRQWLA 29
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Best Local Similarity 46.7%
Matches 14; Conservative.
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A;Molecule type: DNA
A;Residues: 1-371 <STO>
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A; Residues: 1-440 <MAT>
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A;Cross-references: EWBL:U46005; NID:g1335871; PIDN:AAC51112.1; PID:g1335872
B;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell, B;Ochem. Biophys. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM A;Reference number: PC4263; MUID:97168971
A;Reference number: PC4263
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                   yeave, year of year of year of years of years of years of years. Chandipura virus c; Species: Chandipura virus c; Species: Chandipura virus c; Species: Chandipura virus c; Species: Chandipura virus c; Species: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999 C; Accession: A34443 R; Wasters, P. S.; Bella, R. S.; Butcher, M.; Patel, B.; Ghosh, H.P.; Banerjee, A.K. N; Yarology 171, 285-290, 1989 A; Pitcher, M.; Patel, B.; Ghosh, H.P.; Banerjee, A.K. A; Reference number: A3443; MuD:89299473 A; Residues: 1-524 AAS> A; Residues: 1-524 AAS> A; Residues: 1-524 AAS> A; Cross references: GB:J04350; NID:g323376; PIDN:AAA42916.1; PID:g323377 C; Genetics: A; Cass references: GB:J04350; NID:g323376; PIDN:AAA42916.1; PID:g323377 C; Genetics: A; Cass references: GB:J04350; NID:g323376; PIDN:AAA42916.1; PID:g323377 C; Reywords: glycoprotein; spike protein; transmembrane protein C; Reywords: glycoprotein; spike protein; transmembrane #status predicted ASGS> F; 28-524/Product: spike glycoprotein G #status predicted ATMN> F; 472-491/Domain: transmembrane #status predicted ATMN> F; 184,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Species: Homo sapiens (man)
C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
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                                           Indels
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                                                                                                                                                                                                      249 EDPSVREWVLRARATWOPPEWQVVHLSNGIEGPQDRR 285
                                                                                                                             2 EGPTLRQW-LAARAG------PNGIEGPTLRQ 26
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44.8%; Pred. No. 53;
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                                                   4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLROWLAARAGPNGIEGPTLROW 27
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Best Local Similarity 44.8%
Matches 13; Conservative
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A; Accession: G02390
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Best Local Similarity
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A; Residues: 1-814 <HER>
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                                                                     Matches
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A;Introns: 12/2
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
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A;Nolecule type: DNA
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A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Experimental source: strain PAOl
C;Genetics:
A;Gene: hasD; PA3406
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTS-binding protein sp105 - Pacific electric ray
C:Species: Torpedo californica (Pacific electric ray)
C:Species: Torpedo californica (Pacific electric ray)
C:Daces: 30-30n-1993 **sequence_revision 30-Jun-1993 **text_change 22-Jun-1999
C:Accession: S04987; S30070
R:Jentsch, T.J.; Garcia, A.M.; Lodish, H.F.
Biochem. J. 261, 155-166, 1989
A:Title: Primary structure of a novel 4-acetamido-4'-isothiocyanostilbene-2,2'-disulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transport protein HasD PA3406 [imported] - Pseudomonas aeruginosa (strain PAOI)
                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Caenorhabditis elegans
Cibecies: Caenorhabditis elegans
Cibate: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 31-Jan-2000
Cibacesion: T29299
RiJohnson, D.; Stellyes, L.
Sibmitted to the EMBL Data Library, November 1995
Aibescription: The sequence of C. elegans cosmid C50F7.
AiReference number: 220601
AiReference number: 220601
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: DNA
A; Residues: 1.589 < JOH>
A; Residues: 1.589 < JOH>
A; Cross-references: EMBL:U41557; PIDN:AAA83307.1; CESP:C50F7.2
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                                                                                                                                                                                                                                                                                                                               hypothetical protein C50F7.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.8%; Score 51; DB 42.9%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 ESPSFFQWIFGRPKPSGPAGP 559
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                                                              290 GPDLRRWLVARLG 302
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A; __Cross.references: GB: AE004556; GB: AE004091; NID: 99947194; PIDN: AAG04656.1; GSPDB: GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takabawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339
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A,Experimental source: strain Kl
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UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galU [similarity] - Mycobacter
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A; Authors: Sqares, R.; Sutston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MUID:98295987
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-306 < COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein APE0867 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: G72680
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C.Superfamily: Escherichia coli UTP--glucose-1-phosphate uridylyltransferase
C.Keywords: nucleotidyltransferase
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Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
Accession: D70601
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                                                                                                                                                                                                                                        30.1%; Score 51.5; DB 2; Length 371;
31.0%; Pred. No. 32;
tive 7; Mismatches 9; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.8%; Score 51; DB 2; Length 306; 69.2%; Pred. No. 30; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|| :|| | :|| | 145 | 145 | 146 | 147 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 146 | 
                                                                                                                                                                                                                                                                                                                                                                                                                 4 PTLRQWLAARAGP-----NGIEGPTLR----QWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Experimental source: strain PAO1
                                                                                                                                                                                                                                                                Best Local Similarity 31.09
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 69.2*
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A: Molecule type: DNA
A: Residues: 1-281 <KAW>
                                                                                                                                                 A; Gene: PA1267
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                                                                                           C;Genetics:
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Junearyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha chain - Pseudomo N; Alternate names: 2-oxoisovalerate dehydrogenase (lipoamide) E1-alpha chain; branche C; Species: Pseudomonas putida C; Species: Pseudomonas putida C; Species: Pseudomonas putida C; Species: Janar-1992 #text_change 05-Nov-1999 C; Accession: S01317; B36133; S63475 R; Burns, G.; Brown, T.; Hatter, K.; Idriss, J.M.; Sokatch, J.R. R; Burns, G.; Brown, T.; Hatter, K.; Idriss, J.M.; Sokatch, J.R. A; Picheren number: S01317; MUD:88329084 A; Reference number: S01317; MUD:88329084 A; Residues: 1-410 <BMB. X13004 A; Residues: 1-410 <BMB. X13004 A; Residues: 1-410 <BMB. X13004 A; Residues: 1-410 <BMB. X13004 A; Residues: 1-410 <BMB. X13004 A; Residues: 1-410 <BMB. X1301 A; MUD:91008935 A; Rittle: Transcriptional analysis of the promoter region of the Pseudomonas putida br A; Recession: B36133 A; Rulb: A361333 MUD:91008935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE001931; GB: AE000513; NID: 96458461; PIDN: AAF10338.1; PID: 9645
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Accession: C75479
C; Accession: C75479
C; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID:20036896
                                                                                                                                                                                  A;Residucs: 1-150 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL54241.1; PID:917985213; GSPDB:GN00191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| | ||: |:|| || 206 QGIADRFGPHRIDGPDYRQRGTEPAQPLSEAEFAAWLA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%; Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 TLKAWMAAQ--PSGIEG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.8
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 TLRQWLAARAGPNGIEG 21
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                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-351 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                          A; Status: preliminary
                                                                                                                                                                       DNA
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                                                                                            A; Accession: AF3634
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                                                                                                                                                                                                                                                                                                                                       A; Gene: BMEII0999
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                                                                                                                                                                       A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: DR0759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AF3634
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Dates: 04-Aug-2001 #Seguence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Datession: B93235
R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
Falman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Froc. Natl. Acad. Scl. U.S.A. 98, 9883, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-719 < ROR>
A; Residues: 1-719 < ROR>
A; Cross-references: GB:AE006469; PIDN:AAK65164.1; PID:g14523607; GSPDB:GN00165
A; Cross-references: GB:AE006469; PIDN:AAK65164.1; PID:g14523607; GSPDB:GN00165
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
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A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;503-521/Domain: transmembrane #status predicted <TM2>
F;542-562/Domain: transmembrane #status predicted <TM3>
F;25,112,134,162,386,405,470,568/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein SMa0937 [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 2-11;435-449, X',451-452, X',454-459;634-649 <JEN2>
A; Residues: 2-11;435-449, X',451-452, X',454-459;634-649 <JEN2>
C; Superfamily: SITS-binding protein spl05
C; Keywords: disulfide bond; glycoprotein; homodimer; transmembrane protein
F; 2-697/Product: SITS-binding protein #status experimental <MAT>
F; 30-50/Domain: transmembrane #status predicted <TML>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                       A; Cross-references: EMBL:X16078; NID:964403; PIDN:CAA34209.1; PID:964404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 71;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 LDDPEVRQWLTAKQAAAPAAATTPAGLASQWIA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAAR--AGPNGIEGPT--LRQWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%; Score 51; 36.4%; Pred. No.
                                            A; Reference number: S04987; MUID:89374082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.19
Matches 8; Conservative
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                                                                                                               A; Molecule type: mRNA
A; Residues: 1-697 <JEN1>
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                                                                                 A; Accession: S04987
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GSPDB:GN00066; SPDB:SPAC23H4.04

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A;Cross-references: EMBL:298977; PIDN:CAB11659.1; A:Experimental source: strain 972h-; cosmid c23H4
                                                                                                                                           C;Genetics:
A;Gene: SPDB:SPAC23H4.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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S06469
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
S; Ztover, C.K.; Pham, X.Q.; Erwin, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, Pham, P
                                                                                                                                                                                                              R;Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.
Blochem. 233, 828-836, 1995
A;Title: Purlification of active E1-alpha(2)-beta(2) of Pseudomonas putida branched-chair
A;Reference number: S63475; MUID:96085147
A;Accession: S63475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin C; Keywords: lipoamide; oxidoreductase; phosphoprotein; thiamin pyrophosphate F; 2-410/Product: 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) alpha chain #status p F; 202-251/Domain: thiamin pyrophosphate-binding domain homology <TPB>
F; 313/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -oxoisovalerate dehydrogenase (alpha subunit) PA2247 [imported] - Pseudomonas aeruginos
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Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Specie
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Pred. No. 55;
4; Mismatches 3; Indels
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53.3%;
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R,Hester, K.; Luo, J.; Burns,
Eur. J. Blochem. 233, 828-836,
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hes 8; Conservative
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A:Molecule type: protein
A:Residues: 1-13 <HES>
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Best Local Similarity
Matches 8; Conserv
                                                       A; Molecule .type: DNA
A; Residues: 1-17 <MAD>
A;Status: preliminary
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C; Superfam:1...
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Matches
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photosystem II chlorophyll a-binding protein psbC - Synechocystis sp. (strain PCC 680 N;Alternate names: chlorophyll-binding protein, 43K; photosynthetic reaction center 4 c;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 07-Jun-1990 #sequence_revision 19-Jan-1996 #text_change 20-Jun-2000
C;Accession: S06469; S07497; S02380; S74838
R;Chisholm, D.; Williams, JG.K.
Plant Mol. Biol. 10, 293-301, 1988
A;Title: Nucleotide sequence of psbC, the gene encoding the CP-43 chlorophyll a-bindi
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A.Residues: 'MKTLSSLRRFSPV',2-54,'N',56-149,'I',151-288 <DZE>
A.Residues: 'MKTLSSLRRFSPV',2-54,'N',56-149,'I',151-288 <DZE>
A.Residues: 'MKTLSSLRRFSPV',2-54,'N',56-149,'I',151-288 <DZE>
A.Cross-references: EMBL:XO7018; NID:q48064; PIDN:CAA30071.1; PID:q48066
A.Note: the authors translated the codon CAT for residue 131 as Phe; this sequence us R.Kaneko, T.; Sato, S.; Rotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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A; Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BAA17799.1; PID:g165
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A; Note: this sequence uses an incorrect initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Residues: 1-7 <CAR>
A Note: the authors definitely establish that the Met-1 GTG is the initiation codon a R;Dsclkalns, V.A.; Bogorad, L.
BEMBO J. 7, 333-338, 1988
A;Title: Molecular analysis of a mutant defective in photosynthetic oxygen evolution A; Reference number: S02379; MUID:88211542
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C;Keywords: chlorophyll; membrane-associated complex; photosynthesis; photosystem II;
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A; Residues: 'MKTLSSLRRESPV', 2-460 (CHI>
A; Residues: 'MKTLSSLRRESPV', 2-460 (CHI>
A; Cross-references: GB: M21538; NID: 934609; PIDN: AAA85378.1; PID: 91161272
A; Note: this sequence uses an incorrect initiation codon
R; Carpenter, S.D.; Charite, J.; Eggers, B.; Vermaas, W.F.J.
A; Carpenter, 260, 135-137, 1990
A; Ritle: The psbc start codon in Synechocystis sp. pcc 6803.
A; Reference number: S07496; MUID: 90127396
A; Accession: S07497
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A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                         Length 415;
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Pred. No. 62;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                11;
                                                                                                                     DB 2;
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A, Status: not compared with conceptual translation
A;Introns: 34/1; 54/3
C;Superfamily: probable membrane protein YDL033c
                                                                                                                                                                                            4; Mismatches
                                                                                                                                                         56;
                                                                                                                     Score 50;
Pred. No.
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                                                                                                                  29.2%;
37.0%;
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35.0%;
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Best Local Similarity
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                       R;Meijer, W.G.; Arnberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuiz Mol. Genet. 225, 320-330, 1991
A;Title: Identification and organization of carbon dioxide fixation genes in Xanthoba A;Reference number: S13573; MUID:91172133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
A,Accession: A13083
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-341 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45087.1; PID:917742754; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monooxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11.Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: A13083
                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: Z22705; NID: 9297851; PIDN: CAA80406.1; PID: 9581832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL:X17252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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264 VEGLPVVRQWLAVRA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEG-PTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-333 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-150 <MEI>
                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S13578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: Atu4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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A;Cross references: GB:Z95554; GB:AL123456; NID:g3261771; PIDN:CAB08882.1; PID:g2113913
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL; Z81054; PIDN: CAB02881.1; GSPDB: GN00022; CESP: F01D4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 *sequence_revision 17-Jul-1998 *text_change 20-Jun-2000
C;Accession: C70559
                                                                                                                                                                                                                                                      hypothetical protein F01D4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20454
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                      Gaps
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                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                        Indels
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                        13;
                                                                                                                            340 GETMRFWDFRGPWLEPLRGPNGLDLDKLRNDIQPWQVRRA 379
                                                                          3 GPTLR-----QWLAARAGPNGIEGPTLRQ-----WLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.2%; Score 50; DB 2; 1
hilarity 42.4%; Pred. No. 1.2e+02;
Conservative 1; Mismatches R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-472 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1996 A; Reference number: 219278 A; Accession: T20454
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 LAAAGGPEVDEGFDVRGGALAPGTVRQWLAEHA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: polA
C;Superfamily: DNA-directed DNA polymerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 4
A;Introns: 59/3; 127/3; 334/3; 455/3
C;Superfamily: human carboxypeptidase H
                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone F01D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.20)
Best Local Similarity 47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 PAQRQWLTGRSNINGVD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PTLROWLAARAGPNGIE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: F01D4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C70559
                        14;
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                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 27
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Ricoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
A; Accession: H98202
A; Accession: H98202
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-355 < CUR>
A; Cross-references: GB: AB007870; PIDN: AAK89146.1; PID:g15158956; GSPDB: GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F58B3.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: T22B96
R; Harris, B.
submitted to the EMBL Data Library, May 1996
A; Reference number: Z19633
A; Reference number: Z19633
A; Reference number: Z19633
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1.214 < WIL>
A; Rossidues: 1.214 < WIL>
A; Cross-references: EMBL:Z73427; PIDN:CAA97801.1; GSPDB:GN00022; CESP:F58B3.3
C; Genetics: Cource: clone F58B3
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A,Map position: 4
A;Introns: 68/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F58B3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
28.9%; Score 49.5; DB 2; Length 355;
Best Local Similarity 35.1%; Pred. No. 55;
Matches 13; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

28.7%; Score 49; DB 2; Length 214;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EGPTLRQWLAAR----AGPNGIE--GPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: AGR_L_1143
A;Map position: linear chromosome
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Search completed: October 9, 2002, 09:05:00 Job time: 7.19438 secs

||: || ||| |: 191 PTIHQWEGTTAGPCGV 206

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:51:41; Search time 3.82201 Seconds (without alignments) 324.181 Million cell updates/sec Run on:

US-09-422-838C-23 171 Title: Perfect score:

1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

•	Description	1 1	3819	_		torpe	Q9hbhl homo sapien	paste	_	O13947 schizosacch	_				homo ean	-			٠,	n /	n (		Q9cbu0 mycobacteri			O9yit9 aeropyrum p		_	P41643 pinus thunb	Ol5067 homo sapien	<u> </u>	P33479 pseudorabie	P11675 pseudorabie	Q64612 rattus norv	P12107 homo sanien	15 1
	ID	COO many	SCOZ_HUMAN	VGLG_CHAV	AUTO HOMAN	SFIS_IORCA		TONE_PASHA		T.KMU_SCHPO	PSBC_SYNY3		CBBR_XANFL	ODPA_BACST	DIAC_HUMAN	CNG1_CHICK	CA1B BOVIN	UROC MOUSE	VXIS RP434	VXTS LAMBD	VI.76 VIBCU	APPO MACE II	APACLE ODDA BACKE	CDFA_BACSU	CAZI_BUMAN	FRT HIMAN	DVBD MVCTI	DEDI DIME	FORC_FINIA	FUR4_HUMAN				P.P.PO_RAT	AIB_HUMAN	XERC_MYCTU
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dР	Query	31 3	0.15	30.7	000	20.00	2000	20.00	2.00	9.00	2.62	700	٠.	7.87	7.87	28.7	28.7	28.4	28.1	28.1	28.1	28.1	28.1	28.1	27.8	27.5	27.5	27.5	27.5		77.70	7.70		0.10	6.72	6.97
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	Result No.	-	7	m	4	'n	S	7	- α	σ	, ,	2 -	1.5	1 5 C	, .	14 1	ς; ;	16	17	18	19	20	21	22	23	24	25	26	27	28	50	0	, t	1 0	9 (	ç

006399 mycobacteri P02460 gallus gall P04471 odontella s P54234 clarkia arc P54236 clarkia fra P54239 clarkia wil P54240 clarkia wil P54243 centhera m P54243 centhera m P54235 clarkia con P34796 clarkia lew P54238 clarkia lew P54238 clarkia lew
FABH_MYCTU CA12_CHICK PSBB_ODOSI G6P1_CLAFR G6P1_CLAFR G6P1_CLAWI G6P1_CLAWI G6P1_CLAWI G6P1_CLACO G6P1_CLACO G6P1_CLACO G6P1_CLACO G6P1_CLACO
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## ALIGNMENTS

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InterPro; IPR003782; SCOl\_SenC.
Pfam; PF02630; SCOl-SenC; 1.
Mitochondrion; Transit peptide; Disease mutation; Polymorphism.

AND

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBUNIT: TRIMERS IN THE ENDOPLASMIC RETICULUM.
-:- PTM: THIS PROTEIN IS MODIFIED BY THE COVALENT ADDITION OF PALMITIC ACID VIA A THOETHER LINKAGE TO A CYSTEINE. IT COULD BE EITHER ON POSITION 479 OR 484.
-:- SIMILARITY: 39% IDENTITY TO THE G PROTEINS OF VSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J04350; AAA42916.1; -.
PIR; A32443; VGVNCV.
Interpro; IPRO1903; Rhabd_glycop.
Pfam; Pro974; Rhabd_glycop; 2.
Pransmembrane; Envelope protein; Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIOLOGY 171:285-290(1989).

-1- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.

-1- FUNCTION: THIS PROTEIN FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE IT IS RESPONSIBLE BOTH FOR THE UPTAKE OF THE VIRUS BY THE CELL.

HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL.

THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND THE PORTION OF THE GLXCOPROTEIN BXPOSED ON THE CYTOPLASMIC PACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure and expression of the glycoprotein gene of Chandipura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                      21;
                                                                                                                                                    31.3%; Score 53.5; DB 1; Length 266; 33.3%; Pred. No. 4.8; 2; Mismatches 9; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89299473; PubMed=2741347;
Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; sarNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Vesiculovirus.
NCBI_TaxID=11273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                  33 LRSWLLSRQGPAETGGQGQPQGPGLRTRLLITGLFGAGLGGAWLALRA 80
                                                                                                                                                                                                                    --- QWLAARA 32
MITOCHONDRION (POTENTIAL).
                                                                       /FTId=VAR_008874.
S -> F (IN FIC).
/FTId=VAR_008875.
BC2F40E057329BF3 CRC64;
          SCO2 PROTEIN HOMOLOG.
R -> P (IN DBSNP:140523).
/FTId=VAR_011738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPIKE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                             E -> K (IN FIC)
                                                                                                                                                                                                                                                                                                                                  524 AA
                                                                                                                                                                                                                       6 LRQWLAARAGP-----NGIEGPTLR------
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                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandipura virus (strain 1653514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2741347;
                                                                                                                             266 AA; 29810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 Spike glycoprotein precursor.
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524
472
496
524
184
 41
266
20
                                                                 140
                                                                                                 225
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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22
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473
497
184
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TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                      VGLG_CHAV
                                                                                                                                SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
                                   VARIANT
                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
      TRANSIT
                                                                                                  VARIANT
                       CHAIN
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                       VGLG_CHAV
                                                                                                                                                                                                                                                                                                                                                     FT
FT
FT
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SO
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Kraetzschmar J., Lum L., Blobel C.P.;
"Metargidin, a membrane-anchored metalloprotease-disintegrin protein
with an RGD integrin binding sequence.";
J. Biol. Chem. 271:4593-4596(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Umbilical vein;
MEDLINE=97192141; PubMed=9039960;
Herren B., Raines E.W., Ross R.;
"Expression of a disintegrin-like protein in cultured human vascular
                                                                                                                                                                                                                                        013444; 013493; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 01-MMR-2002 (Rel. 41, Last annotation update) 47 Appan 15 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cystelnerich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang X.P., Kamata T., Yokoyama K., Puzon-WcLaughlin W., Takada Y.,
"Specific interaction of the recombinant disintegrin-like domain of
MDC-15 (metargidin, ADAM-15) with integrin alphavbeta3.";
J. Biol. Chem. 273:7345-7350(1998).
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SORTING NEXIN 9 (BY SIMILARITY).
-!- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHAV-BETA3.
-!- PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
.) (POTENTIAL)
                                                                                                 ;;
0
                                                                  Score 53; DB 1; Length 524; Pred. No. 11;
                                                                                                  13; Indels
                                            58826 MW; A84AF0A5FFFB73CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
 N-LINKED (GLCNAC. ... PALMITATE (POTENTIAL) PALMITATE (POTENTIAL)
                                                                                                                                                                                                                              814 AA.
                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH INTEGRIN ALPHAV-BETA3. MEDLINE=98184837; PubMed=9516430;
                                                                                                                                                          359 IDGPVLKEPKGKRESPSGISSDIWTQW 385
                                                                                                                                1 IEGPTLRQWLAARAGPNGIEGPTLRQW 27.
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Breast carcinoma;
MEDLINE=96214870; PubMed=8617717;
                                                                           31.0%;
37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells and in vivo.";
FASEB J. 11:173-180(1997).
                                                                                                     Conservative
                                                                                                                                                                                                                               STANDARD;
                                   484
                                                                                         Local Similarity
                                                  524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                        ADAM15 OR MDC15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
        344
479
484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN:
                                                                                                                                                                                                                                                                                                                                              (Metargidin)
                                                                                                          10;
                                                                                                                                                                                                                                  AD15_HUMAN
                                                   SEQUENCE
           CARBOHYD
                                                                              Query Match
                                                                                                                                                                                                                     AD15_HUMAN
                         LIPID
                                      LIPID
                                                                                                                                                                                                        RESULT 3
                                                                                              Best
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728 LKGPTC-QYRAAQSGPSERPGPPQRALLA 755

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                                                                                                                                                                                                                                                                                                                               PROSITE: PS50215; ADAM_MEPRO; 1.
PROSITE: PS50214 DISINTEGRIN_1; FALSE_NEG.
PROSITE: PS50014 DISINTEGRIN_2; 1.
PROSITE: PS00102; EGF_2; 1.
PROSITE: PS01166; EGF_2; 1.
PROSITE: PS00144; ZINC_PROTEASE; 1.
PROSITE: PS00546; CTSTEINE_SWITCH; FALSE_NEG.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Transmembrane; EGF_like domain; E319-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
G -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL ATTACHMENT SITE (POTENTIAL). ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD2EC26CB1314576 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3-BINDING (POTENTIAL). SH3-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G -> S (IN REF. 2)
A -> P (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYSTEINE SWITCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY. SIMILARITY.
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                                                                                                                                                                                                 InterPro: IRR001818; Matrixin.
InterPro: IPR001818; Matrixin.
InterPro: IPR001890; Reprolysin.
InterPro: IPR001890; Reprolysin.
Pfam; PF00200; disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAM 15
                                                                                                                                                                             InterPro; IPR001762; Disintegrin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY
BY
                                                                                                             EMBL; U46005; AAC51112.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87686 MW;
                                                                                                                              EMBL; U41767; AAC50404.1;
HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                           SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       684
                                                                                                                                                   MEROPS; M12.215; -.
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                                                                                                                                                                  MIM; 605548;
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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DOMAIN
DOMAIN
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Query Match

30.7%; Score 52.5; DB 1; Length 814;

Best Local Similarity 44.8%; Pred. No. 20;

Matches 13; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

1 IEGPTLROWLAARAGPNGIEGPTLROWLA 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE CHLORIDE CHANNEL.
-1- SUBGINIT: HOMODIMER; DISULFIDE-LINKED.
-1- TISSUE SPECIFICITY: ELECTROPLAX TISSUE, BRAIN (200-FOLD LESS), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEARY (300-FOLD LESS).

-I- MISCELLANEOUS: BINDS 4-ACETAMIDO-4'-ISOTHIOCYANOSTILBENE-2,2'-DIS ULPHONIC ACID (SITS), AN INHIBITOR OF A VARIETY OF ANION TRANSPORT
                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-201 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
15-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               californica electroplax.";
Biochem. J. 261:155-166(1989).
-!- FUNCTION: THIS GLYCOPROTEIN IS PROBABLY NOT A FUNCTIONAL PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SITS) -binding membrane protein highly expressed in Torpedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89374082; Pubmed-2775201;
Jentsch T.J., Carcia A.M., Lodish H.F.;
"Primary structure of a novel "Primary structure of a novel 4-acetamido-4'-isothiocyanostilbene-2,2'-disulphonic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%; Score 51; DB 1; Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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PIR; S04987; S04987
InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; Iransmembrane; Glyco_hydro_31; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 WLAARAGPNGIEGPTLROW 27
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                      SP15_TORCA
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                                                                                                              P19965;
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RESULT 4
SP15_TORCA
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ID DEFM
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09HBH1;

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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                            STRAIN=SEROTYPE A1 / ATCC 43270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-NOV-1988 (Rel. 09, Created)
1-FEB-1996 (Rel. 33, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GPEIKQGIVAKAIPNAAEG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 47.4 es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 246 AA;
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                                                                                SEQUENCE FROM N.A.
                                          NCBI_TaxID=75985;
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                            Mannheimia
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O
                                                                                                                                                                                                                                                                                                                                                                            Lonetto M.A., Zhu Y., Li X., Southan C.;
Lonetto M.A., Zhu Y., Li X., Southan C.;
"A human homolog of bacterial peptide deformylases.";
Submitted (NOV-2000) to the EMBL/GenBank/DDhJ databases.
Submitted (NOV-2000) to the EMBL/GenBank/DDhJ databases.
I. FUNCTION: Removes the formyl group from the N-terminal Met of
newly synthesized proteins (By similarity).
I. CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate +
methionyl peptide.
I. COFACTOR: Binds 1 iron(II) ion (By similarity).
I. SUBELLULAR LOCATION: Mitochondrial (Fotential).
I. TISSUE SPECIFICITY: Ubdquitous.
I. SIMILARITY: BELONGS TO THE POLYPEPFIDE DEFORMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000181; Pep_deformylase.

Pfam; PF01327; Pep_deformylase; 1.

ProDom; PD003844; Pep_deformylase; 1.

Protein biosynthesis; Hydrolase; Iron; Mitochondrion; Transit peptide.

PRANSIT ? MITOCHONDRION (POTENTIAL).

CHAIN ? 243 PEPTIDE DEFORMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                  01-MMR-2002 (Rel. 41, Created)
01-MMR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
peptide deformylase, mitochondrial precursor (EC 3.5.1.88) (PDF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                   Giglione C., Serero A., Pierre M., Boisson B., Meinnel T.;
"Identification of eukaryotic peptide deformylases reveals
universality of Niterminal protein processing mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 1; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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BY SIMILARITY.
IRON (BY SIMILARITY).
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                       MEDLINE-20514156; PubMed-11060042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF239156; AAG33968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27013 MW;
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                                                                                                                                                                                                                                                                                                                                EMBO J. 19:5916-5929(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK15624.1
                                                                                                       (Polypeptide deformylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AARAGPNGIEGPTLRQ 26
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                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
215
218
                                                                                                                                                                                                     NCBI_TaxID=9606;
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METAL
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P72204;

TONB.

TONB\_PASHA

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not content.
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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4) (Branched-chain alpha-keto acid dehydrogenase component alpha chain (El))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   MEMBRANE PROTEINS (BY SIMILARITY).
SUBCELLULAR LOCATION: ANCHORED TO THE CYTOPLASMIC
MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE
PERIPLASM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U62565; AAB09530.1; -.
Transport; Protein transport; Inner membrane; Periplasmic; Transmembrane; Signal anchor.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 SIGNAL-ANCHOR (POTENTIAL).
246 PERIPLASMIC (POTENTIAL).
27785 MW, C9582F619FCBA5B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 1;
Pred. No. 13;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 AA
                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE TONB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown D. Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                        MEDLINE-99356017

MEDLINE-99356017

MEDLINE-99356017

Mevarsson A., Seger K., Turley S., Sckatch J.R., Hol W.G.J.;

Crystal structure of 2-oxoisovalerate and dehydrogenase and the architecture of 2-oxo acid dehydrogenase multienzyme complexes.";

Nat. Struct. Biol. 6:785-792(1999)

-!- FUNCTION: THE BRANCHED-CHAIN ALPHA-KETO DEHYDROGENASE COMPLEX CAPALYZES THE OVERALL CONVESION OF ALPHA-KETO ACIDS TO ACID. TO COMPAINS MULTIPLE COPIES OF 3 ENZYMATIC COMPONENTS:

BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE (E1), LIPOAMIDE ACYLTRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E1), LIPOAMIDE

ACYLTRANSFERASE (E2) AMD LIPOAMIDE DEHYDROGENASE (E3).

-!- CAPALYTIC ACTIVITY: 3-methyl-2-oxobutanoate + lipoamide = S-(2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Probable tRNA (5-methylaminomethyl 2-thiouridylate)-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Madhusudhan K.T., Huang G., Burns G., Sokatch J.R.; Transcriptional analysis of the promoter region of the Pseudomonas putida branched-chain Keto acid dehydrogenase operon."; J. Bacteriol. 172:5655-5663(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Flavoprotein; Thiamine pyrophosphate; 3D-structure. SEQUENCE 410 AA; 45268 MM; 0C998460CCFB9CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 1; Length 410; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                methylpropanoyl)dihydrolipoamide + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE TRMU FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
                                                                                                        X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00676; E1_dehydrog; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M57613; AAA65614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001017; E1_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:| :|: ||||:
298 GPSLIEWVTYRAGPH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GPTLRQWLAARAGPN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S01317; DEPSXA.
PDB; 1QS0; 18-AUG-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thiouridylate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896
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013947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=972;
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the Swiss Institute of Bioinformatics and the EMBL outstation -

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                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on any as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chisholm D., Williams J.G.K.; "Nucleotide sequence of psbC, the gene encoding the CP-43 chlorophyll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-80211542; PubMed-3130247; Dzelzkalns V.A., Bogorad L.; "Molecular analysis of a mutant defective in photosynthetic oxygen evolution and isolation of a complementing clone by a novel screening
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97061201; PubMed=8905231; Ranaka A., Asamizu E., Nakamura Y., Ranaka A., Asamizu E., Nakamura Y., Randajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S., Salamada M., Yasuda M., Tabata S., Saguence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THE 43 KDA PROTEIN (PG) IS A COMPONENT OF THE CORE OF PHOTOSYSTEM II. IT IS A CHLOROPHYLL BINDING PROTEIN. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN; CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Last sequence update)
LoCY-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kba reaction center protein (P6 protein) (CP43).
PSBC OR SLL0851.
                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a-binding protein of photosystem II, in the cyanobacterium Synechocystis 6803.";
                                                                                                                                                                                                                                                 DB 1; Length 415;
                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                     InterPro; IPR004135; tRNA_Me_trans.
Pfam; PF03054; tRNA_Me_trans; 1.
Transferase; Methyltransferase; tRNA processing.
SEQUENCE 415 AA; 47626 MW; D2B604335B7A935F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PSBB / PSBC FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 AA
                                                                                                                                                                                                                                                                    Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                 Score 50;
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGPNGIEGPTLRQW 27
                                                                                                                                                                                                                                                                                                                                                                       58 VEGVFMRNWLDEDSAPSGC--PAERDW 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 10:293-301(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSBC_SYNY3 STANDARD; P P09193; P73749; 01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                               29.2%;
                                                                                                                        EMBL; Z98977; CAB11659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-300 FROM N.A.
                                                                                                                                                                                                                                                                  Best Local Similarity 37.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:333-338(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THYLAKOID MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             procedure.";
                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSBC_SYNY3
δy
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Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98395987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeder K., Gas S., Barry C.E. III, Terkaie F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Culver S., Seeger K., Ketch A., McLean J., Solver S., Squares R., Sulston J.E., Taylor K., Whitehead S., Squares R., Scelphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizrahi V., Huberts P., Dawes S.S., Dudding L.R.;
"A PCR method for the sequence analysis of the gyra, polA and rnhA gene segments from mycobacteria.";
Gene 136:287-290(1993).
                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                     DB 1; Length 472;
                                                                                                                                                                                                                                                         3; Mismatches 13; Indels
                                                                                      Photosystem II; Thylakoid; Chlorophyll;
                                                                                                                                                                                 R -> A (IN REF. 2).
T -> N (IN REF. 3).
Y -> I (IN REF. 3).
; D94D9FE73F66192D CRC64;
                                                                                                                                                                                                                                                                                            352 GETMRFWDFRGPWLEPLRGPNGLDLDKLRNDIQPWQVRRA 391
                                                                                                                                                                                                                                                                             3 GPTLR-----QWLAARAGPNGIEGPTLRQ-----WLAARA 32
                                                                                                                                                                                                                                                                                                                                                                         01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
POLA POLYMETASE I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                      PRT; 904 AA
                                                                                                                                                                                                                                    Score 50;
Pred. No. 2
                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94124016; PubMed-8294019;
                                                                                                                                                                                                                51760 MW;
             EMBL; M21538; AAA85378.1; -. EMBL; D90909; BAA17799.1; -.
                                                                                                                                                                                                                                     29.2%;
                                  CAA30071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                  InterPro; IPR000932; PSII.
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.03
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                           PF00421; PSII; 1.
                                                                                                                              182
224
259
291
445
                                            PIR; S06469; S06469.
PIR; S02380; S02380.
                                                                                                                                                                                                      162 1
472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                        Photosynthesis;
                                                                                                  Transmembrane;
                                   x07018;
                                                                                                                                                                                                                                                                                                                                 RESULT 10
DPO1_MYCTU
ID DPO1_MYCTU
                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
                                                                                                                                TRANSMEM
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                     TRANSMEM
                                                                                                                                                    TRANSMEM
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                        EMBL;
EMBL;
                                                                             Pfam;
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                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 904 AA; 98471 MW; 1C8E560FE5F74323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Gaps
Bishai W ; "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Hyphomicrobium group; Xanthobacter.
                                                                                                                                                                                                              + {DNA}(N).
-!- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-!- SIMILARITY: BELONGS TO DNA POLYMBRASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LAARAGPNGIEG------PTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002298; DNA_pol.
InterPro; IPR001998; DNA_pol.A.
InterPro; IPR001998; DNA_pol.A.
InterPro; IPR003583; HHH.1.
InterPro; IPR003584; HHH.2.
Ffam; PF001367; 5_3 exonuclease; IPfam; PF00476; DNA_pol.A; IPFam; PF00476; DNA_pol.A; IPFAMT; SW00476; DNA_pol.A; IPRINTS; PR00468; DNA_pol.A; IPRINTS; PR00476; DNA_pol.A; IPRINTS; PR00476; DNA_pol.A; IPRINTS; SW00476; SBEXOC; ISMART; SW00476; SBEXOC; ISMART; SW00476; SBEXOC; ISMART; SW00476; SBEXOC; ISMART; SW00476; SBEXOC; ISMART; SW00476; SBEXOC; ISMART; SW00479; HHHI; IL
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MEDLINE=94012468; PubMed=8407781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007030; AAK45935.1; -. HSSP; P19821; 1BGX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L11920; AAB46393.1; -.
EMBL; Z95554; CAB08882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.2%;
Best Local Similarity 42.4%;
Matches 14; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00482; POLAC; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P25545;
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Mol. Gen. Genet. 225:320-330(1991).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE CBB OPERON (CBBLSXFP)
FOR RUBISCO AND OTHER CALVIN CYCLE GENES. BINDS SPECIFICALLY TO
TWO BINDING SITES IN THE CBBR-CBBL INTERGENIC REGION.
-!- SIMILARIY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                            Meijer W.G., Arnberg A.C., Enequist H.G., Terpstra P., Lidstrom M.E.,
Dijkhuizen L.;
                                                                                                                                                                                                                                                                                                                                         "Identification and organization of carbon dioxide fixation genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
van den Bergh E., Dijkhuizen L., Meijer W.G.; "CbbR, a LysR-type transcriptional activator, is required for expression of the autotrophic CO2 fixation enzymes of Xanthobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MOV-1995 (Rel. 32, Last annotation update)
Pyruvate dehydrogenase El component, alpha subunit (EC 1.2.4.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  j;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00126; HTH_1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
PRASCription regulation; Activator; DNA-binding.
DNA_BIND
SEQUENCE 333 AA; 36003 MW; 9B375B4FB2D1EE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49.5;
Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X17252; -; NOT_ANNOTATED_CDS.
PIR; S13578; S13578.
InterPro: IPR000847; HTH_LysR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                        Bacteriol. 175:6097-6104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NCA 1503;
MEDLINE=90345939; PubMed=2200674;
                                                                                                                                                                                                                                             MEDLINE=91172133; PubMed=1900916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z22705; CAA80406.1; -
                                                                                                                                                                                    SEQUENCE OF 1-150 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| | :||||| 1|
264 VEGLPVVRQWLAVRA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEG-PTLROWLAARA 14
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                                                                                                                                                                                                                   STRAIN=H4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ODPA_BACST
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fisher K.J., Aronson N.N. Jr.; "Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase di-N-acetylchitobiase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Jr.; Liu B., Aronson N.N. Jr.; "Structure of the human gene for lysosomal di-N-acetylchitobiase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCCSAMINE (1-4) N-ACETYLGLUCCSAMINE CHITOBLOSE CORE FROM THE REDUCING END OF THE BOND. IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE. SUBCELLULAR LOCATION: Lysosomal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             InterPro; IPR001017; El dh.
Pfam; PF00676; El_dehydrog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLIBRATY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 1; Length 368; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                  acetyldihydrolipoamidė + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE.
SUBUNIT: HETERODIMER OF AN ALPHA AND A.BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                368 AA; 41338 MW; 46199FEF69EE4662 CRC64;
(E3).
-!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Di-N-acetylchitobiase precursor (EC 3.2.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 267:19607-19616(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 EGPTLIETLCFRYGPHTMSGDDPT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92406917; PubMed=1527079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EGPTLRQWLAARAGPNGIEG--PT 23
                                                                                                                                                                                                                                                      EMBL, X53560; CAA37628.1; -. PIR; S10798; DEBSPF. HSSP; P09060; 1020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           283
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Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOTORECEPTORS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLECTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CNG channel 1) (CNG-1).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cyclic nucleotide gated channel, cone photoreceptor, alpha subunit
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91264082; PubMed=7684234;
Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
Molday R.S., Kaupp U.B.;
"Rod and cone photoreceptor cells express distinct genes for
                                                                                                                                                                                                                                                                                                                               28.7%; Score 49; DB 1; Length 385; 37.9%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                         4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 AA.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  4 PTLROWLAARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                              AF085701, AAC35852.1; JOINED.
AF085702, AAC35852.1; JOINED.
AF085703; AAC35852.1; JOINED.
AF085704; AAC35852.1; JOINED.
                                   AF085706; AAC35852.1; -. AF085700; AAC35852.1; JOINED.
                                                                                                                    AF085705; AAC35852.1; JOINED
                                                                                                                                                                     IPR001579; Chitinase_2.
                          EMBL; M95767; AAA35684.1; -.
                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                              S27959; S27959.
                                                                                                                                PIR; A44102; A44102
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9031;
                                                                                                                                                         600873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNG1_CHICK
Q90805;
                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                      ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNG1_CHICK
                                                                  EMBL;
                                                                              EMBL;
                                                                                           EMBL;
                                                                                                         EMBL;
                                                                                                                    EMBL;
                                                                                                                                                                                                                           CHAIN
                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                       Ionic channel; Ion transport; cAMP-binding; Transmembrane; Vision;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LINKED (GLCNAC. . .) (POTENTIAL). A67ADFDD942CEFCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
H3 (POTENTIAL).
H4 (POTENTIAL).
H4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
H6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CAMP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                         H1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTL------RQWLAARAGPNGIEGPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-LUL-1998 (Rel. 36, Last annotation update)
05-lagen alpha 1(XI) chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911 AA.
                                                                                                                                                                                                                                                                                                                      H2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                     InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR000595; cNMP_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49;
Pred. No. 5
                                                                                                                SMART; SMO0100; CNMP; 1.
PROSTIE; PSO0889; CNMP_BINDING_1; 1.
PROSTIE; PSO089; CNMP_BINDING_2; 1.
PROSTIE; PS50042; CNMP_BINDING_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                              Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%;
34.1%;
EMBL: X89598; CAA61757.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.7'
Best Local Similarity 34.1'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum-smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA1B_BOVIN
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                                                                                                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM
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   the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 50:23-33[1998].

-!- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF ADRENOCORFOLCOTROPIC HORMONE (ACTH). BINDS WITH HIGH AFFINITY TO CRF RECEPTOR TYPES. 1, 2-ALPHA, AND 2-BETA.

-!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
                                                                                                                                                                                                                           AMINO-TERMINAL PROPEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                             TRIPLE-HELICAL REGION (INTERRUPTED).
                                                                                                                                                                    Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                               28.7%; Score 49; DB 1; Length 911; 47.8%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98292491; PubMed-9628819;
Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
"The structures of the mouse and human urocortin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                             COLLAGEN ALPHA 1(XI) CHAIN.
                                                                                                                                                                                                                                                                                                                                                            911 911
911 AA; 89259 MW; C05C4B3350749CFC CRC64;
                                                                                                                                                                                                                                                                                                 SHORT NONHELICAL SEGMENT
                                                                                                                                                                                                                                                                                                                               TRIPLE-HELICAL REGION. CROSSLINKING.
                                                                                                                                                                                                                                                             NONHELICAL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNCC_MOUSE STANDARD; PRT; 122 AA. P81615; 088390; STANDARD; PRT; 12999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                               TELOPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD005970; Urocortin_CRF; 1. SMART; SM00039; CRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000187; CRF.
InterPro; IPR003620; Urocortin_CRF.
Pfam; PF00473; CRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 IEGPPGPAGPAGLMGPPGLQGPT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLROWLAARAGPNGIEGPT 23
                                                                                                                                    InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 11.
                                                                                                                    EMBL; M82977; AAA30369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF038632; AAC24202.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                         Collagen.
                                                                                                                                                                                                                                           >911
                                                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Urocortin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                               AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY SIMILARITY).
D2969756F36F5DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Limberger R.J., Campbell A.M., "Functional elements of DNA upstream from the integrase operon that are conserved in bacteriophages 434 and lambda.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker J., Limberger R., Schneider S.J., Campbell A.; "Recombination and modular exchange in the genesis of new lambdoid
                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsbNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                  1;
             Cleavage on pair of basic residues; Signal. 25
                                                                                                                   28.4%; Score 48.5; DB 1; Length 122; 41.7%; Pred. No. 9.6;
                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA recombination; DNA-binding.
SEQUENCE 72 AA; 8635 MW; 0E6A4843503344AA CRC64;
                                                                                                                                                                                                                                                                        P11683; P16408;
01-OCT-1989 (Rel. 12, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                 72 AA.
                                       BY SIMILARITY.
                                                                                                                                             2; Mismatches
                                                     UROCORTIN
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=Phage 434;
MEDLINE=91346141; PubMed=1715186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88167849; PubMed=2965063;
                                                                                                                                                                      4 PTLRQWLAARAGPNGIEGPTLRQW 27
                                                                                                                                                                                     21 PESSQWSPAAAATGVQDPNLR-W 43
                                                                                        122 AA; 13557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M60848; AAA67901.1; -. EMBL; X51962; CAA36222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Biol. 3:297-308(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-64 FROM N.A.
PS00511; CRF; 1.
                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Lambda phage group.
NCBI_TaxID=10712, 10742;
                          25
80
120
120
                                                                                                                                                                                                                                                                                                                                                           Bacteriophage 434, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 61:135-144(1987).
             Amidation;
                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage HK022.
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                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                 Excisionase.
                                                                                                                                                                                                                                                                 VXIS_BP434
                                                                                         SEQUENCE
PROSITE;
             Hormone;
                                                                                                                   Query Match
                                                 PEPTIDE
MOD_RES
                          SIGNAL
                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phages
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                                                                                                                                            Matches
NA KW KW FT FT FT FT FT SQ SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 77:2482-2486(1980).
-!- FUNCTION: EXCISIONASE AND INTEGRASE ARE NECESSARY FOR THE EXCISION OF PROPHAGE FROM THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION AT THE ATT SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-80234646; PubMed-6446713; Hoess R.H., Foeller C., Bidwell K., Landy A.; Foeller C., Bidwell K., Landy A.; Foeller crecombination functions of bacteriophage lambda: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequence of the int-xis-Pi region of the bacteriophage lambda; overlap of the int and xis genes."; Nucleic Acids Res. 8:1765-1782(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of regulatory regions and overlapping structural genes for
                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10710;
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"Nucleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 1; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
   DB 1; Length 72;
                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA recombination; DNA-binding.
SEQUENCE 72 AA; 8605 MW; 0E6A4843502200AA CRC64;
                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.5;
28.1%; Score 48; DB 1
37.5%; Pred. No. 6.5;
tive 7; Mismatches
                                                                                                                                                                                        72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83189071; PubMed-6221115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-81053845; PubMed-6253947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TLROWLAARAGPNGIEGPTLROWL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TLQEWNARQRRPRSLE--TVRRWV 25
                                                                                        5 TLRQWLAARAGPNGIEGPTLRQWL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J02459; AAA96563.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                      Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A04321; RSBPXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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YL76_VIBCH
ID YL76_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davies R.W.;
                                                                                                                                                                                       VXIS_LAMBD
P03699;
                                                                                                                                                                                                                                                                             Excisionase.
        Query Match
                                                                                                                                                                        VXIS_LAMBD
                                                                                                                                                            RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Jagels K., Lacroix C., Maclean J., Monle S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                 'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein; Complete proteome.
270 AA; 30984 MW; 1EC54ACDEED8AB92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-!- SIMILARITY: BELONGS TO THE UPF0162 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 TLQAWLVGHKGPLAKLKPQHLQSVDNPTIIGRWLA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TLROWLAARAGP-----NGIEGPT-LROWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable integrase/recombinase xerC. XERC OR ML1600 OR MLCB250.62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.1%;
                                                                   Hypothetical protein VC2176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004289; AAF95321.1;
TIGR; VC2176; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 31.4 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XERC_MYCLE S
O9CBUO; 033037;
                                                                                                             Vibrio cholerae.
                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 27
                                                                                                                                                                                                                                                                                                                                                         Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                               cholerae
Q9KQ28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: Participates in site-specific recombination. Acts by catalyzing the cutting and rejoining of the recombining DNA molecules. Acts jointly with XerD (By similarity).
-!- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyruvate dehydrogenase El component, alpha subunit (EC 1.2.4.1) (S complex, 42 kDa subunit) (Vegetative protein 220) (VEG220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caldwell R.M., Ferrari E.; "Sequence analysis of the mobA-ampS region of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemila H., Palva A., Paulin L., Arvidson S., Palva I.; "Secretory S complex of Bacillus subtilis: sequence analysis and identity to pyruvate dehydrogenase."; J. Bacteriol. 172:5052-5063(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winters P., Caldwell R., Enfield L., Ferrari E.;
"The amps-nprE (124 degrees-127 degrees) region of the Bacillus
subtilis 168 chromosome: sequencing of a 27 kb segment and
identification of several genes in the area.";
Microbiology 142:3033-3037(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%; Score 48; DB 1; Length 297; 37.9%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
E70FA43F15286053 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                               Leproma; ML1600; -.
InterPro; IPR002104; Phage_integrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLRQWLAARAGPNGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 PVLRSWLATAAGAGAARTTLARRISAVKA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                      EMBL; 297369; CAB10656.1; ALT_INIT.
EMBL; AL583922; CAC30551.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90368558; PubMed=1697575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODPA_BACSU STANDARD; P
P21881; Q59227;
01-MAY-1991 (Rel. 18, Created)
15-JUL-1998 (Rel. 36, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 AA; 32180 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDHA OR ACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ODPA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                        regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1).
DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE B.SUBTILIS PDH COMPLEX POSSESSES ALSO BRANCHED-CHAIN
                                                                                                                                            "First steps from a two-dimensional protein index towards a response-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de Wet W.J., Bernard M.P., Benson-Chanda V., Chu M.-L., Dickson L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00676; El_deh_drog; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                     Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weil D., Ramirez F.; "Organization of the human pro-alpha 2(I) collagen gene."; J. Biol. Chem. 262:16032-16036(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: THIAMÎNE PYROPHOSPHÂTE.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 178 A -> R (IN REF. 1).
370 AA; 41417 MW; 3183EB8881E1BD6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          2-OXOACID DEHYDROGENASE (BCDH) ACTIVITY.
CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-acetyldihydrolipoamide + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POB123; PO2464; Q9UEB6; Q9UPH0; PO8123; PO2464; Q9UEB6; Q9UPH0; O1-AuG-1988 (Rel. 08, Created) D6-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                          MEDLINE-97443988; PubMed-9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 EGPTLIETLTFRYGPHTMAGDDPT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88058962; PubMed=2824475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF012285; AAC24932.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z99111; CAB13331.1; --
PIR; B36718; DEBSPA.
HSSP, P090600; 1QSO.
Subtilist; BG10207; pdhA.
InterPro; IPR001017; E1_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M57435; AAA62681.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE OF 1-15.
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                              STRAIN-IS58;
                                                                                                                       Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
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Korkko J.M., Earley J.J., Ala-Kokko L., Prockop D.J.; "Analysis of the COLIA1 and COLIA2 genes by CSGE and DNA sequencing in 14 patients with mild OI (Type I). Identification of common sequences for null allele mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 145-198 FROM N.A.
MEDLINE-88298792; PubMed-3403536;
Kuivaniemi H., Sabol C., Tromp G., Sippola-Thiele M., Prockop D.J.;
"A 19-base pair deletion in the pro-alpha 2(I) gene of type I
procollagen that causes in-frame RNA splicing from exon 10 to exon 12
in a proband with arypical osteogenesis imperfecta and in his asymptomatic mother.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97255959; PubMed-9101290; Kuivaniemi H., Tromp G., Prockop D.J.; "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of a cDNA for the pro alpha 2 chain of human type I procollagen. Comparison with chick cDNA for pro alpha 2(I) identifies structurally conserved features of the protein and the gene."; Biochemistry 22:1139-1145(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Click E.M., Bornstein P.; "Isomorphic and characterization of the cyanogen bromide peptides from "Isolation and characterization of human skin collagen."; the alpha 1 and alpha 2 chains of human skin collagen."; Biochemistry 9:4699-4706(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fietzek P.P., Furthmayr H., Kuehn K.; "Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-skin collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maekelae J.K., Vuorio T., Vuorio E.;

Growth-dependent modulation of type I collagen production and mRNA

levels in cultured human skin fibroblasts ";

Blochim. Biophys. Acta 1049:171-176(1990).
                                                                                                                                                                                     Kuivaniemi H., Tromp G., Chu M.-L., Prockop D.J.; "Structure of a full-length cDNA clone for the prepro alpha 2(I) chain of human type I procollagen. Comparison with the chicken gene confirms unusual patterns of gene conservation.";
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 623-1366 FROM N.A.
MEDLINE-83178919; PubMed-6687691;
Bernard M.P., Myers J.C., Chu M.-L., Ramirez F., Eikenberry E.F.,
                                                                                             Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                            Kalicki J., Wamsley P., Gibson A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91184577; PubMed-2010058;
Kuivaniemi H., Tromp G., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 263:11407-11413(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Blochem. 47:257-261(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-75008198; Pubmed-4412529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90304220; PubMed-2364107;
                                                                                                                                                         TISSUE=Placenta;
MEDLINE=88339824; PubMed=3421913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-71038625; PubMed-5529814;
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                                                                                                                                                                                                                                                                         Biochem. J. 252:633-640(1988).
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 181-1366 FROM N.A.
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                                                                                                                                    SEQUENCE OF 1-765 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 417-447.
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SEQUENCE FROM N.A.
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Well D., D'Alessio M., Ramirez F., Eyre D.R.; "Structural and functional characterization of a splicing mutation in the pro-alpha 2(I) collagen gene of an Ehlers-Danlos type VII MEDLINE=89123407; PubMed=2914942; Baldwin C.T., Constantinou C., Dumars K.W., Prockop D.J.; Baldwin C.T., Constantinou C., Dumars K.W., Prockop D.J.; A single base mutation that converts glycine 907 of the alpha 2(I) chain of type I procollagen to aspartate in a lethal variant of osteogenesis imperfecta. The single amino acid substitution near the carboxyl terminus destabilizes the whole triple helix."; J. Biol. Chem. 264:3002-3006(1989). MEDLINE 91291136; PubMed = 2064612; Bateman J.F., Hannagan M., Chan D., Cole W.G.; Bateman J.F., Hannagan M., Chan D., Cole W.G.; Characterization of a type I collagen alpha 2(I) glycine -586 to valine substitution in osteogenesis imperfecta type IV. Detection of the mutation and prenatal diagnosis by a chemical cleavage method.; Biochem. J. 276:765-770(1991). Variant Ol-II CYS-877.
Fertala A., Westerhausen A., Morris G.M., Rooney J.E., Prockop D.J.; Fertala A., Westerhausen A., Morris G.M., Rooney J.E., Prockop D.J.; "Two cysteine substitutions in the type I procollagen genes (COLIA1 and COLIA2) that cause lethal osteogenesis imperfecta. The location of glycine substitutions does not in any simple way predict their Am. J. Hum. Genet. 47:A216-A216(1990). associated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseases of bone, cartilage, and blood vessels."; Hum. Mutat. 9:300-315(1997). SECURINCE OF 1090-1107 FROM N.A., AND VARIANT OI-IV ARG-1102. MEDLINE-88227975; PubMed-2897363; Wenstrup R.J., Cohn D.H., Cohen T., Byers P.H.; "Arginine for glycine substitution in the triple-helical domain of the products of one alpha 2(I) collagen allele (COLIA2) produces the osteogenesis imperfecta type IV phenotype."; J. Biol. Chem. 263:7734-7740(1988). MEDLINE-88059013; PubMed-3680255; Wirtz M.K., Glanville R.W., Steinmann B., Rao V.H., Hollister D.W.; Wirtz M.K., Glanville R.W., Steinmann B., Rao V.H., Hollister D.W.; "Ehlers-bands syndarome type VIIB. Deletion of 18 amino acids comprising the N-telopeptide region of a pro-alpha 2(I) chain."; J. Biol. Chem. 262:16376-16385(1987). Byers P.H., Wallis G.A., Willing M.C.; Ostcogenesis imperfecta: translation of mutation to phenotype."; J. Med. Genet. 28:433-442(1991). MEDITION 29380165; PubMed=2777764; MEDITION 2018 11.-H.M., Cole W.G., Bateman J.F.; Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.; CollAl and "Characterization of point mutations in the collagen COLIAl and COLIA2 genes causing lethal perinatal osteogenesis imperfecta."; J. Biol. Chem. 264:15809-15812(1989). "The human type I collagen mutation database."; Nucleic Acids Res. 25:181-187(1997). Biol. Chem. 265:16007-16011(1990). MEDLINE=90368825; PubMed=2394758; VARIANTS OI CYS-349 AND CYS-736. MEDLINE=91115889; PubMed=1990009; MEDLINE=91374476; PubMed=1895312; MEDLINE=97169389; PubMed=9016532; VARIANTS OI-IV VAL-676. VARIANT OI-II SER-955. REVIEW ON OI VARIANTS. REVIEW ON OI VARIANTS VARIANT EDS-VII-A2. EDS-VII-A2. Dalgleish R.; patient VARIANT [19] 

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              Byers P.H., Cohn D.H.,
"The effects of different cysteine for glycine substitutions within
alpha effects of different cysteine for glycine substitutions within
type I collagen triple helix.",
J. Biol. Chem. 266:2590-2594(1991).
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                                                                                                                                                                                                                                                                                                                                             "Mutation in a gene for type I procollagen (COLIA2) in a woman with postmenopausal osteoporosis: evidence for phenotypic and genotypic overlap with mild osteogenesis imperfecta."; Proc. Natl. Acad. Sci. U.S.A. 88:5423-5427(1991).
                                                                                                                                                                                                                                                                           VARIANT OI-IV SER-751.
MEDLINE-91271401; PubMed=2052622;
Spotila L.D., Constantinou C.D., Sereda L., Ganguly A., Riggs B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bateman J.F., Moeller I., Hannagan M., Chan D., Cole W.G.;
Lethal perinatel osteogenesis imperfecta due to a type I collagen
alpha 2(I) Gly to Arg substitution detected by chemical cleavage of
an mRNA:CDNA sequence mismatch."
                                                                                                                                                     Tsuneyoshi T., Westerhausen A., Constantinou C.D., Prockop D.J.; "Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of type I procollagen in lethal osteogenesis imperfecta. The conformational strain on the triple helix introduced by a glycine substitution can be transmitted along the helix."; J. Biol. Chem. 266:15608-15613(1991).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lysyl-trnA synthetase (EC 6.1.1.6) (Lysine--trnA ligase) (LYSRS).
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 Shrago-Howe A.W., Lever L.W., Phillips C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 1; Length 100. Pred. No. 1.38+02;
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                                                                                                                                      MEDLINE=91340689; PubMed=1874719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.1%;
50.0%;
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 Wenstrup R.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002904; tRNA-synt_lys_I.
Pfam; PF01921; tRNA-synt_lys_I.
PROSITE; PS00118 AA_TRNA_LIGASE_I; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimelman D.; ^{\circ} "GBP, an inhibitor of GSK-3, is implicated in Xenopus development and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla: Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                             Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yost C., Farr G.H. III, Pierce S.B., Ferkey D.M., Chen M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 93:1031-1041(1998).
-!- FUNCTION: BINDS GSK-3 AND PREVENTS GSK-3-DEPENDENT
-!- FUNCTION: MAY BE IMPLICATED IN TUMOR PROGRESSION
-!- SIMILARITY: BELONGS TO THE GSK-3-BINDING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
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                                                                                                                                                                                                                                                                                                                                                      65114 MW; 753664E2937FBF27 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                         27.8%; Score 47.5; DB 1; 35.7%; Pred. No. 61;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GSK.3 binding protein FRAT2 (Fragment).
                                                                                                                                                                                                                                                                                                                                      "KMSKS" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
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53.3%; Pred. No.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                   309
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., Deboy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khourl H., Gill J., Mikula A.,
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-:- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
-:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- SUBUNIT: LOCATION: INNER SIDE OF THE MEMBRANE (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE DIHYDROOROTATE DEHYDROGENASE FAMILY.
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S)-dihydroorotate + 0(2) = orotate +
      5; Indels
      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DHOdehase) (DHODase) (DHOD).*
PYRD OR RV2139 OR MT2197 OR MTCY270.29C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001295; DHO_dh.
InterPro; IPR003009; FMN_enzyme.
Pfam; PF01180; DHOdehase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z95388; CAB08654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE007067; AAK46481.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
         8; Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rv2139; -
                                                                  14 AGPNGIEGPTLRQWL 28
                                                                                                                            15 AGPSALPGPCRRGWL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MT2197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H(2)0(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList;
                                                                                                                                                                                                                                                                                  PYRD_MYCTU
006236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
            Matches
                                                                                                                                                                                                                        RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Photosynthesis; Photosystem II; Thylakoid; Chlorophyll; Chloroplast;
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Loss of all ndh genes as determined by sequencing the entire chloroplast genome of the black pine Pinus thunbergii."; Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=3350;
                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kDa reaction center protein (P6 protein) (CP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOTOSYSTEM II. IT IS A CHLORÒPHÝLL BINDING PROTEIN.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN; CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.5%; Score 47; DB 1; Length 473; 32.5%; Pred. No. 59; ive 5; Mismatches 12; Indels
Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
                                                                                DB 1; Length 357;
                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 AA; 51826 MW; 0E05E8FC7268465C CRC64;
                                                3D9D107DD9B4FCB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Pinus thunbergii (Green pine) (Japanese black pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THYLAKOID MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 GETMRFWDLRAPWLEPLRGPNGLDLSKLRKDIOPWOERRS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GPTLR-----QWLAARAGPNGIEGPTLRQ-----WLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUR4_HUMAN STANDARD; PRT; 1338 AA.
015067;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
                                   FMN (POTENTIAL)
                                                                                                                                                                                                                                                                          473 AA.
                                                                                                      Pred. No. 45;
0; Mismatches
                                                                                                    45;
                                                                                     Score 47;
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=95024047; PubMed=7937893;
                                   294 F
37998 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D17510; BAA04424.1; -. Mendel; 10000; PINth;psbC;1. InterPro; IPR000932; PSII.
                                                                                    27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                       Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                          256 RLGPGGISGPPLAQ 269
                                                                                                                                                        13 RAGPNGIEGPTLRQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00421; PSII
                                       286
357 AA;
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                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                                                              PSBC_PINTH
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                                                       SEQUENCE
                                                                                       Query Match
                                         NP BIND
                                                                                                                                                                                                                                                                                            P41643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 27
PUR4_HUMAN
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                                                                                                                                                                                                                                                              PSBC_PINTH
                                                                                                                                                                                                                                            RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO TYPE-1 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                  Patterson D., Bleskan J., Gardiner K., Bowersox J.; "Human phosphoribosylformylglycinamide amidotransferase (FGARAT): regional mapping, complete coding sequence, isolation of a functional genomic clone, and DNA sequence analysis."; Gene 239:381-391(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new CDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
-!- CATALYTIC ACTIVITY: ATP + 5'-phosphoribosylformylglycinamide + Logutamine + Hi(2)0 - ADP + phosphate + 5'-photamidine + Logutamine + Hi(2)0 - ADP + phosphate + Similarity - PATHWAY: DE NOVO DURINE BIOSYNHERSIS; FOURTH STEP.
-!- SAPHWAY: DE NOVO PURINE BIOSYNHERSIS; FOURTH STEP.
-!- SUBCELLULAR LOCATION: CYLOPIASMIC BY SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pirity District Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of the Proposition of t
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                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) (FGAM
synthase) (FGAMS) (FORM)glycinamide ribotide amidotransferase)
(FGARAT) (Formylglycinamide ribotide synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1158 1158 GATASE (BY SIMILARITY).
1338 AA; 144663 MW; 9741F8EDB5E1FEE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB002359; BAA20816.1; ALT_INIT.
MIM; 602133; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 QWLAARAGP----NGIEGPTLRQWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence
01-MAR-2002 (Rel. 41, Last annotatio
Collagen alpha 2(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20018191; Pubmed=10548741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97349984; PubMed-9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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1158 1158
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                                                                                                                                    PFAS OR KIAA0361.
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA21_MOUSE
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SEQUENCE
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CA21_MOUSE
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                                                                                                                                  Phillips C.L., Morgan A.L., Lever L.W., Wenstrup R.J.;
"Sequence analysis of a full-length cDNA for the murine pro alpha
2(1) collagen chain: comparison of the derived primary structure with
human pro alpha 2(1) collagen.";
Genomics 13:1345-1346(1992).
                                                                                                                                                                                                                                                                                                                                                                                                          'Construction of a full-length murine pro alpha 2(I) collagen cDNA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONVERTED TO AN ALDEHYDE GROUP THAT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
-!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A43291; A43291.
MGD: MGI: 88468; Colla2.
InterPro; IPR000887; Collagen.
InterPro; IPR000885; Fib_collagen_C.
Pfam; PF01410; CoLFI; 1.
Propom: PF002078; Fib_collagen_C; 1.
SMART; SM00038; CoLFI; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rossi P., de Crombrughe B.;
"Identification of a cell-specific transcriptional enhancer in first intron of the mouse alpha 2 (type I) collagen gene.";
Proc. Natl. Acad. Sci. U.S.A. 84:5590-5594(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID (BY
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                                                                                                                                                                                                                                                                                        Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       Phillips C.L., Lever L.W., Pinnell S.R., Quarles L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO-TERMINAL PROPEPTIDE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                          the polymerase chain reaction.";
J. Invest. Dermatol. 97:980-984(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                  MEDLINE=92372043; PubMed=1505972;
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92084969; PubMed=1748823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-23 FROM N.A.
MEDLINE=87289650; Pubmed=3039494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FIBRILLAR FORMING COLLAGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X58251; CAA41205.1; -.
EMBL; BC007158; AAH07158.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; K01832; AAA37331.1; -.
                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-110 FROM N.A.
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musculus (Mouse)
                                                                                                                                                                                                                                                          TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROXYAPATITE.
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
1109
                                                                                                                                                                                                                                                                                                                                           TISSUE=Calvaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                    TISSUE-Calvaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                            Wenstrup R.J.;
                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
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P11675;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91021039; PubMed-2171211; VICER C., KOZMIK Z., Paces V., Schlrm S., Schwyzer M.; Fordik z., Paces V., Schlrm S., Schwyzer M.; Pseudorables virus immediate-early gene overlaps with an oppositely oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enhancer regions.";
Virology 179:365-377(1990).
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-! SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTW: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF PHOSPHORYLATION.
              (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
V -> A (IN REF. 4).
R -> TT (IN REF. 1).
AM, OD17DFSD6C1452D1 CRC64;
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347 354 POLY-SER.
                                                                                                                     Score 47; DB 1; Length 1372;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.5%; Score 47; DB 1; Length 1446; 44.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                         10; Indels
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W; 81F43A3DE3DDA068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
INVOLVED IN CROSS-LINKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1461 AA.
                                                                                                                                                                                                                                                                                                                     PRT; 1446 AA.
                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudorabies virus (strain Kaplan) (PRV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GPSAAPRWSPARGDPVGEPGPAAR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTL--RQWLAARAGPNGIEGPTLR 25
                                1273 1273 N-LI
15 15 V->
1167 1167 R->
1372 AA; 129557 MW;
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                                                                                                                                                                                                                758 IVGPTGSVGAAGPSGPNGPPGP 779
                                                                                                                                                                                            1 IEGPTLRQWLAARAGPNGIEGP 22
                                                                                                                                                                                                                                                                                                                                                                                                     fmmediate-early protein IE180.
                                                                                                                     27.5%;
50.0%;
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                                                                                                                                                         11; Conservative
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hes 11; Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-33703;
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ID IE18_PRVIF
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SEQUENCE
                                                                 CONFLICT
                                  CARBOHYD
                                                                                                                        Query Match
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                                                     CONFLICT
                                                                                                                                                                                                                                                                                RESULT 29
IE18_PRVKA
                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                   Cheung A.K.;
Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRAPING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                                                                       Cheung A.K.; "DNA nucleotide sequence analysis of the immediate-early gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                            Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

390 405 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 47; DB 1; Length 1461; 44.0%; Pred. No. 1.9e+02; tive 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER.
W; 7F31E7ABE403B208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
            01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 9, 2002, 09:00:08
                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:4637-4646(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 GPSAAPRRWSPARGDPVGEPGPAAR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GPTL--RQWLAARAGPNGIEGPTLR 25
                                                                                                                                                                                                                                MEDLINE=89315207; PubMed=2546124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1461 AA; 149833 MW;
                                                                         Immediate-early protein IE180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 44.0 nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S04713; EDBEIF.
                                                                                                                                                                                                                                                                                              pseudorabies virus.
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=31523;
                                                                                                                                                                                                                                                                                                                                                     REVISIONS
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δy
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:52:16; Search time 11.466 Seconds (without alignments) 482.803 Million cell updates/sec Run on:

US-09-422-838C-23 Perfect score:

1 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 32

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_19:\*

sp\_unclassified:\* sp\_invertebrate:\* sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\* sp\_rvirus:\*
sp\_bacteriap:\* sp\_organelle:\* sp\_archea:\* sp\_bacteria:\* sp\_plant:\* sp\_mammal:\* sp\_fungi:\* sp\_human:\* sp\_phage: \* sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

SUMMARIES

Description		Op1841 cleponella p	Cores poryangium	Observed Streptomyce	Obstact dioSopulla	Ogano, caulobacter	DOZO11 terrococold1	P9/UIL Streptomyce	C91544 pseudomonas	Casuma deinococcus	Warteb deinococcus	Q96c78 homo sapien	Q9x7n5 streptomvce	016161 mytilus adu	Obbade atmost and	Ogran streptomyce	U91096 streptomyce	Q9i477 pseudomonas
ID	083436	091,804	09S5E5	0972.82		094192						0990/8	SN/X6Ö	016161	0982.05	00100	V2L096	091477
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Query Match Length DB	683	607	509	869	361	1744	420	1095	305	326	2 6	# \ 0 C	390	902	196	1349	1	3 / T
Query Match	36.8	36.3	35.1	34.2	32.7	32.5	32.2	31.6	31.0	31.0	30.7		4.00	30.4	30.4	30.4		30.1
Score	63	62	9	58.5	26	55.5	55	54	53	53	5.2.5		7 0	25	52	52	1 1 1	0.10
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Gaps . 0

Query Match 36.8%; Score 63; DB 16; Length 683; Best Local Similarity 46.4%; Pred. No. 4.6; Matches 13; Conservative 3; Mismatches 12; Indels

Q9ydq0 aeropyrum p 005576 mycobacteri Q9rk51 streptomyce Q9xK57 ktebsiella	່ໝວາ	V9190/ pagrus majo Q981n1 rhizobium 1 O90v79 leishmenia	093178 streptomyce 098141 rhizobinm	Ogf2fo deinococcus	Q9xdb0 mycobacter1	Q9t5b8 agrobacteri O9ilm2 pseudomonas	017754 caenorhabdi	Q98p10 rhizobium l Q9uqhl homo sapien	Q9bxa9 homo sapien	OS41XO PERILLA IRU OSWV74 mns mnschlu	Q9aqh5 achromobact	020968 caenorhabdi	Q913h3 rhizobium 1	Q9as26 oryza sativ	Q43416 cenchrus ci	Q9rkm5 streptomyce
Q9YDQ0 Q05576 Q9RK51 Q9X757	Q94XJ8 Q92ZH9 Q91407	Q981N1 Q9GY79	Q93LY8 Q98LG1	Q9RWB0 09F2F9	Q9XDB0	Q9F3B8 Q9I1M2	017754	Q90GH1	Q9BXA9 O94LXO	Q9WV74	Q9AQH5	020968	09г3н3	09AS26	043416	Q9RKM5
17 16 2 2	16 16	16	2 16	1 <sub>6</sub>						11				2;		
281 306 322 381 589	600 719 1820	526 1460	250	351	400	410	472	1272	1300	336	133	214	249	250	307	319
22000 2000 2000 8000 8000	29.8 29.8	29.5	29.2 29.2	29.5 29.2	29.2	29.5	29.2	29.5	26.5 28.5	28.9	28.7	28.7	7.87	7.87	7.87	7.87
51 51 51 51	51 51 51	50.5	20	50	500	20	50 00 00 00	000	6	49.5	49	49	4. 4 2) (	n (	4 • V (	4. V
17 18 19 20 21	22 23 24	25	23	30	31	33	9. 6. 4. 7.	36	3 / 3 8	39		41	7 7	7 4	4 ·	<b>4</b> C

## ALIGNMENTS

Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Rhalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowmen C., Cotton M.D., Fujii C., Garland S., Wenter B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., "Complete genome sequence of Treponema pallidum, the syphilis 683 AA; 74518 MW; F91407FA7094AAD1 CRC64; Bacteria; Spirochaetales; Spirochaetaceae; Treponema NCBL\_TaxID=160; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PRT; STRAIN=NICHOLS; MEDLINE=98332770; PubMed=9665876; spirochete.";
Science 281:375.388(1998).
EMBL; AE001220; AAC65409.1;
TIGR; TP0421; -.
InterPro; IPR001258; NHL.
InterPro; IPR001440; TPR.
Pfam; PF01456; NHL, 4. CONSERVED HYPOTHETICAL PROTEIN. PRELIMINARY; Treponema pallidum. SEQUENCE FROM N.A. Complete proteome. SEQUENCE 683 AA; RESULT 1 083436 

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MEDLINE=97000351; PubMed=8843436;
                                                                                                 SEQUENCE
                                                                                                                     Query Match
                                                                                                                                                                                                                                           09VZ82
                                                                                                                                            Matches
                                                                                                                                                                                                                        RESULT 4
                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
ORF1, ORF2, ORF3, ORF4, ORF5 GENES, COMPLETE CDS (PUTATIVE DNA-BINDING
                                                                                                                                                                                                                STRAIN-SO CE90;
MEDIZHRE-2013045; PubMed-10662695; Milnamow M.,
Molnar I., Schupp T., Ono M., Zirkle R.E., Milnamow M.,
Nowak-Thompson B., Engel N., Toupet C., Stratmann A., Cyr D.D.,
Gorlach J., Mayo J.M., Hu A., Goff S., Schmid J., Ligon J.M.;
The biosynthetic gene cluster for the microtubule-stabilizing agents
epothliones A and B from Sorangium cellulosum So ce90.";
Chem. Biol. 7:97-109(2000).
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                      36.3%; Score 62; DB 2; Length 607; 34.8%; Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                     Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococales; Soranqineae; Polvanaiaceae: Dolvanaium
                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Umeyama T., Ping Chin L., Horinouchi S.; "Multicopy suppressor gene of afsR mutant."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     96 VDGPALVRWLAARGAP----GPLREYEEERERARTAQEARRLWLAA 137
                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGPNCIEGP-------TLRQWLAA 30
                                                                                                                                                                                                                                                                                                                                607 AA; 66326 MW; F113CA299B25048E CRC64;
                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 66.3 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 AA.
                                                                                607 AA.
                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
                   PRT;
      4 PTLRQWLAARAGPNGIEGPTLRQWLAAR 31
                                                                                                       1-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
                                                                                   PRELIMINARY;
                                                                                                                                                 Polyangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 16; Conserv
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                                                                                                                                                                                   NCBI_TaxID=56;
                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
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RADINE-20196006; Pubmed-10731132;

RADINE-20196006; Pubmed-10731132;

RADINE-20196006; Pubmed-10731132;

RA Adams M.D. (Cenliker S.E., Holt R.A., Galle R.F., Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Stutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Hedrerson S.N.,

RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Barlaw R.M. Basu A., Baxendale J., Baytektargoll L., Beatley B.D.,

RA Barlaw R.W., Basu A., Baxendale J., Baytektargoll L., Beatley E.M.,

RA Bortkow D., Botchan M.R., Bouck J., Broktater P., Blochankov S., Dunkov D., Botchan M.R., Bouck J., Broktater P., Blochankov S., Dunkov B.C., Dunne R.A.

RA Burls K.C., Busam D.A., Buller H., Caddeu E., Center A., Chandre I.,

RA Burls K.J., Benos P.V., Bernam B.P., Brottler P., Botchan M., Buller H., Caddeu E., Center A., Chandre I.,

RA Burls K.J., Bevangelista C.C., Ferriac S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Bevangelista C.C., Ferriac S., Pleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Hehman A.P., Inseywan C.,

RA Lasko P., Edi Y., Levitsky A.A., Li J. Will M.H., Ibeywan C.,

RA Lasko P., Lei Y., Levitsky A.A., Li Z., Kenlison J.A., Morbison D.L.,

RA Lasko P., Lei Y., Levitsky A.A., Li Z., Lina Y., Morly D.M., Nessen M.G.,

RA Reinert R., Raringer C.D., McLeod M.P., Morpherson D.L.,

RA Reinert R., Randingen K.A., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Morphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warphy B., Warph
                                                                    "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AB017438; BAA82701.1;
EMBL; AL356529; CAB92204.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                      y match 35.1%; Score 60; DB 2; Length 509; Local Similarity 44.1%; Pred. No. 8.2; hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                   509 AA; 54398 MW; 7BB074DAAE0F1867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       869 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQW---LAARAGPNGIE-GPTLRQWLAA 30
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STRAIN=ATCC 19089 / CBI5;
MEDLINE=2117368; PubMed=11259647;
MEDLINE=2117368; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.E., Alley W.R.K., Ohta N., Maddock J.R., Deboy R.T., Dodson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.",
Proc. Natl. Acad. Sci. Natl. 1864 186-4141 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                            34.2%; Score 58.5; DB 5; Length 869; 40.6%; Pred. No. 22;
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Rembl. AE003482: ARA-1943.11.
Rembl. AE003482: ARA-1943.11.
Rembl. AE003482: ARA-1943.11.
Rembl. AE003482: ARA-1947.11.
Rembl. AE003482: TRNA-synt_la.
Rembl. AE003302: TRNA-synt_la.
Rembl. AE00333: TRNA-synt_la.
Rembl. AE00333: TRNA-Synt_la.
Rembl. PROSITE; PRO00383: TRNA-SYNTHLEO.
Rembl. PROSITE; PRO00178; AA_TRNA-LIGASE_I; I.
SEQUENCE 869 AA; 99299 MW; E87AlECBEBBZ7B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.7%; Score 56; DB 16; Length 361; 54.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATION EFFLUX FAMILY PROTEIN.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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InterPro; IPR002395; Kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01545; Cation_efflux; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 40.69
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE 361 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"Cloning of a gene encoding a sorbitol oxidase from Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces sp. Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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                                                        Paracoccidioides brasiliensis.
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.
NCBL_Tax1D=121759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00242; MYSC; 1.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
SEQUENCE 1744 AA; 193777 MW; DB7622D0A69F0705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF107624; AAD19613.2; -
InterPro; IPR0012923; Chitio_synth.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR001699; myosin_head.
Pfam; PF00063; myosin_head; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nino-Vega G.A., San-Blas G.;
"Sequence analysis of the CHS4 gene of Paracoccidioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AB00519; BAA19135.1; -InterPro: IPR001575; Oxid_FAD_bind. Ffam; PF01565; FAD_binding_4; 1. SEQUENCE 420 AA; 45181 MW; EF3189045CAF0649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.5%; Score 55.5; DB 3; 51.7%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 GPVGQVWLKQRVGDEGARSVMPAEWLGAR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPTLRQWLAARAGPNGIEGPTLRQWLAAR 31
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20210320; PubMed=10746225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 11; Conserv
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CHITIN SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brasiliensis.
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033747; BAA85759.1; -.
Endonuclease.
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                                               SEQUENCE
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Kloyama S., Rikuctural gene of an alternative incision enzyme for DNA
damage in Deinococcus radiodurans.";
                                                                                                                                                                                                                                 Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey W.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Rcomplete genome sequence of Pseudomonas aeruginosa PAOL, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
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0
                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34370FB8BEC201AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFGATE PFO2785; BIOCÍTO_CÍT.

PFAM: PFO02785; BIOCÍTO_LIPOYI; 1.

PFAM: PFO0389; CZPSASE_L_Chain; 1.

PFAM: PFO0289; CPSASE_L_Chain; 1.

PFAM: PFO0289; CPSASE_L_CD2; 1.

PROSITE: PSO0188; BIOTIN; 1.

PROSITE: PSO0225; CRSTALLIN BETACAMMA; UNKNOWN_1.

PROSITE: PSO0225; CRSTALLIN BETACAMMA; UNKNOWN_1.

PROSITE: PSO0225; CRSTALLIN BETACAMMA; 34370FB8BECZO1AD CRC SEQUENCE 1095 AA; 116876 MW; 34370FB8BECZO1AD CRC
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 AA
                                        PRT; 1095 AA.
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EMBL; AE004569; AAG04789.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001249; Accoa_biotinCC.
Interpro; IPR001882; Biotin.
Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR000022; Carboxyl_trans.
Interpro; IPR000901; CPSase.
                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001064; Crystallin.
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                                                                                                          PROBABLE PYRUVATE CARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                              opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
                                           PRELIMINARY;
                                                                                                                                     Pseudomonas aeruginosa
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                                                                                                                                                                          NCBI_TaxID=287;
                                                                                    01-MAR-2001
01-DEC-2001
                                                                                                                                                               Pseudomonas
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                    RESULT 8
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MEDLINE-20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson D.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang D., Pamphlle W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
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                                                                                                                    12;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 15 (METARGIDIN).
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                                                    Score 53; DB 2; Length 305;
Pred. No. 37;
4; Mismatches 6; Indels
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TIGR: DR1819; -.
Endonuclease; Complete proteome.
SEQUENCE 326 AA; 35693 MW; C4EAUDOAD2C38988 CRC64;
305 AA; 33592 MW; B94D333243E2FEA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
UV DAMAGE BNDONUCLEASE, PUTATIVE.
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                                                                                                                                                                                                                                      228 EDPSVREWVLRARATWOPPEWOVVHLSNGIEGPODRR 264
                                                                                                                                                                               2 EGPTLRQW-LAARAG------PNGIEGPTLRQ 26
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                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Science 286:1571-1577(1999).
                                                                   31.0%;
                                                                                                  40.5%;
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Matches 15; Conservative
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                                                                                                  Best Local Similarity 40.5
Matches 15; Conservative
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Coyne K.J., Qin X.X., Waite J.H.;
                                                                                                                                                                                                                                                          Local Similarity
Hes 11; Conserv
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SEQUENCE
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coeliscolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL049587; CAB40679.1;
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
MCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                  Query Match

30.7%; Score 52.5; DB 4; Length 814;
Best Local Similarity 44.8%; Pred. No. 1.2e+02;
Matches 13; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.4%; Score 52; DB 2; Length 396; 34.4%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
814 AA; 87717 MW; 683A8368AD30996B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 396 AA; 41908 MW; BCB465197F3A3F6E CRC64;
                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                       396 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PTLRQWLAARAGPNGIEGPT----LRQWLAAR 31
                                                                                                                                            128 LKGPTC-QYRAAQSGPSERPGPPQRALLA 755
                                                                                                                      1 IEGPTLROWLAARAGPNGIEGPTLROWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                         PRT;
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MEDLINE=97000351; Pubmed=8843436;
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                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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es 11; Conserv
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SEQUENCE
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Q9X7N5
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"Extensible collagen in mussel byssus: A natural block copolymer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Kinashi H., Hopwood D.A.,
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                                                                                                                                                                                30.4%; Score 52; DB 5; Length 902; 52.4%; Pred. No. 1.6e+02; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 967;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           21 902 COLLAGEN P.
902 AA; 78526 MW; DIEF09DEA2BD9EF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
I COMPLEX, SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 2;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                   967 AA.
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                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                 Science 277:1830-1832(1997).
EMBL, AF015539; AAB80719.1; -
InterPro; IPR000087; Collagen.
Pfam: PF01391; Collagen; 7.
Signal; Collagen.
                                                                                                                                                                                                                                                                         :||| | | ||||| 527 KGPTGAQGPAGPAGPSGEQGP 547
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53.68;
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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902
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InterPro; IPR000205; NAD\_binding.

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Mol. Microbiol. 21:77-96(1996).
EMBL; AL163003; CAB86115.1; -
InterPro; IPR000719; Euk.Pkinase.
InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 15692 / PAO1:
STRAIN-ATCC 15692 / PAO1:
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.4%; Score 52; DB 2; Length 1349; larity 51.6%; Pred. No. 2.4e+02; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                       Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    Prostre: PF00069; pkinase; 1.
PROSTRE: PF50011: PROTEIN KINASE_DOM; 1.
PROSTRE: PS00136; SUBTILASE_ASP: UNKNOWN.1.
ATP-binding: Hypothetical protein; Transferase.
SEQUENCE 1349 AA; 145671 MW; F0902A235D694B38 CRC64;
                                                                                                                                           STRAIN-A3(2);
Brown S.P., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN PA1267.
  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 145.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                            STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                    Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                          NCBI_TaxID=1902;
                                                                                                                                                                                                               STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas.
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A KAWATADAYASI Y., HINO, Y., HOLIKAWA H., YAMAZAKI S., HAIKAWA Y.,
A Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
A Hosoyama A., Fukul S., Magai Y., Nishijima K., Nakazawa H.,
A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Makamura Y., Nomura N., Sako Y., Kikuchi H.;
A Complete genome sequence of an aerobic hyper-thermophilic
Complete genome sequence of an aerobic hyper-thermophilic
Complete genome sequence of an aerobic hyper-thermophilic
BEBL; AP000060; BAA79847.1; -.
II DNA Res. 101(1999)
REBLS: AND COMPLETE: NOROWALI.
REBLS: AND COMPLETE: UNKNOWN_I.
REBLS: AND COMPLETE: ORD PREAFE; UNKNOWN_I.
REQUENCE 281 AA, 32123 MW; 09AC9AF6F92CB4IE CRC64;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                 Gaps
                                                                                                                            13;
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8
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                                                                     30.1%; Score 51.5; DB 16; Length 371; 31.0%; Pred. No. 72; ive 7; Mismatches 9; Indels 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.8%; Score 51; DB 17; Length 281; 34.4%; Pred. No. 62;
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Hypothetical protein; Complete proteome.
SEQUENCE 371 AA; 39174 MW; 016D60440BAD50D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHERICAL 32.1 KDA PROTEIN APE0867.
                                                                                                                                                                                        4 PTLRQWLAARAGP-----NGIEGPTLR----QWLAARA 32
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                                                                                                                                                                                                                                                                                                                                                                                       281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TLRQWLAARAGPN----GIEGPTLRQWLAAR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                             Best_Local Similarity 31.0%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
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005576
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Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Honsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulter S., Seeger K., Skelton S., Squares S., Squares R., Stalton J.E., Taylor K., Whitehead S., Barrell B.G.; Complete genome sequence."

Nature 393:37-544(1998).
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL117669; CAB56131.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy L., Harris D.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                306 AA; 32378 MW; 24C2387443B0A3E8 CRC64;
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SEQUENCE 322 AA; 35339 MW; DD55BB0480090638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 35.3 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB
Pred. No. 68;
                                                                                                                                                                                                                EMBL: 294752: CAB08153.1; --
Tuberculist; Rv0993; --
InterPro; IPR001825; NTP_transferase.
Pfam; PF00483; NTP_transferase.
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                          69.28;
                                                                                                                                                                                                                                                                                                                                                                                                   29.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GPTLROWLAARAG 15
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Best Local Similarity
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nes 8; Conserv
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381 AA.

PRT;

PRELIMINARY;

09X757

RESULT 20

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Q9X757

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MEDLINE-94150718; PubMed=7906398;
MEDLINE-94150718; PubMed=7906398;
Milson R., Alinacough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favelio A., Fulton L.,
Gardher A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Shiton J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                  Papanicolaou G.A., Medeiros A.A., Jacoby G.A., "Novel plasmid mediated beta-lactamase (MIR-1) conferring resistance to oxyimino- and alpha-methoxy-beta-lactams in clinical isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Jacoby G.A., Tran J.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, M37839, AAD22636.1; -.
HSSP; P05364; 2BLT.
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                           Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                        Klebsiella pneumoniae.";
Antimicrob. Agents Chemother. 34:2200-2209(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00144; beta-lactamase; 1.
PROSITE; PS00336; BETA_LACTAMASE_C; 1.
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01, Last sequence 19, Last anno
          Created)
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InterPro; IPR001586; Beta_lactam_C.
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12,
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33.3%;
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
BETA-LACTAMASE.
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01-NOV-1996 (TrEMBLrel.
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                                                                                                    Klebsiella pneumoniae.
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                                                                                                                       Plasmid pMG230.
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                                                                                                                                                                   Klebsiella
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:959-964(2000).
-i- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS).
EMB. AE004761; AAG06794.1; -.
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                                                                                                                                                                     Query Match

29.8%; Score 51; DB 5; Length 589;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 9; Indels
                                                                                   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U41557; AAA83307.1; -.
InterPro; IPRO00087; Collagen.
SEQUENCE 589 AA; 55491 MW; 038508B5221A5EB9 CRC64;
"The sequence of C. elegans cosmid C50F7.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Complete_proteome; Transport.
600 AA; 63454 MW; D3DEA5FB1A56FB2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSPORT PROTEIN HASD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 AA.
                                                                                                                                                                                                                                                                                                                                                                     PRT; 600 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001140; ABC_transporter_tmem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0211; ABC_TRANSPORTER; 1. ATP-binding; Complete proteome; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003439; ABC_transportr.
Interpro; IPR001687; APL_GTP_A.
Pfam; PP00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                 539 ESPSFFQWIFGRPKPSGPAGP 559
                                                                                                                                                                                                                                                2 EGPTLRQWLAARAGPNGIEGP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 LDGADLRQWSAAALGPH 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGPN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P13569; INBD.
InterPro; IPR003593; AAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HASD OR PA3406
                                                                        Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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0922H9;
                                                                                                                                                                                                                                                                                                                                                                       96 чуз
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0922H9
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Q9HYJ8
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MEDLINE-21240220; PubMed=11342118;

A Touhata K., Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;

A Touhata K., Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;

A Touhata K., Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;

A Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;

Chain of red seabream.";

L Blochin. Biophys. Acta 1517:323-326(2001).

R EMBL; AB045975; BAB02287.;

R InterPro; IPR000087; Collagen.

R InterPro; IPR001290; Fail_collagen.C.

R InterPro; IPR001290; Frenyltn.

R InterPro; IPR001219; TSPN.

R Pfam; PF01410; ColFf; 1.

R Pfam; PF02210; TSPN; 1.

R ProDom; PR002078; Fib_collagen.C; 1.
                                                                                                                                                                                                                                                            Barnett M.J. Fisher R.R. Jones T., Komp C., Abola A.P.,
Barnett M.J. Fisher R.R. Capela D., Galibert F., Gouzy J.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Hulzar L., Hyman R.W., Kahn D., Kann M.L.,
Kallan S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
Nucleotide sequence and predicted functions of the entire
Sinorhizobium mellioti psym megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBE, AE007241, AAK65164.1;
Plasmid; Hypothetical prothetin; Complete protecome.
SEQUENCE 719 AA, 77245 MW; 045DBBCCB1691789 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pagrus major (Red sea bream) (Chrysophrys major).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                          Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.8%; Score 51; DB 16; Length 719; 36.4%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1820 AA; 181678 MW; 46E45E8AF7AD3DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN SMA0937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 LUDDEVROWLTAKQAAAPAAATTPAGLASQWIA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAAR--AGPNGIEGPT--LRQWLA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00294; PRENYLATION; UNKNOWN_1. Collagen.
                                                                                                                                                                                                                                                  MEDLINE=21396509; PubMed=11481432;
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SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.8%
Best Local Similarity 36.4%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sparidae; Pagrus
                                                                                                                                                                          NCBI_TaxID=382;
                                                                                                                                                                                                                                      STRAIN=1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLV/XIA1.
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                                                                                  SMA0937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  091907
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.
Oliver K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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29.8%; Score 51; DB 13; Length 1820; 52.6%; Pred. No. 4.5e+02; Live 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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EMBL; AL390114; CAC01975.2; -.
InterPro: IPR001313; PUM.
Pfam; PF00066; PUF; Dumilio; 7.
SEQUENCE 1460 AA: 153236 MW; 7B5EF90010364DD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
REPLICATION PRIMASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE HYPOTHETICAL 21.3 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50.5; DB 16;
Pred. No. 1.4e+02;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                   526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1460 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21082930; PubMed=11214968;
                                                                                                                                         1403 GPVGPQGLAGKAGPEGLRG 1421
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50.0%;
                                                                                                       3 GPTLRQWLAARAGPNGIEG 21
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
Query Match
Best Local Similarity
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Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pMLa
                                                  10;
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Q981N1;
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Q981N1
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                                                  Matches
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Q9GY79
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Length 1460;

DB 5;

29.5%; Score 50.5;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                   Gaps
                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PGA64;
Metsa Ketela M., Kantola J., Ylihonko K.;
Metsa Ketela M., Kantola J., Ylihonko K.;
"Cloning and Characterization of a Silent Angucycline-type Gene Cluster from a Rubromycin B Producing Streptomyces sp. PGA64.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AV034378; AAK57521.1;
NON_TER 250 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 50; DB 2; Length 250; 38.5%; Pred. No. 74;
Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 AA; 26031 MW; 597EE6581FFF8C97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 AA; 27788 MW; 86698FFD04036653 CRC64;
                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
PROBABLE SHORT CHAIN DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LRQWLAARAGPNGIEGPT-----LR--QWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 AA
         37.9%; Pred. nv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                           4 PTLRQWLAARAGP----NGIEGPTLRQW 27
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti)
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EMBL, AP002996; BAB48502.1; -.

InterPro; IPR002198; AbH.short.

InterPro; IPR00205; NAD_binding.

Pfam; PF001.06; adh.short; 1.

PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                             Streptomyces sp. PGA64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
            Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=161235;
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                             PGAK (FRAGMENT).
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Q98LG1
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                                                                                                                                                                                                                                                                                                                                                                                                       White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphlle W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=47716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blanco G., Patallo E.P., Brana A.F., Trefzer A., Bechthold A., Rohr J., Mendez C., Salas J.A.; "Identification of a sugar flexible glycosyltransferase from Streptomyces olivaceus, the producer of the antintumor polyketide
                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                   8; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 351;
29.2%; Score 50; DB 16; Length 268; 40.0%; Pred. No. 79; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 351 AA; 38454 MW; 31B01305A7B28694 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 16; L4
Pred. No. 1.1e+02;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| | || :| || || || || || 206 QGIADRFGPHRIDGPDYRQRGTEPAQPLSEAEFAAWLA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 QWLAARAGPNGIEGPTLRQ-------WLA 29
                                                                                     384 AA.
                                                                                                                                                                                 351 AA
                                                                    8 QWLAARAGPNG------IEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=R1;
MEDLINE=20036896; PubMed=10567266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 286:1571-1577(1999).
EMBL; AE001931; AAF10338.1; -.
TIGR; DR0759; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.2%;
Best Local Similarity 34.2%;
Matches 13; Conservative
      Query Match 29.2's
Best Local Similarity 40.0's
Matches 14; Conservative
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                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
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Patallo E.P.; "Decoxysugar methylation during biosynthesis of the antitumor polyketide elloramycin by Strepomyces olivaceus: characterization of three methyltransferase genes."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            "Identification of a sugar flexible glycosyltransferase from Streptomyces olivaceus, the producer of the antitumor polyketide elloramycin.";
                                                                                                                                                                                                                                                                                                                                                                                            ,
                                                                                                                                                                                                                                                                                                                                                   29.2%; Score 50; DB 2; Length 384; 52.2%; Pred. No. 1.2e+02; tive 2; Mismatches 9; Indels
                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AJ300305; CAC16413.1; -- EMBL; AJ309821; CAC32467.1; --
                                                                                                                                                                                                                                                                                                                   384 AA; 39674 MW; A254F56B6ED12F2B CRC64;
                                                                                                                                                                                                                                                             Interpro; IPR000890; Acetate_kin.
PROSITE; PS01076; ACETATE_KINASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 VROLLAERLGPAGSEPPPERYFL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LRQWLAARAGPNGIEGPTLRQWL 28
                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 52.29
Matches 12; Conservative
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Search completed: October 9, 2002, 09:03:03 Job time: 12.5494 secs

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(without alignments) 247.023 Million cell updates/sec
                                                                                                                     October 9, 2002, 08:50:51; Search time 16.1874 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
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                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100
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Maximum DB seq length: 200000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	TPO-mimetic peptid	TPO-MIMELIC Perlin	Thrombopolectin	Thrombopoletin min	TPO-MIMELIC PEPLIA	TPO-MIMECIC PARTOR C. TRACTOR C.	Synthetic implime	TOWN OF TO AT THE TOWN OF THE	Synthelic Imr. Inc	TAP-TAP OF TAPE	HUMBIN THEY THE
	ID	AAB16963	AAB17293	AAY96525	AAY96528	AAB17281	AAB17282	AAB17308	AAY96530	AAB17311	AAB16960	AAY96531
	ЭВ	21	21	21	21	21	21	21	21	21	21	21
	Query Match Length DB	36	36	36	41	42	42	42	42	9	269	269
æ	Query Match I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	194	194	194	194	194	194	194	194	194	194	194
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Fc-TMP-TMP proteir	1 4	,	mimetic pept	ַל כ	TILI OIIIDOPOTECTIII	TPO-MIMecic	TPO-mimetic	TPO-mimeri	TPO-mimetic	TPO-mimetic	Thrombopole	TPO-mimetic	oranim-Od.I.	TPO-mimeric	TPO-mimetic	TPO-mimetic	TPO-mimetic	Cyclic or li	TPO-mim	Linear throm	TPO-mimetic	TPO-mimetic	TEO-mimetic	Oitemim-Con	and mimotic period	to coodmowde	THEOROGOACET	Thrompopoler	TPO-mimetic	OTDANTIN-Odf.	TPO-MIMECIC	TPO-MILMECTO Percenting of the Commercial Percenting Commercial Pe	TPO-INTINGCTO	TPO-IIITIMECTO
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## ALIGNMENTS

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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; CTLA4, minetic; IL-1; TNF; antagonist; MMP; inhibitor; exthropoietin; thrombopoietin; interleukin 1, cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                         TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                  AAB16963 standard; Protein; 36 AA.
                                                                                                                                                                                                                                                                                               99WO-US25044.
                                                                                                                                                                                                                                                                                                                          98US-0105371
                                                                      31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
                                                                                                                                                                                                                                                                                                   25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
                                                                                                                                                                                                                                                                        04-MAY-2000.
                                                                                                                                                                                                                          Synthetic.
                                                AAB16963;
RESULT 1
AAB16963
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FC domain, pharmacologically active peptides, and linkers. Where (I) is: (Al)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L2)d-P2, (L3)e-P3, or -(L1)c-P1, -(L2)d-P2, (L3)e-P3, where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently laws cytostatic, antiasthmatic, thrombolytic and immunosuppressive be used for producing pharmaceutical compositions. The composition can activities DNAs vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are market.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating cancer, astima, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                               The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autolmmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 194; DB 21;
100.0%; Pred. No. 1.7e-16;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:349.
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                                                                                                                                                                Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17293 standard; Peptide; 36 AA.
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                                                                                                 autoimmune diseases -
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P2-(L3)e-P3-(L4)e-P1-(L2)d-P3-(L4)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)
                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating cancer, astura, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 194; DB 21;
100.0%; Pred. No. 1.7e-16;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLROWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin mimetic peptide compound 6.
                                                                         Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96525 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                          autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96525;
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mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2-X_1_1, X_2-X_1_1, X_2-X_1_2, X_2-X_1_1, X_2-X_1_1, X_2-X_1_2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-X_1-2, X_1-2-2, X_1-X_1-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2, X_1-2-2,
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                                                                                                           production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus associated ITP, and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 194; DB 21;
100.0%; Pred: No. 1.7e-16;
Micmatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                         Claim 16; Page 62; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96528 standard; peptide; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20..27
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28..41
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= TMP_1
Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                             WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96528;
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Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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Matches
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 - X_{-1} = 0, X_2 - X_{-1} = 1, X_2 - X_{-1} = 1, X_1 - X_1 - X_1 = 1, X_1 - X_1 - X_1 - X_1 = 1, X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1 - X_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                           production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Pred. No. 1.9e-16;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                             Claim 16; Page 65; 91pp; English.
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                                                       Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371.
99US-0428082.
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Matches 36; Conservative
                                                                                                         WPI; 2000-365108/31.
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(AMGE-) AMGEN INC.
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                                                       Feige U,
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                                                    Liu C,
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re domain, pharmacologically active peptides, and inhers. Where (I) is:

(X1)a *FI-(X2)b, where: FI = an Fc domain; X1 and X2 = are each
independently selected from *(L1)c-P1-(L2)d-P2-(L3)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P3, or *(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
of or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
chalf-life or incorporate functions such as Fc receptor binding, protein
chalf-life or AAA69526 and AAB16955 cand phase of the present invention.

Sequences used in the exemplification of the present invention.
                                                                                                                                                               The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; Immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                               Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17282 standard; Peptide; 42 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                 WPI; 2000-350702/30
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AAB17282
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AA69443 to AAA69256 and AAB16955 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                     The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P2, -(L3)e-P2, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour neorosis factor; vascular endothelial growth factor; matrix metalloproteinase;
             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 194; DB 21; 100.0%; Pred. No. 2e-16;
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                                                                                      Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17308 standard; Peptide; 42 AA.
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99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                    autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
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nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17308
q
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The present invention describes composition of matter (1) comprising an Producin pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain, X2 = are each independently selected from -(L1)c-F1-(L1)c-F1-(L2)d-F2, where P1, P2, P3, and P4 = are each independently sequences of where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently of or L, provided that at least 1 of a and b 1s. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein to AAA69526 and AAB18055 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                        Example 2; Page 327; 608pp; English.
                                                                  autoimmune diseases
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42 AA; Sequence

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Gaps
                         .
0
  Length 42;
                         Indels
DB 21;
                         0;
100.0%; Score 194; DB 2: 100.0%; Pred. No. 2e-16;
                                                 1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                             0; Mismatches
                         36; Conservative
  Query Match
Best Local Similarity
                         Matches
                                                  ŏ
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0

AAY96530 standard; Protein; 42 AA. Thrombopoietin mimetic peptide. 04-SEP-2000 (first entry) AAY96530; RESULT 8 AAY96530 

Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.

Synthetic.

WO200024770-A2.

04-MAY-2000.

99WO-US24834 22-OCT-1999; 98US-0105348 23-OCT-1998;

AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31. N-PSDB; AAA29225 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Example 2A; Page 48; 91pp; English.

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiastmmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antien + tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
Overlapping oligonucleotides were used to construct a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                                                             100.0%; Score 194; DB 21; Length 42; 100.0%; Pred. No. 2e-16;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                7 IEGPTLROWLAARAGGGGGGGGIEGPTLROWLAARA 42
                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 331; 608pp; English
                                                                                                                                                                                                                                                                                                                                           AAB17311 standard; Peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                        Local Similarity
nes 36; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                               AAB17311;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                  AAB17311
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)3-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(I)-C-F1-(I2)d-F2.

(L1)C-P1-(L2)d-F2-(L3)e-F^3, or -(L1)C-P1-(L2)d-F2-(L3)e-F3-(L4)f-F4 where F1, P2. P3, and P4 = are each independently sequences of paramacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer asthma, thrombosis, or autoimmune diseases.

CC activities of an FC domain (rather than a Fab domain) can provide a longer complement fixation, and possibly placental transfer. AAA69443

CC AAA69256 and AAB16956 to AAB1803 represent uncleotide and amino acid cycles are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Score 194; DB 21;
Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 185-186; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                           100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                               60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB16960;
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-F1-(L1)c-F2.

-(L1)c-F1-(L2)d-F2-(L3)e-F^3, or -(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be performed pharmaceutical compositions. The compositions are useful for treating pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer as the incorporate functions such as Fc receptor binding, protein a shift of a second or incorporate functions with a fab domain can be absorbed to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin, IgG1, Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A compound which binds to an mpl receptor comprising a thrombopoletin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2, x_2-x_1_1, x_1-x_1-x_1, x_1-x_1-x_1, x_1-x_1-x_1, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 194; DB 21; Length 269; 100.0%; Pred. No. 1.3e-15; .ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96531 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 1961 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Wed Oct

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X_1-X_1_4. X_1 = 1, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, D. E; X_9 = W, T or F; X_1_0 = L, I, V, A, F, M, or K; X_{1,1} = A, I, V, L, F, G, S, Or Q; X_{1,3} = R, K, T, V, N, Q or G; X_{1,4} = A, I, V, L, F, T, R, E, or G; L_1 = 1 inker occeptising 1 to 20 anino acids; and n = 0 or 1. The compounds bind to and activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. applastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; fimunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNR; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 194; DB 21;
100.0%; Pred. No. 1.3e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB16959 standard; Protein; 268 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB16959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16959
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pharmacologically active peptides; II, L2, I3, and L4 = are each independently linkers; and a. b, c. d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP: inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                           Length 268;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                        97.9%; Score 190; DB 21; 100.0%; Pred. No. 3.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                             234 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                 100.0%; Pred. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17301 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                 268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17301;
                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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The present invention describes composition of matter (I) comprising an

Example 2; Page 182-183; 608pp; English.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -

Feige U, Liu C, Cheetham J, Boone TC;

(AMGE-) AMGEN INC.

22-OCT-1999;

WPI; 2000-350702/30.

N-PSDB; AAA69445

Fc domain, pharmacologically active peptides, and linkers. Where (I) (Xl)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)d-P2, -(L3)d-P2, -(L3)d-P2-(L3)d-P2, or -(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L3

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O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18055 to AAAB18003 represent nucleotide and maino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_L^{-1}(L_L^{-1})_L TMP_L^{-2}], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "optionally modified by bromoacetyl or PEG"
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note- "optionally linked to an Fc molecule"
                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                     Score 186; DB 21;
Pred. No. 1.5e-15;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGKGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin mimetic peptide compound 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        AAY96523 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l5..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                       95.9%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                Ouery Match
Best Local Similarity 97.2°
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                         AAY96523
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10 to 14 residues in length comprising X_-2-X_-1-0, X_-2-X_-1-1, X_-2-X_-1-2, X_-2-X_-1-3, X_-2-X_-1-4, X_-1-X_-1-1, X_-1-X_-1-2, X_-1-X_-1-2, X_-1-X_-1-3, X_-2-X_-1-4, X_-1-X_-1-1, X_-1-X_-1-2, X_-1-2,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thromoblytic; WBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vyctocxio; T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                          Score 186; DB 21; Length 36;
Pred. No. 1.5e-15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17303 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                            / Match 95.9%;
Local Similarity 97.2%;
Nes 35; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                      36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17303;
                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17303
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AaA69443 to AAA69526 and AAB18032 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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Sequence

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                       Gaps
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0
Score 185; DB 21; Length 36; Pred. No. 2e-15;
                      1;
                     0; Mismatches
95.48;
97.28;
         Local Similarity 97.2 ies 35; Conservative
Query Match
                     Matches
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1 IEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 36 ð

1 IEGPTLRQWLAARAGGCGGGGGTEGPTLRQWLAARA 36 g

RESULT 16 AAB17307

AAB17307 standard; Peptide; 36 AA 

AAB17307;

31-OCT-2000 (first entry)

TPO-mimetic peptide sequence SEQ ID NO:363.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

Synthetic.

WO200024782-A2.

04-MAY-2000.

99WO-US25044 25-OCT-1999;

98US-0105371 99US-0428082 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Boone TC Feige U, Liu C, Cheetham J,

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -

Example 1; Page 324; 608pp; English.

Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.
(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently present invention describes composition of matter (I) comprising an The

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Thrombopoietin, mimetic, TMP, TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer Thalf-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB180915 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                Length 36;
                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                21;
                                                                                                                                                                                                                Score 185; DB 2:
Pred. No. 2e-15;
0; Mismatches
                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                 | IEGPTLRQWLAARAGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Cheetham J;
                                                                                                                                                                                                                95.4%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                            Query Match
Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96524;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                AAY96524
      8888888888888
                                                                                                                                                                                                                                                                                δŏ
                                                                                                                                                                                                                                                                                                              g
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10 to 14 residues in length comprising X_2 - X_1 = 0, X_2 - X_{-1} = 1, X_2 - X_{-1} = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_1 - X_1 = 0, X_2 - X_1 = 0, X_3 - X_1 = 0, X_4 - P_1, X_3 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_5 - P_2, X_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an
is:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2e-15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGCGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17294 standard; Peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match . 95.4%;
Best Local Similarity 97.2%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105371
99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 18
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 deast 1 and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNas, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions, or acception are used for producing paramaceutical compositions, or activitions are used of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18035 to AAAB180303 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (x1)a-F1-(x2)b, where: FI = an FC domain; x1 and x2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; Li, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TRE; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                      Ĥ
                                                                                                                                                                                                                                                                                                            94.6%; Score 183.5; DB 21; Length 37; 97.3%; Pred. No. 3.1e-15;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA-GGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 319; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17295 standard; Peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                          37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000
                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17295;
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                                                                                                                                                                                                                                                                                                                                                        Matches
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O or 1, provided that at least 1 of a and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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38 AA; Sequence

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2;
      Length 38;
                                Indels
 Score 183; DB 21;
Pred. No. 3.6e-15;
0; Mismatches 0;
                                                         1 IEGPTLRQWLAARA--GGGGGGGGGIEGPTLRQWLAARA 36
                                                                           1 IEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 38
   94.38;
94.78;
Query Match
Best Local Similarity 94.7'
Matches 36; Conservative
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TPO-mimetic peptide sequence SEQ ID NO:360. AAB17304 standard; Peptide; 39 AA. 31-OCT-2000 (first entry) AAB17304; RESULT 

autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; Modified peptide; therapeutic agent; fusion; Fc domain; cancer; asthma; thrombosis; pharmaceutical.

Synthetic.

WO200024782-A2

99WO-US25044 25-OCT-1999; 04-MAY-2000

99US-0428082 98US-0105371 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Boone TC; Feige U, Liu C, Cheetham J,

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -

Example 1; Page 323; 608pp; English.

Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-FI-(X2)b, where: FI = an Fc domain, XI and XI = are each independently selected from -(LI)c-PI, -(LI)c-PI-(LI)d-P2, (LI)d-P2, (LI)d-P2, (LI)d-P2, P3, or -(LI)c-PI, -(LI)c-PI-(LI)d-P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; LI, LI, LI, LI, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or I, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive The present invention describes composition of matter (I) comprising

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activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA694343 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes composition of matter (I) comprising an (X1)a-F1-(X2)b, where F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombollytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                94.1%; Score 182.5; DB 21; Length 39; illarity 92.3%; Pred. No. 4.2e-15; Conservative 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                1 IEGPTLROWLAARAGGG---GGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17305 standard; Peptide; 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases
                                                                                                                                                                                                                                               Local Similarity
es 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                          39 AA;
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                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69434 to AAA69526 and AAB18095 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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(LI)C-FI-(LZ)d-FZ-(LZ)a-FY-3, or -(LI)C-FI-(LZ)d-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(LZ)a-FZ-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1: TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGG---GGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGCPEGGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.1%; Score 182.5; DB 2 92.3%; Pred. No. 4.2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 92.3
hes 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
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                                                                                                                                                                                                                                                                                    Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human 'immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
half-life or incorporate functions such as Fc receptor binding, protein
           A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69266 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                   Gaps
                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                            'note= "optionally linked to an Fc molecule"
                                                                            Length 36;
                                                                                                   Indels
                                                                             21;
                                                                             93.8%; Score 182; DB 21;
94.4%; Pred. No. 4.5e-15;
iive 0; Mismatches 2.
                                                                                                                         1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                    1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                  Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                    AAY96526 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                            15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                          1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                   19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105348.
                                                                                                                                                                                                                                                (first entry)
                                                                                        Local Similarity 94.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                          36 AA;
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                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                            Sequence
                                                                                                                                                                                                                          AAY96526;
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                      Matches
                                                                                                                                                                                RESULT 23
                                                                                                                                                                                           AAY96526
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                                                                                                                            δ
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thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
activate the c-Mpl receptor which mediates the activity of endogenous
88888888
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36 AA; Seguence

Gaps .; 0 Length 36; Indels Score 182; DB 21; Pred. No. 4.5e-15; 0; Mismatches 93.8%; 94.4%; 34; Conservative Local Similarity Query Match Best Loca Matches

0

1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36 ò

pp

RESULT 24

AAB17296 standard; Peptide; 42 AA

AAB17296;

31-OCT-2000 (first entry)

TPO-mimetic peptide sequence SEQ ID NO:352

autoimmune disease; cytostatic, antiasthmatic; thrombolytic; VEGF; munuosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropojetin; thrombopojetin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; Modified peptide; therapeutic agent; fusion; Fc domain; cancer; asthma; thrombosis; pharmaceutical.

Synthetic.

40200024782-A2.

04-MAY-2000

25-OCT-1999;

98US-0105371. 23-OCT-1998;

99US-0428082 22-OCT-1999;

(AMGE-) AMGEN INC.

Boone TC; Liu C, Cheetham J, Feige U,

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -

Example 1; Page 319; 608pp; English.

The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-FL-(X2)b, where: F1 = an FC domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2.(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

(Inc-P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, e, and f = are each independently linkers; and a, b, c, e, and b is 1. The composition can have exprostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an FC domain (rather than a Fab domain) can provide a longer 

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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (x_1)_{P} = T_P(x_2)_P, where: F_1 = a_1 Fc domain, X_1 and X_2 = a_1 reach independently selected from -(Li)<sub>C</sub>-Pi, -(Li)<sub>C</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-Pi-(Li)<sub>d</sub>-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                        Score 181; DB 21; Length 42; Pred. No. 6.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARA-----GGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                      , ;
0
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17292 standard; Peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                   93.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases -
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                        42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2.
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                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17292;
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 25
         8 × 3 5 5 5 5 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
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SSXSS

qq δ

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re domain, pharmacologically active peptides, and linkers. Where [1] is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
(X1)a-F1-(X2)d-P2-(X3)a-P3. or (X1)a-F1-(X2)d-P2-(X3)a-F3-(X4)f-P4
(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X2)d-P2-(X3)a-F3-(X4)f-P4
(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-F1-(X1)a-
                                                                                                                                                                                                                                                                                                                                                   ij
to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autofimmune disease; cytostatic; antiasthmatic; thrombolytic; VBCF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TMF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vactotoxic T cell lymphocyte antigen, 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                  DB 21; Length 35;
                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                  Score 177.5; DB 2. Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARA-GGGGGGGGIEGPTLRQWLAARA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:358.
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17302 standard; Peptide; 40 AA
                                                                                                                                                                                                                                                       91.5%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
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                                                                                                                                                          35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U,
                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
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ine present inventions describes compositions of marcet (1) compitating and for domain, pharmacologically active peptides, and linkers. Where (1) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4.

(Mere P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a b, b, c, d, e, and f = are each independently (0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be useful for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein can be an incorporate functions such as Fc receptor binding, protein composition, complement fixation, and possibly placental transfer. AAAA6943 complemences used in the exemplification of the present invention.
                                                                                    Ϊ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes composition of matter (I) comprising an
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                      Indels
                                                                                                                                              1 IEGPTLRQWLAARAGGGG----GGGGIEGPTLRQWLAARA 36
                                               Score 174; DB 21;
Pred. No. 4.5e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                            AAB17291 standard; Peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                 89.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0428082
                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases
                                                                   Local Similarity
nes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                  AAB17291;
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                 Sequence
                                                     Query Match
                                                                                          Matches
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                                                                                                                                                                                                                           RESULT 27
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SO
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34 AA;

Sequence

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94.48;

Best Local Similarity

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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-FI-(X2)b, where: FI = an FC domain, XI and X2 = are each independently selected from -(L1)C-PI-(L1)C-PI-(L2)d-P2.

-(L1)C-FI-(L2)d-F2-(L3)e-F3, or -(L1)C-PI-(L2)d-P2-(L3)e-F3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently active part at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be useful for treating pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an FC domain (rather than a Fab domain) can provide a longer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; famunosoppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                     2;
    Length 34;
                                                                                     Indels
                                                                                 ;
    Score 171; DB 21;
Pred. No. 8.6e-14;
                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                    1 IEGPTLRQWLAARA--GGGGGGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17298 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J,
Query Match 88.1%;
Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17298;
                                                                                                                                                                                                                                                                                                                                                       RESULT 28
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86.6%; Score 168; DB 21; Length 36;

36 AA;

Sequence

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an (X1)a-FI-(X2)b, where FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-PI-(L2)d-P2.

(L1)c-PI-(L2)d-P2-(L3)e-P^3, or -(L1)c-PI-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating cancer, asthma, thrombosis, or autoimmue diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; imunosoppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                             Indels
Pred. No. 2.1e-13;
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Pred. No. 2.1e-13;
0; Mismatches 2;
                                                                 1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                     1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                 IPO-mimetic peptide sequence SEQ ID NO:355.
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                  AAB17299 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.68;
94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.6 Best Local Similarity 94.4 Matches 34; Conservative
                             34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2
                                                                                                                                                                                                                                                                           31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                       AAB17299;
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                           Matches
                                                                                                                                                              RESULT 29
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1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
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AAY96521 standard; peptide; 36 AA.

AAY96521;

04-SEP-2000 (first entry)

Cyclic or linear thrombopoietin mimetic peptide compound 2.

Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.

Synthetic

'note= "optionally linked to an Fc molecule" Location/Qualifiers /label- TMP\_1 Disulfide-bond Modified-site Peptide 

'note= "optional" 15..22 /label= linker Peptide Peptide

23..36 /label= TMP\_2

WO200024770-A2

04-MAY-2000

99WO-US24834. 22-OCT-1999;

98US-0105348. 23-OCT-1998;

(AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31.

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Claim 16; Page 61; 91pp; English.

mimetic peptide (TMP) dimer joined by a linker [TMP]-[(L.1)\_nTMP\_2],

s new. TMP\_1 and TMP\_2 are amino acid sequences varying from at least

10 to 14 residues in length comprising X\_2-X\_1\_0, X\_2-X\_1\_1, X\_2-X\_1\_2,

X\_2-X\_1\_3, X\_2-X\_1\_4, X\_1^2, X\_1^

36 AA; Sequence

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Gaps
                                   ;
0
86.6%; Score 168; DB 21; Length 36; 94.4%; Pred. No. 2.1e-13; ive 0; Mismatches 2; Indels
              Best Local Similarity 94.4
Matches 34; Conservative
     Query Match
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1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36 δŏ

1 IEGPTLRQCLAARAGGGGGGGGIEGPTLRQCLAARA 36

Search completed: October 9, 2002, 08:58:55 Job time: 16:1874 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:55:27; Search time 5.98595 Seconds (without alignments) 146.898 Million cell updates/sec Run on:

Title: Perfect score:

US-09-422-838C-24 194 1 IEGPTLROWLAARAGGGGGGGGGGTEGPTLROWLAARA 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

231628 seqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

231628

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		фp			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
1	76.5	39.4	25	7	US-08-764-640-231	Sequence 231, App
7	76.5	39.4	25	m	US-09-244-298A-231	
e	76.5	39.4	25	4	-09-516-	231,
4	73	7	14	7	US-08-764-640-13	13,
S	73	37.6	14	7	-80-	19
9	73	ζ.	14	m	-08-973-	13,
7	73	7	14	m	-08-973-	193,
8	73		14	m	US-09-244-298A-13	13,
σ	73		14	e	-09-244	193,
10	73		14	4	-09-516-	13,
11	73		14	4	US-09-516-704-193	193,
12	73		15	7	-08-764-640-1	17.
13	73	37.6	15	7	-08-764-	
14	73		15	e	-08-973-	17,
15	73		15	m	US-08-973-225-185	
16	73		15	m	-09-244-	17,
17	73		15	٣	-09 - 244	
18	73		15	4	US-09-516-704-17	17,
19	73		15	4	US-09-516-704-185	185,
20	73		16	~	US-08-764-640-18	18,
21	73		16	~	US-08-764-640-194	194,
22	73		16	7	-764-	232,
23	73		16	m	US-08-973-225-18	18,
24	73		16	m	-08-973-	_
25	73		16	က	US-08-973-225-220	220
56	73	37.6	16	3	244-	18,
27	73	37.6	16	3	US-09-244-298A-194	

4	Appl											App	App	App	App	App	App			
232	28.	194	232	195,	199	195,	199	195,	199	195	199	196,	200,	209	215,	196,	200			
egueines	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence			
115-09-244-2984-232	US-09-516-704-18	US-09-516-704-194	US-09-516-704-232	US-08-764-640-195	US-08-764-640-199	US-08-973-225-195	US-08-973-225-199	US-09-244-298A-195	US-09-244-298A-199	US-09-516-704-195	US-09-516-704-199	US-08-764-640-196	US-08-764-640-200	US-08-764-640-209	US-08-764-640-215	US-08-973-225-196	US-08-973-225-200		ALIGNMENTS	
c	4	4	4	7	7	m	m	3	c	4	4	2	7	~	7	ĸ	٣			
7	16	16	16	14	14	14	14	14	14	14	14	15	15	15	15	15	15			
37.6	37.6	37.6		35.6	5.			35.6					35.6				35.6			
73	73	73	73	69	69	69	69	69	69	69	69	69	69	69	69	69	69			
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45			

Applic 69451 69451 69451 Dower Dower Barre Gates Schat Wagst Hendi	JANT: YID, WUN OF INVENTION: PEPTIDES OF INVENTION: RECEPTOR R OF EXQUENCES: 244 SPONDENCE ADDRESS: 244 RESSEE: Glaxo Wellcome EFT: Five Moore Drive, E R: Research Triangle Par RE: NC TYRY: USA TYPY: USA TYPY: USA TER READABLE FORM: TER READABLE FORM: THE READABLE FORM: THE READABLE FORM: THE TER READABLE FORM: THE READABLE FORM: THE READABLE FORM: THE TER THE POOSYMIN SATING SYSTEM: PC-OMPALIALE	H KONKCHZZ4ON T
RESULT 1 US-08-764 Sequence Patent 1 Patent 1 Patent APPL APPL APPL APPL APPL APPL APPL APPL	APPLIC TITLE NUMBE CORRES STR STR STA STA COUNT	CURRE ALTON NAME TELEGO

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                                                                              39.4%; Score 76.5; DB 2; Length 25; 40.6%; Pred. No. 0.0058; tive 8; Mismatches 2; Indels
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.4%; Score 76.5; DB 3; Length 25; 40.6%; Pred. No. 0.0058; tive 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                              Dower, William J.

Barrett, Ronald W.

Cwirla, Steven E.

Gates, Christian
Schatz, Peter J.

Balasubramanian, Palaniappan
Wagstrom, Christopher R.
                                                                                                                                                 2 EGPTLROWLAARAGGGGGGGGGGEGPTLROWLA 33
                                                                                                                                                                               2 DGPTLREWISFXA-----DGPTLREWIS 24
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                             ; OTHER INFORMATION: /product= "Ava" US-08-764-640-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: /product= "Ava"
US-09-244-298A-231
                                                                                                                                                                                                                                                               Sequence 231, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                             Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hrubiec, Robert T.
REGISTATION UNMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glaxo Wellcome
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.69
Matches 13; Conservative
                                                                                    Query Match
Best Local Similarity 40.69
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                  RESULT 2
US-09-244-298A-231
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 NAME/KEY:
LOCATION:
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STATE:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.4%; Score 76.5; DB 4; Length 25; Best Local Similarity 40.6%; Pred. No. 0.0058; Matches 13; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
CTHER INFORMATION: /product= "Ava";
SEQUENCE DESCRIPTION: SEQ ID NO: 231:
US-09-516-704-231
                                                                                                                                                                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3281
:|||||:|:: | :|||||:|::
2 DGPTLREWISFXA------DGPTLREWIS 24
                                                                                                                                                                                                                                                                                                                                           Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
                                                                                                                                   Sequence 231, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 13, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                     APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                US-09-516-704-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-764-640-13
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                                                                                           RESULT 3
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0
                                                                                                                                                                                          TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.6%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.008; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                              STREET: Five Moore Drive, P.O. Box 13398
                                                                       Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Balasubramanian, Palaniappan
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REGISTRATION NUMBER: 392
REFRENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEBHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                             Deprince, Randolph B. Podduturi, Surekha
Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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Best Local Similarity 100.
Matches 14; Conservative
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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APPLICANT: Dower,
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                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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APPLICANT:
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APPLICANT:
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Gaps
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.6%; Score 73; DB 2; Length 14; Best Local Similarity 100.0%; Pred. No. 0.008; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                       E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
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APPLICATION NUMBER: US/08/973,225A
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                   PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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                                                                                 Research Triangle Park
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                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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COMPUTER READABLE FORM:
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LENGTH: 14 amino acids
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                         ADDRESSEE:
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US-08-973-225-13
                                                                                                                             COUNTRY:
                                                                STREET:
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US-08-973-225-193

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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100.0%; Pred. No. 0.008;
tive 0; Mismatches C
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HINDIEC, ROBERT T.
REGISTRATION NUMBER: 36.392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
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Mattheakis, Larry C.
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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STRANDEDNESS: <Unknown>
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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Matches 14; Conservative
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                      Score 73; DB 3; Length 14; Pred. No. 0.008; 0; Mismatches 0; Indels
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37.6%; Score
100.0%; Pred. No. v...
... 0; Mismatches
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TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CWILL, CRISTIAN APPLICANT: Gates, Christian APPLICANT: Schatz, Peter J. APPLICANT: Balasubramanian, Palaniappan APPLICANT: Balasubramanian, Palaniappan APPLICANT: Hendren, Richard W. APPLICANT: Hendren, Richard W. APPLICANT: Podduturi, Surekha
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US-09-244-298A-193
; Sequence 193, Application US/09244298A
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
- LENGTH: 14 amino acids
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                              Query Match 37.6 Best Local Similarity 100. Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                   APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73; DB 3; Length 14;
Pred. No. 0.008;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09516704
Fatent No. 6251864
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWITA Steven E.
GATES, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                            STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                        Schatz, Peter J.
Balasubramanian, Palaniappan
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Hendren, Richard W.
                                                                                                                            Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                                                                Deprince, Randolph B.
Podduturi, Surekha
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100.0%; Pre
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           Barrett, Ronald W. Cwirla, Steven E. Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                             Glaxo Wellcome
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LENGTH: 14 amino acids
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Best Local Similarity 100.
Matches 14; Conservative
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MOLECULE TYPE: peptide
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GENERAL INFORMATION: APPLICANT: DOWER,
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                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.6%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.008; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                           COMPUTER: IBM PC rentatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                           ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
FLASSIFICATION: <UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,392
REFERENCE/COCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 193, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 244
                                                                                                                                                        ZIP: 27709
COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 14, Conservative
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                                                                                                               STATE: NC
COUNTRY: USA
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TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-17
TYPE: amino acid
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                   STRANDEDNESS:
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US-08-764-640-185
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.6%; Score 73; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 0.008; Matches 14; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT PR3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: CWILLA, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-516-704-193
                                                           ATTORNEY/AGENT INFORMATION:
NAME: HULDLG., ROBERT T.
REGISTRATION NUMBER: 36, 392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08764640 Patent No. 5869451 Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun
                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
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37.6%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.0086; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schatz, Peter J.
APPLICANT: Balasaubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Pin, Qun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                   Sequence 185, Application US/08764640 patent No. 5869451 patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gwirla, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLROWLAARA 14
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                                                                                             1 IEGPTLROWLAARA 14
                                                                                                                       1 IEGPTLROWLAARA 14
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.6%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.0086; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-08-973-225-185
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagstrom, Christopher R. Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Five Moore Drive, P. (CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSE
                                                                 NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                             ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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ZIP: 27709
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                 Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 37.6%; Score 73; DB 3; Length 15; Best Local Similarity 100.0%; Pred. No. 0.0086; Matches 14; Conservative 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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APPLICATION NUBBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HINDIGEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 973065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWILLA Steven E.
Duffin, David J.
                                                                                                                 APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                        Sequence 17, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Glaxo Wellcome
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Mattheakis, Larry C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 232
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                      Query Match
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244.2002
                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 185, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Bower, William J.
APPLICANT: Cwirla, Stewen E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
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11-DEC-1996
11-DEC-1996
11-DEC-1996
     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                   NAME: HILDLEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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COUNTRY: USA
ZIP: 27709
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Hendren, Richard W.
Deprince, Randolph B.
Poddiucri, Surekha
Prodiucri, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.6%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.0086; tive 0; Mismatches 0; Indels
                                                                                                                                      Length 15;
                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                      Score 73; DB 3; 1 Pred. No. 0.0086;
                                                                                                                         37.6%; Scor.
100.0%; Pred. No. v.
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Balasubramanian, Palaniappan
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RAPPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Research Triangle Park
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 244
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Best Local Similarity 100.0
Matches 14; Conservative
  15 amino acids
                                                                                                                                                         Best Local Similarity 100.
Matches 14; Conservative
                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-244-298A-185
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LENGTH: 15 amino TYPE: amino acid STRANDEDNESS:
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                      E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: /product= "Beta-ala" US-08-764-640-18
  Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 194, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
                                                             Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REPERRNCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     STREET: Five Moose Land.
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.6
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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ADDRESSEE: Glaxo Wel
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-764-640-194
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                       APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                       Deprince, Randolph B.
Podduturi, Surekha
TILE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.6%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.0086; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                        Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 185: US-09-516-704-185
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                             Sequence 185, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                        APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.6
Best Local Similarity 100.
Matches 14; Conservative
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1 IEGPTLROWLAARA 14
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ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NC
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                                                       RESULT 19
US-09-516-704-185
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us-09-422-838c-24.rai

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MOLECULE TYPE: peptide
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APPLICANT: Balsaubramanian, Palaniappan
APPLICANT: Balsaubramanian, Palaniappan
APPLICANT: Balsaubramanian, Palaniappan
APPLICANT: Beptince, Randolph B.
APPLICANT: Deptince, Randolph B.
APPLICANT: Poduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: BECEPTOR
TITLE OF INVENTION: RECEPTOR
MUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.6%; Score 73; DB 2; Length 16; Best Local Similarity 100.0%; Pred. No. 0.0092; Matches 14; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                   EE: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
ETLING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM.PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 232, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                         PK3281
                                                                Research Triangle Park
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/POCKET NUMBER: PKS TELECOMMUNICATION INFORMATION: 919-248-1000 INFORMATION FOR SEQ ID NO: 194: SEQUENCE CHRRACTERISTICS: LENGTH: 16 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: CWITLIA, Steven E.
APPLICANT: Gates, Christian
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; MOLECULE TYPE: peptide
US-08-764-640-194
                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS
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                                                                                                              USA
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                                                                                                              COUNTRY: US
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                                                                CITY: F
STATE:
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Wagstrom, Christopher R. Wrighton, Nicholas C. Wrighton, Nicholas C. TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THROMBOPOIETIN RECEPTOR
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY FAGENT INFORMATION:
NAME: HILDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFRENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S. 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Research Triangle Park
STATE: NC
APPLICATION NUMBER: US/08/764,640 FILING DAFE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Hrubiec, ROBERT 7. REGISTRATION NUMBER: 36,392 REFERENCE/DOCKET NUMBER: PK13281
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Mattheakis, Larry C.
Schatz, Peter J.
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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STRANDEDNESS: <Unknown>
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                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
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                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IEGPTLROWLAARA 15
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RESULT 25
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBORPOLETIN RECEPPOR
                                                                                                                                         37.6%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0092; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                           OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.6%; Score 73; DB 3; Le Best Local Similarity 100.0%; Pred. No. 0.0092; Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-08-973-225-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                        Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEG ID NO: 194:
SEQUENCE CHARACTERISTICS:
                   NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schatz, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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ZIP: 27709
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Matches 14; Conserva
                                         LOCATION:
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                                                                                                                                                                                                                                                                                                                                                       US-08-973-225-194
FEATURE:
                                                                                                US-08-973-225-18
                                                                                                                                              Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                               STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                    THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HYDDEC, RODERT T
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-973-225-220
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Balasubramanian, Palaniappan
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                Sequence 220, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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                                                                                                                                                                            Haselden, Sherril S.
Mattheakis, Larry C.
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 220:
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; Patent No. 6121238
                                                                          APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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                                                                                                                                                           Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                       Schatz, Peter J
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 232
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US-08-973-225-220
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US-09-244-298A-18
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APPLICANT:
APPLICANT:
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APPLICANT:
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COUNTRY:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
               APPLICANT: YIN, OUN
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
ADDRESSEE: GlaxO Wellcome
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HILDLEC, ROBERT T.
REGISTRATION NUMBER: 36,392
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STREET: Five Moore Drive, P.O. Box 13398
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APPLICANT: CWILLS, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balaubramanian, Palaniappan
APPLICANT: Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 194, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
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Podduturi, Surekha
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REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
    APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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Best Local Similarity 100.0
Matches 14; Conservative
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                 USA
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STATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.6%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0092; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A FILING DATE: 11.DEC-1996 CLASSIFICATION: 514
                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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Barrett, Ronald W.

Cwirla Steven E.

Gates, Christian

Schatz, Peter J.

Balasubramanian, Palaniappan

Wagstrom, Christopher R.

Hendren, Richard W.
                                                                                                                                                                                                                     NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 232, Application US/09244298A; Patent No. 6121238; GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ZIP: 27709
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Podduturi, Surekha
Yin, Qun
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Five Moore Drive,
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NAME: Hrubiec, Robert T.
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.(
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-244-298A-194
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MEDIUM TYPE: Floppy
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APPLICANT:
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REFERENCE/DOCKET NUMBER: PK3281

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Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                           37.6%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.0092; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.0092; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                             Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 9, 2002, 09:06:30 Job time: 6.98595 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                   Sequence 194, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J. Barrett, Ronald W. Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                         Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEOUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                1 IEGPTLROWLAARA 14
                                                                                                                                                                            1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IEGPTLROWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                           Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NC
                                                                                                                                                                                                                                                                 US-09-516-704-194
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US-09-516-704-18
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                                                                                                                                                                                                                                            RESULT 30
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                          37.6%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0092; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-516-704-18; Sequence 18, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
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             TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 15
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                     LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-232
                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                        2 IEGPTLRQWLAARA 15
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                                                                                                                            amino acid
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Matches 14; Conserv
                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                            Query Match
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Gaps

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:54:17; Search time 8.09368 Seconds Run on:

(without alignments)
427.397 Million cell updates/sec

US-09-422-838C-24 194 Title: Perfect score:

1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
: pir4:\* 4 3 2 ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	hypothetical prote- probable ATP/GTP-b hflX protein - Myc probable Hilx - My probable Hilx - My hypothetical prote- hypothetical prote- laccase (EC 1.10.3 laccase (EC 1.10.3 laccase (EC 1.10.3 hypothetical 20.2k phosphatidylinosit neurotrophin-4 pre- subtilisin-like pr- subtilisin-like	
SUMMARIES		
DB	000000000000000000000000000000000000000	
% Query Match Length	500 500 5188 5488 5188 5199 5199 510 510 510 510 510 510 510 510	
% Query Match	33.00 3.00	
Score	88 80 80 80 80 80 80 80 80 80 80 80 80 8	
Result No.	100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

hypothetical prote	tyrosine kinase -	receptor-like prot	hypothetical prote	hypothetical prote	hypothetical prote	homeotic protein H	hypothetical prote	probable deoxyribo	hypothetical prote		hypothetical prote	. Ω	heterogeneous ribo	helix-loop-helix t	glycine-rich prote
T13690	158378	T04124	T13386	B84781	T06612	A53662	E96495	S57795	T10550	T48099	H85067	T35365	S35500	JC6087	T49109
~1	7	N	~	7	~	7	~	~	~	C)	N	~	Н	7	7
908	888	962	1325	327	339	403	443	867	80	199	250	270	346	367	396
30.9	30.9	30.9	30.9	30.7	30.7	30.7	30.7	30.7	30.4	30.4	30.4	30.4	30.4	30.4	30.4
9	9	9	9	59.5	59.5	59.5	59.5	59.5	59	29	59	59	59	59	59
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-500 (WHIL>
A; Cross -references: EMB::Z78013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5
A; Experimental source: clone F15B9
                                               hypothetical protein F15B9.5 - Caenorhabdítis elegans
C.Species: Caenorhabdítis elegans
C.Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999
C.Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: CESP:F15B9.5
A;Map position: 5
A:Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1
                                                                                                                                                       R.Percy, C. Submitted to the EMBL Data Library, August 1996 A:Reference number: Z19351 A:Accession: T20961 A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.55
Matches 13; Conservative
RESULT 1
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Graviolate ATP/GTP-binding protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001
C;Accession: G87031
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Davtes, R.M.; Devilin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A;Title: Massive gene decay in the leprosy bacillus.
A;Title: Massive gene decay in the leprosy bacillus.
A;Accession: G87033
A;Accession: G87033
A;Accession: G87034
A;Accession: G87034
A;Residues: 1-488 <STO>
A;Cossion: G8:AL450380; NID:g13093026; PIDN:CAC31378.1; GSPDB:GN00147

C;Genetics: A;Gene: Mi0997 C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology

Query Match

Length 488; 35.3%; Score 68.5; DB 2; Ĥ

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hypothetical protein Y41C4A.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
R;Steward, C.
Submitted to the EMBL Data Library, October 1998
A;Reference number: 220269
A;Reference number: 220269
A;Reference number: 220269
A;Accession: T26808
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y41C4A.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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**Reference number: 220269

**Accession: T25807

**Ascession: T25807

**Ascession: T25807

**Ascession: T25807

**Ascession: P125807

**Ascession: P125807

**Ascession: P125807

**Ascession: P125807

**Assidue: DNA

**Ascions: Laterances: EMBL: AL032627; PIDN: CAB54381.1; CESP:Y41C4A.4a

**Ascession: P125807

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A;Cross-references: EMBL:AL032627; PIDN:CAB54382.1; CESP:Y41C4A.4b
A;Experimental source: clone Y41C4A
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
A;Experimental source: BAC clone B9J10; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.0%; Score 64; DB 2; Length 331; 76.9%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.0%; Score 64; DB 2; Length 201; 57.1%; Pred. No. 4.9; 3; Indels .ive 2; Mismatches 3; Indels
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A; Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C; Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CESP:Y41C4A.4b
A;Introns: 24/3; 50/2; 81/3; 161/1; 230/1; 294/3
C;Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 RAGGGGGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 RGGGGGGGGVNG----RWSA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57,19
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GGGGGGGGIEGPT 27
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Best Local Similarity
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A; Residues: 1-201 <SCH>
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                                                                                                                                                                                                                                                                              A; Status: preliminary
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T26808
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
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                                                                                                                                                                                                                                                                                                                                                                                                                                      hilly protein - Mycobacterium leprae
N:Alternate names: B2135_C2_202 protein
C;Species: Wycobacterium leprae
N:Alternate names: B2135_C2_202 protein
C;Species: Wycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72938
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2235.
A;Reference number: S72587
A;Accession: S7298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-518 <SMI>A;Cross-references: EMBL:U00019; NID:q467079; PIDN:AAA17274.1; PID:q467091
C;Genetics:
A;Start codon: GTG
C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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C;Species: Wycobacterium tuberculosis
C;Date: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
C;Accession: D70505
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34.3%; Score 66.5; DB 2; Length 495;
Best Local Similarity 46.7%; Pred. No. 6;
Matches 14; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.3%; Score 68.5; DB 2; Length 518; Best Local Similarity 46.7%; Pred. No. 3.9; Matches 14; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein B9J10.290 [imported] - Neurospora crassa C;Species: Neurospora crassa
                                                                     Indels
                                                                     7;
                              Pred. No. 3.7;
                 46.7%; Pred. ....
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                                                                                                                                                                                                        4 PTLRQW-----LAARAGGGGGGGGGEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PTLROW-----LAARAGGGGGGGGIEGP 26
                                                                                                                                                        4 PTLRQW-----LAARAGGGGGGGGIEGP 26
                                                                     14; Conservative
                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-495 <COL>
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                                                                     Matches
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A; Residues: 1-490 <MOL>
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F.12-49/Domain: propeptide #status predicted <PRO>
F.50-619/Product: laccase #status predicted <PRO>
F.50-619/Product: laccase #status predicted <PRO>
F.415-50main: amino-terminal beta-barrel #status predicted <PRO>
F.136.72Domain: middle beta-barrel #status predicted <PRO>
F.1319.282,295,340,422,444/Binding site: carbohydrate (ASN) (covalent) #status predicted <PRO-
F.134,480/Binding site: copper (His) (type 2) #status predicted <PRO-
F.146,189,191,482,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status predicted <PRO-
F.146,189,191,482,548,550/Binding site: Copper (His) (type 1) #status predicted <PRO-
F.477,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricermann, U.A.; Lerch, K.

Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
Arithe: Isolation and partial nucleotide sequence of the laccase gene from Neurospora can partial nucleotide sequence of the laccase gene from Neurospora can Arithe: A29762, MUID:87067412
Arcession: A29762
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Arcession: A39763
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Arcession: A2976
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: A28523; A29762
R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
R;Germann, U.A.; Maeller, G.; Hunziker, P.E.; Lerch, K.
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A;Reference number: A28523; MUID:88087214
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R; Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
A; Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A; Reference number: A28523; MUID: 88087214
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A; Residues: 1-619 <CER>
A; Cross-references: EMBL:M18334; NID:g168827; PIDN:AAA33592.1; PID:g168828
C; Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
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N;Alternate names: urishiol oxidase
C;Species: Neurospora crassa
C;Date:: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)
N;Alternate names: urishiol oxidase
     Length 333
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C; Keywords: copper; glycoprotein; oxidoreductase
F;1-21/Domain: signal sequence #status predicted <SIG>
Score 64; DB 2;
Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 63.5; DB
57.7%; Pred. No. 15;
ive 0; Mismatches
                                                                                               2; Mismatches
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33.0%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-619 <GER>
A;Cross-references: EMBL:M14554
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                               169 GGGGGGGGVPGPS 181
                                                                                                                                                                                    15 GGGGGGGIEGPT 27
                                        Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A28523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: B28523
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Query Match
Best Local S
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                                                                                Matches
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A.introns: 86/3
C.Superfamily: laccase
C.Keywords: Coopper; glycoprotein; oxidoreductase
C.Keywords: Coopper; glycoprotein; oxidoreductase
F.12-24/Domain: signal sequence #status predicted <PRO>
F.22-49/Domain: propeptide #status predicted <PRO>
F.50-619/Product: laccase #status predicted <MAT>
F.50-619/Product: laccase #status predicted <MAT>
F.50-619/Product: accase #status predicted <BB1>
F.316-372/Domain: middle beta-barrel #status predicted <BB2>
F.431-580/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F.431-580/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F.139, 282, 295, 340, 422, 444/Binding site: carbohydrate (Asn) (covalent) #status predict F.144, 480/Binding site: copper (His) (type 2) #status predicted
F.146, 189, 191, 482, 548, 550/Binding site: 2Cu-o cluster (His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09084
R;Molendijk, A.J.; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylino A;Reference number: 216411; MUID:98281574
A;Accession: T09084
A;Status: prediminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: genomic RNA
A;Residues: 1-201 <ROT>
A;Cross-references: GB:D12477; GB:D01129; NID:g222674; PIDN:BAA02044.1; PID:d1002526;
A;Experimental source: strain raspberry
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A;Experimental source: strain cw-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: tomator ringspot virus
C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C.Accession: JQ1091 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C.Accession: JQ1091 #Sequence_revision D.M.
J. Gen. Virol. 72, 1505-1514, 1991
A.Title: Nucleotide sequence of tomator ringspot virus RNA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 63.5; DB 1; Length 619; 57.7%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical 20.2K protein - tomato ringspot virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 265/3; 331/3; 370/3; 455/1; 481/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: JQ1093; MUID:91311402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ROWLAARAGGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 RQDSQAERYGGGGGGCNSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 RAGGGGGGGIE----GPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 RAGGGGGGGKEVFKAGRTLLKVLKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%;
61.5%;
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A;Status: translation not shown
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Best Local Similarity 61.55
Matches 16; Conservative
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2;
                                           DB
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                                                                                                                                     1; Mismatches
                                 Score 61.5;
Pred. No. 20;
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A)Map position: 15q26-15q26
                                                                                                                                                                                                                                11 AARAGGGGGGGGIEGPTLR-----OWL 32
                                                                                                                                                                                                                                                                                                                      24 AAGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AARAGGGGGGGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AAGAGGAGGAGGPGFRPLAPRPWRWL 52
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A;Status: nucleic acid sequence not shown
                                           31.7%;
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Best Local Similarity 48.3%;
Matches 14; Conservative
Query Match
Best Local Similarity 46...
Best Local 14; Conservative
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A.Molecule type: DNA
A.Residues: 1-209 <BER>
A.Accession: JH0505
A.Residues: 1-209 <BER>
A.Molecule type: MRNA
A.Residues: 1-176, /P / 178-209 <BER1>
A.Molecule type: mRNA
A.Residues: 1-176, /P / 178-209 <BER1>
A.Residues: 1-176, /P / 178-209 <BER1>
A.Residues: 1-176, /P / 178-209 <BER1>
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A.Residues: 1-176, /P / 178-209 <BER1>
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A.Residues: 1-176, /P / 178-209 <BER1>
A.Residues: 1-176, /P / 178-209 <BER1>
A.Residues: 1-176, /P 
                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Vorway rat)
C;Species: Rattus norvegicus (Vorway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: B42687; JH0504; JH0505
R;Ip, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, L. Proc. Natl. Acad. Sci. U.S.A. 89, 3066-3064, 1992
A;Title: Mammallan neurotrophin-4: structure, chromosomal localization, tissue distribut A;Reference number: A42687; MUID:92212967
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A;Residues: 1-487 <KIE>
A;Note: the lack of a domain necessary for correct folding and activity of other serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: DNA'

A Residues: 1-209 <IPA-

A) Residues: 1-209 <IPA-

A) Cross-references: GB: M86742; NID:g205775; PIDN: AAA41728.1; PID:g205776

A) Cross-references: GB: M86742; NID:g205775; PIDN: AAA41728.1; PID:g205776

B: Berkemeier, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenthal, Meuron, T. 857-866, 1991

A) Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.

A) Reference number: JH0503; MUID:92075279
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DNA Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A;Reference number: A39490; MUID:92075167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form B NAlternate names: subtilisin homolog precursor, short splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 31-Mar-2000
C;Accession: B39490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.2%; Score 62.5; DB 2; Length 209; Best Local Similarity 42.5%; Pred. No. 7.3; Matches 17; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 GSPLROYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GPTLRQWL-----AARAGGGG---GGGGIEGPTLRQWLA 33
                                                                                                                                          231 GP----LLAAGGGGGGGGGGSSPGDGSTARWDEWL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:131390; OMIM:167405
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C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5571
E;Mori, R; Kii, S; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.;
Biochem: 121, 941-948, 1997
A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyacession: JC2191
R;Tsuji, A.; Higashine, K.; Hine, C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y.
Biochem: Biochem: B. Commun. 200, 943-956, 1994
A;Title: Identification of novel cDNAs encoding human kexin-like protease, PACE4 isof A;Reference number: JC2191; MUID:94235049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Residues: 1-652 <TSU>
C,Comment: This protein consists of a signal peptide, a propeptide, a substilisin-lik
C;Comment: This protein cleaves precursor proteins at dibasic amino acid residues.
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                                                                                                                                                                                                                                                                                                                 subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form C N.Alternate names: kexin-like protease isoform
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A;Cross-references: DDBJ:D87994; NID:92330550; PIDN:BAA21792.1; PID:92330551
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
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Gaps
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A)Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: alternative splicing; hydrolase; serine proteinase
F;196-434/Domain: subtiliain homology <SBT>
F;205,246,420/Active site: Asp, His, Ser #status predicted
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Indels
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Gaps

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hypothetical protein T12P18.5 [imported] - Arabidopsis thaliana Cipaces: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D96664
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.Wi, Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
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N;Alternate names: class III POU domain protein brain-2; transcription factor Oct-3
N;Contains: transcription factor Brn-2; transcription factor Oct-5a; transcription fac;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Dec-2000
C;Accession: S29334; S05043; S30296
R;Schreiber, E; Tobler, A.; Malipiero, U; Fontana, A.
Submitted to the EMBL Data Library, April 1992
A;Description: The human N-Oct 3 cDNA encodes three neuroectodermal cell lineage rest
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A;Reference number: S05042; MUID:89295573
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R; He, X.; Treacy, M.N.; Simmons, D.M.; Ingraham, H.A.; Swanson, L.W.; Rosenfeld, M.G.
Nature 340, 35-42, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE005173; NID: 96358783; PIDN: AAF07364.1; GSPDB: GN00141
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A;Molecule types: mRNA
A;Residues: 1-443 <CCH>
A;Cross.references: EMBL;211933; NID:q35084; PIDN:CAA77990.1; PID:q35085
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A,Residues: 280-350;351-404,<HEX>
A,Cross-references: GB:Z11933; NID:g35084
R;Schreiber, E.; Tobler, A.; Malipiero, U.; Schaffner, W.; Fontana, A.
F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                     Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.4%; Score 61; DB 2; Length 415; 54.5%; Pred. No. 19; tive 1; Mismatches 9; Indels
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A,Status: preliminary; not compared with conceptual translation
                                                                         DB 2;
                                                                  Score 61.5; Di
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                 -----QWL 32
                                                                                                                                                                                                                                                                                    24 AAGAGGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 SGGGGGGGGNKTTERSWSFGR 206
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                                                                  31.7%;
ilarity 48.3%;
Conservative
                                                                                                                                                                                                              11 AARAGGGGGGGGIEGPTLR-
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                                                                                                   Best Local Similarity
Matches 14; Conserv
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-415 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: D96664
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                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
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                                                                                                                                                                                                                                                                                    a
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A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing A;Reference number: JC5570; MUID:97335942
A;Accession: JC5570
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                     subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - hum N;Alternate names: kexin homolog
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Experimental source: brain cerebellum
C;Comment: This enzyme is a processing protease and responsible for processing of variou ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J. DNA Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps A;Reference number: A39490; MUID:92075167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-I
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C;Superfamily: subtilisin-like proteinase PACE4, subtilisin homology
C;Superfamily: subtilisin-like proteinase PACE4, subtilisin homology
C;Reywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F;1-62/Domain: signal sequence #status predicted <SIG>
F;63-149/Domain: propeptide #status predicted <PRO>
F;195-434/Domain: subtilisin homology <SBT>
F;195-434/Domain: hydrophobic cluster #status predicted <HCL>
F;205-246,347,420/Active site: Asp, His, Asn, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C;Accession: A39490
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C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
                                                                                                       Gaps
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C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: diternative splicing; hydrolase; serine proteinase
F;150-969/Product: serine proteinase PACE4 #status predicted <SIG>F;196-434/Domain: subtilisin homology <SBT>
                                    Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 969;
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                                                                                                       Indels
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                                 DB 2;
                         Score 61.5; DE Pred. No. 37; 1; Mismatches
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                                                                                                                                                                  11 AARAGGGGGGGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                        24 AAGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AARAGGGGGGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AAGAGGAGGAGGAGFRPLAPRPWRWL 52
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                      ch 31.7%;
1 Similarity 48.3%;
14; Conservative
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                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-969 <KIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A39490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: PACE4
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                                                                                            Matches
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C; Genetics
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A; Residues: 1-25, 'G', 27-443 <SCW>
A; Residues: 1-25, 'G', 27-443 <SCW>
A; Residues: 1-25, 'G', 27-443 <SCW>
A; Residues: 1-25, 'G', 27-443 <SCW>
A; Cross-references: EMBL: L11933
A; Experimental source: tissue-type brain
C; Genetics:
A; Genetics: OBE: 222816; OMIM: 600494
A; Map position: 6416-6416
C; Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C; Keywords: alternative initiators; DNA binding; homeobox; nucleus; transcription factor Brn-2 #status experimental <AMTI>
F; 68-90/Region: glutamine-rich
F; 125-149/Region: plutamine-rich
F; 181-443/Product: transcription factor Oct-5a #status experimental <AMTI>F; 180-443/Product: transcription factor Oct-5b #status experimental <AMTI>F; 209-336/Domain: POU domain homology <POU>F; 355-411/Domain: homeobox homology <POU>F; 355-411/Domain: homeobox homology <POU>F; 355-411/Domain: homeobox homology <POU>F; 355-411/Domain: POU<FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRED FIRE
A; Reference number: $30296; MUID:93181199
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N.Alternate names: class III POU domain protein brain-2

S.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Accession: S31224

R.Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M.

Proc. Natl. Acad. Sci. U.S.A. 89, 3380-3284

A.Fitle: Structure and evolution of four POU domain genes expressed in mouse brain.

A.Reference number: S31223; MUID:92228768

A.Status: preliminary

A.Recession: S31224

A.Status: preliminary

A.Residues: 1-445 cHRN-

A.Cross-references: BMBL:M88300; NID:9200446; PIDN:AAA39961.1; PID:9200447

C.Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology

C.Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology

F. 68-90/Region: glutamine-rich

F. 153-165/Region: histidine/proline-rich

F. 213-261/Region: histidine/proline-rich

F. 211-21/Region: histidine/proline-rich

F. 211-338/Domain: Pow domain homology < CHOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.4%; Score 61; DB 1; Length 443; 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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Pred. No.
                                                                                                                                                                                             A; Status: nucleic acid sequence not shown
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66.7%;
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N;Alternate names: cytokeratin 10
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 10; Conservative
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60 QWITALSHGGGGGG 74
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Best Local Similarity
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S31224
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A, Molecule type: DNA
A, Residues: 452-463, 'P', 465-507, 'Y', 523-593 <KOR2>
A, Cross-references: PIDN:AAB21314.1; PID:9244508
A, Note: sequence extracted from the Piskovsky, V.V.; Shvets, Y.P.; Kisselev, L.L.
B; Tkachenko, A.V.; Buchman, V.L.; Bliskovsky, V.V.; Shvets, Y.P.; Kisselev, L.L.
Gene 116, 245-251, 1992
A; Title: Exons I and VII of the gene (Kerl0) encoding human keratin 10 undergo struct A; Reference number: PC1102; MUID:92339897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 130-278, YrV, 281-311, 'I', 313-339, 'V', 341-373, 'R', 375-407, 'Q', 409-459, 'RS'
56-579, 'P', 581-593 *CDARL>
A; Cross-references: EMBL: M19156; NID: 9186769
A; Note: the sequence from Fig. 3 is inconsistent with the nucleotide sequence from Fi
F; Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
Submitted to the EMBL Data Library, May 1988
A; Reference number: S14667
                                                                                                                                                                                                                                                                                                       A; Wolecule type: mRNA
A; Residues: 'G'. 198-407,'Q', 409-450,'G', 452-486,491-524,534-593 <TKA>
A; Cross-references: GB:M77663; NID:9186629; PIDN:AAA59199.1; PID:9186629
A; Cross-references: GB:M77663; NID:9186629; PIDN:AAA59199.1; PID:9186629
A; Experimental source: embryonic skin, clone HK51
R; Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
Mol. Biol. Rep. 12, 277-283, 1987
A; Title: Sequence of a cDNA encoding human keratin No 10 selected according to struct
A; Reference number: S14666; MUID:88122104
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A;Note: the translated sequence in GenBank entry HUMKRT10A, release 111.0, differs fr
A;Molecule type: mRNA
A;Residues: 130-278,′YV′,281-311,′I′,313-339,′V′,341-373,′R′,375-407,′Q′,409-459,′RS′
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A;Amap position: 17q12-17q21
A;Introns: 209/3; 237/2; 289/3; 343/3; 385/3; 458/2; 592/3
A;Note: this gene encodes variants with considerable length polymorphism
A;Note: mutations in this gene and cause epidermolytic hyperkeratosis and keratosis; c;Complex: heterotetramer of two type I and two type II proteins, usually keratin I;C;Complex: heterotetramer of two type I and two type II proteins, usually keratin I;C;Keywords: coiled coil; heterotetramer; intermediate filament; polymorphism
F;I-145/Domain: head <HEA>
F;146-456/Domain: helical rod *status predicted <ROD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 452-593 <KOR1>
A;Cross-references: PIDN:AAB21315.1; PID:9244509
A;Notes: sequence extracted from NCBI backbone (NCBIP:79427)
A;Accession: B38182
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Pred. No. 27;
5; Mismatches
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52.6%;
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Matches 10; Conserv
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                                                                                                                                                                                                                  A; Accession: S02158
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Aymolecule type: DNA
A;Residues: 1-210 <IP1>
A;Rolecule type: DNA
A;Residues: 1-210 <IP1>
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A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
C. Comment: In this protein, the coiled-coil rod-like region found in many myosin heav
be protein is globular and does not self-associate into filaments.
C. Comment: In this protein, the coiled-coil rod-like region found in many myosin heav
be protein is globular and does not self-associate into filaments.
C. Genetics:
A. Introns: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 321/3; 4
A. Introns: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 331/3; 4
C. Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 hom
C. Keywords: actin binding: MTP, hydrolase; nucleotide binding; P-loop; phosphoprotein
F.101-108/Region: nucleotide-binding motif A (P-loop)
F.543-564/Region: carboxyl-terminal <CTD>
F. 671-1168/Domain: carboxyl-terminal <CTD>
F. 672-893/Region: alanine/glycine/proline-rich
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C; Species: Homo sopiens (man)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C; Accession: A42687; Juh0503
R; Ip, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A; Title: Manmabalian neurotrophin 4: structure, chromosomal localization, tissue distrin A; Reference number: A42687; MUID:92212967
A,Note: this gene and protein are called MIB in this paper
R;Brzeska, H.; Lynch, T.J.; Martin, B.; Korn, E.D.
J. Biol. Chem. 264, 19340-19348, 1989
A;Title: The localization and sequence of the phosphorylation sites of Acanthamoeba A;Reference number: A34448; MUID:90037074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;983-1030/Domain: SH3 homólógy <$H3>
F;034-Life8/Region: alanine/glycine/proline-rich
F;107/Binding site: AFP (Lys) #status predicted
F;311/Binding site: phosphate (Ser) (covalent) #status experimental
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C;Superfamily: nerve growth factor beta chain
C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
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Pred. No. 12;
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35.0%;
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Matches 12; Conservative
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(Species: Acarthamoeba castellanii
(Species: Acarthamoeba castellanii
(Spaties: Acarthamoeba castellanii
(Spaties: Acarthamoeba castellanii
(Spaties: 30-Sep-1990 % sequence—revision 30-Sep-1990 % text_change 19-Jan-2001
(SAccession: A33891; C34446; A44146
(R;Jung, G.; Korn, E.D.; Hammer III, J.A.
(R;Jung, G.; Korn, E.D.; Hammer III, J.A.
(A;Jung, G.; Korn, E.D.; Hammer III, J.A.
(A;Title: The heavy chain of Acarthamoeba myosin IB is a fusion of myosin-like and non-my A;Reference number: A33891; MUID:88016163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richen, C.N.; Denome, S.; Davis, R.L. 
Proc. Natl. Acad. Sci. US.A. 83, 9313-9317, 1986
A:fitle: Molecular analysis of cDNA clones and the corresponding genomic coding sequence
A:Reference number: A26651; MUID:87092243
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A;Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 262/3; 294/1; 407/3; 496/2; 534/2; 588/3; 7 (;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase lB, calmodulin-dependent; 3',5'-C;Superfamily: 3',5'-cyclic-nucleotide phosphoric diseater hydrolase alternative splicing; phosphoric diseater hydrolase alternative splicing; phosphoric diseater hydrolase F;137-777/Product: cAMP-dependent 3',5'-cyclic-nucleotide phosphodiesterase splice form F;439-667/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology CCNP>
                                                                                                                                                                                                                                                                                                                                                                                                                  3.55. "cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific, splice form II N; Contains: 3'.5' "cyclic-nucleotide phosphodiesterase, CAMP-specific, splice form III C; Species: Drosophila melanogaster in 19-Jul-1996 #text_change 17-Nov-2000 C; Date: 28-Oct-1995 #sequence_revision 19-Jul-1996 #text_change 17-Nov-2000 C; Accession: 855543; 855642; 85544; A26651 R; Qiu, X:; Chen, C.N.; Malone, T.; Richter, L.; Beckendorf, S.K.; Davis, R.L. J. Mol. Biol. 222, 553-565, 1991 Mol. Biol. 222, 553-565, 1991 Mol. Biol. 222, S53-565, 1991 Mol. Biol. 222, S53-565, 1991 Mol. Biol. 255.55 Mull: Biol. 222, S53-565, 1991 Mol. Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.55 Mull: Biol. 255.5
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A;Residues: 416-777 <CHE>
A;Cross-references: GB:M14982; NID:9157278; PIDN:AAC34201.1; PID:9157280
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A;Residues: 'WQAEQ', 86-87,'IG', 90-91,'QKYHSRYLKNRRHTLANVR',94-777 <Q13>
A;Cross-references: EMBL:X55174
A;Accession: S65544
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A;Residues: 'MYCSFCCCYNFRN',4,'P',6,'S',94-777 <Q14>
A;Cross-references: EMBL:X55174
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                                                                                      9 KHYSSSRSGGGGGGGGG 27
                        7 ROWLAARAGGGGGGGGIEG 25
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A;Residues: 137-777 <012>
A;Cross-references: EMBL:X55174
A;Accession: S65542
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A;Accession: S19662
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A; Residues: 1-1168 <JUN>
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nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-777 <QIU>
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1; Mismatches
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C,Keywords: coiled coil; intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transforming protein junD - chicken
                                                                                                                                                                                                                                                                                                                  30.9%;
ilarity 57.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 LPPNAGGGGGGGGAGAPAI 254
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72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LAARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AAAAGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-323 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                               A; Gene: MIPS:YLR338w
   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S20099
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C;Species: indox sapisans (nam)
C;Species: indox sapisans (nam)
C;Date: 16-Feb-1994 #sequence_revision 12-Apr-1996 #text_change 04-Feb-2000
C;Accession: A48266; S17423; A60189
R;TOyoshima, H.; Mcautsumi, H.; Maru, Y.; Hadiwara, K.; Furuya, A.; Mioh, H.; Hanai, N.;
Proo. Natl. Aced. Sci. U. S.A. 90, 5404-5408, 1993
R;TOyoshima, H.; Mcautsumi, H.; Maru, Y.; Hadiwara, K.; Furuya, A.; Mioh, H.; Hanai, N.;
A;Title: Differently spliced cDMAs of human leukocyte tyrosine kinase receptor tyrosine
A;Attle: Ted 48266; MUID:93296146
A;Accession: A48266
A;Accession: A48266; MUID:93296146
A;Accession: A48266
A;Accession: A48266; MUID:93296146
A;Accession: A5204
A;Accession: A5204
A;Accession: A5204
A;Accession: A5204
A;Attle: Tell ky dene encodes a novel receptor-type protein tyrosine kinase.
A;Rodessides: Latk gene encodes a novel receptor-type protein tyrosine kinase.
A;Rodession: S17422
A;Attle: Tell ky dene encodes a novel receptor-type protein tyrosine kinase.
A;Rodession: S17422
A;Attle: Tell ky dene encodes a novel receptor-type protein tyrosine kinase genes.
A;Rodession: S17422
A;Attle: Tell ky dene encodes a novel receptor-type protein tyrosine kinase genes.
A;Rodession: A141, R*A;3-19, L*, Z21-273, 335-864 <KRO>
A;Rodession: S17422
A;Attle: Tell ky dene encodes a novel receptor-type protein tyrosine kinase genes.
A;Rodession: A50189
A;Attle: Tell ky dene encodes a novel receptor-type protein kinase genes.
A;Reference number: A60189; MUID:90191712
A;Ratus: preliminary
A;Reference number: A60189; MUID:9019172
A;Reference number: A60189
A;References: G8-716 <KRO>
A;References: G8-716 <KRO>
A;References: G8-716 <KRO>
A;References: G8-716 <KRO>
A;References: G8-716 <KRO>
A;References: G8-716 <KRO>
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A;References: G8-716 <KRO>
A;References: G8-717 kopinalis Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afrikase Afri
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N;Alternate names: hypotherical protein L8300.13-a
C.Species: Saccharomyces cerevisiae
C.Species: 20-Jul_1996 #sequence_revision 23-Aug-1996 #text_change 05-Nov-1999
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
   6
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Pred. No. 43;
1; Mismatches 2; Indels 5
   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, January 1994
A;Description: The sequence of S. cerevisiae cosmid 8300.
A;Reference number: S69312
                                                                                                                        129 GSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                          3 GPTLRQWL------AARAGGGGGGGGGTEGPTLRQWLA 33
   Mismatches
                                                                                                                                                                                                                                                                                                                  N; Alternate names: protein-tyrosine kinase tykl
                                                                                                                                                                                                                                                                                    protein-tyrosine kinase (EC 2.7.1.112) 1tk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EG-PTLRQWLAARAGGGGGGG 22
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63.6%;
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Matches 14; Conservative
14; Conservative
                                                                                                                                                                                                                                                                                                                                                      C; Species: Homo sapiens (man)
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   Matches
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Rikrieg, T.M.; Schafer, M.P.; Cheng, C.K.; Filpula, D.; Flaherty, P.; Steinert, P.M.; J. Biol. Chem. 260, 5867-5870, 1985
A;Title: Organization of a type I keratin gene. Evidence for evolution of intermediat A; Reference number: A02940; MUID:85207552
A;Accession: A02940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Comment: Fourier analysis has identified a 7-residue repeating pattern (heptad) bet forms a stable alpha helical coiled coil but is interrupted by three short regions wi C; Comment: Most of the introns of the gene encoding this protein are located within the sequence at or near the beginning of heptad repeats. Several of these sites are co C; Comment: The amino and carboxyl ends are rich in glycine, serine, and aromatic resi
A,Residues: 1-285 <DU2>
A;Cross-references: EMBL:U19028; NID:g609380; PID:g2340034; GSPDB:GN00012; MIPS:YLR33
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A;Residues: 1-569 <KRI>
A;Cross-references: GB:L00193; GB:K00391; NID:g198625; PIDN:AAA39391.1; PID:g387397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #Sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S2009
R;Hartl, M.; Hutchins, J.T.; Vogt, P.K.
Oncogene 6, 1623-1831, 1991
A;Title: The chicken jun 991 and its product.
A;Reference number: S20099; MUID:92019832
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C;Species: Mus musculus (house mouse)
C;Date: 15-Nov-1984 #sequence_revision 04-Dec-1986 #text_change 10-Dec-1999
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Note: initiator Met not shown A,
Note: the authors translated the codon GAG for residue 41 as Gly
                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 2; Length 285;
Pred. No. 18;
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Pred. No. 20;
0; Mismatches 5; Indels
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                                                                                                                                                                  A;Map position: 12R
C;Keywords: transmembrane protein
F;140-158/Domain: transmembrane #status predicted <TMI>
F;201-217/Domain: transmembrane #status predicted <TM2>
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δ
                                                                                          Db
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submitted to the EMBL Data Library, July 1995
A;Description: Hdc, an imaginal specific gene required for adult morphogenesis in Drosop
A;Reference number: $58064
A;Accession: $58064
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A;Molecule type: DNA
A;Residues: 1-806 <MUR>
A;Residues: BMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA21318.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein EG0003.2 - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Bate: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C.Accession: T13690
R.Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A.Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A.Reference number: 217699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hdc protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1998
C;Accession: S58064
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                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: FlyBase:hdc
A;Cross-references: FlyBase:FBgn0010113
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F;144-457/Domain: rod <RQD>
F;144-178/Region: coil 1A
F;179-192/Region: coil 1B
F;193-293/Region: coil 1B
F;204-309/Region: coil 2A
F;310-328/Region: coil 2A
F;337-457/Region: coil 2B
F;395/Region: stutter
                                                                                                                                                                                                                                     F;458-569/Domain: tail <END>
F;458-569/Region: V2 and E2 subdomains
                                                                                                                                                                                                                                                                                                                                                                                                7 ROWLAARAGGGGGGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                         9 KQFSSSRSGGGGGGGSVRVSSTR 31
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54.5%;
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F;1-143/Domain: head <HED>
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Best Local Similarity
Matches 10; Conserv
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A;Molecule type: mRNA
A;Residues: 1-649 <WEA>
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Best Local Similarity
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        Mismatches
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        Indels
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        Gaps
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        GGGGGGCIEGPTLRQWLAARA
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein . protein search, using sw model

October 9, 2002, 08:51:41; Search time 4.29977 Seconds (without alignments) 324.181 Million cell updates/sec Run on:

US-09-422-838C-24 194 1 IEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 36 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	es	P06811 neurospora			rattus	homo sa	omou ?	qallu	homo s	mus r	P12252 drosophila			P93527 sorghum bic		homo	gallı		٠	O60548 homo sapien		snm 8	P22293 drosophila	_	009029 mesocricetu	9 ношо	095948 homo sapien		l lucil			P28357 mus musculu	Q9v5n1 homo sapien	у
SUMMARIES		LAC1_NEUCR	LAC2 NEUCR	YR21_TRSVR	NT5_RAT	SCO2_HUMAN	PAC4_HUMAN	FXD3_CHICK	OC3N_HUMAN	OC3N_MOUSE	CNA1_DROME	K1CJ_HUMAN	MYSC_ACACA	PHYB_SORBI	NT5_HUMAN	KLTK_HUMAN	JUND_CHICK	SXL_CERCA	DCO_DROME	FXD2_HUMAN	K1CJ_MOUSE	KLTK_MOUSE	SUS_DROME	SOX1_MOUSE	BET3_MESAU	HB9_HUMAN	ONC2_HUMAN	ZIN_HUMAN	ECR_LUCCU	DYHA_CHLRE	HXD9_HUMAN	HXD9_MOUSE	HH3R_HUMAN	EVX2_HUMAN
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											P04632 homo sapien
BRN1_MOUSE	BRN1_RAT	BRN1_HUMAN	Y967_TREPA	EOMD_MOUSE	KF3C_RAT	PHYB_ORYSA	INS_BOVIN	INS_SHEEP	TTF1_CAVPO	CANS_PIG	CANS_HUMAN
Н	<del></del>	,	Н	7	_	-	_	Н	Н	Н	7
495	497	200	517	688	962	1171	105	105	112	266	268
29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.6	29.6	29.4	29.4	29.4
58	28	28	28	28	58	28	57.5	57.5	22	57	57
34	35	36	37	38	39	40	41	4.2	43	44	45

## ALIGNMENTS

us-09-422-838c-24.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 40, Last amnotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS).
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-:- SUBCELLULAR LOCATION. Secreted (Potential).
-:- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                  COPPER (TYPE 1) (PROBABLE).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 619;
                                                                                                                        COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
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COPPER (TYPE 1) (PROBABLE).
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FDED6D78B65048E3 CRC64;
                                                                                     PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                32.7%; Score 63.5; Dilarity 57.7%; Pred. No. 9.9; Conservative 0; Mismatches
                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                             LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ROWLAARAGGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 RODSOAERYGGGGGGGCNSPTNROCW 64
                                                                                                                                                                                                                                                                                                                                                            68198 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                        146
189
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477
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548
                            Repeat
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444
619 AA;
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5141;
                                                 22
50
607
84
216
431
                            Glycoprotein;
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P10574;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on
ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                   PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
COPPER (TYPE 3) (PROBABLE).
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Rott M.E., Tremaine J.H., Rochon D.M.;
"Nucleotide sequence of tomato ringspot virus RNA-2.";
J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBB6CCDE18841145 CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 20.2 kDa protein in RNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
     European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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N-LINKED
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InterPro: IPRO01117; Cu-oxidase.
InterPro: IPRO02355; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 RQWLAARAGGGGGGGGGEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68120 MW;
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P25245;
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                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              4,
                                                                                                                                                                                                         Score 63; DB 1; Length 201;
Pred. No. 4.1;
                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                  POLY-GLY.
9038506E18D7B450 CRC64;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                    POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                     13 RAGGGGGGGIE----GPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                 13 RAGGGGGGGKEVFKAGRTLLKVLKA 38
                                                                                     PIR; JQ1094; JQ1094.
HSSP: P04002; INFR.
Hypothetical protein.
DOMAIN 15 66 POLS
DOMAIN 61 66 POLS
DOMAIN 144 148 POLS
SEQUENCE 201 AA; 20194 MW; 90
                                                                                                                                                                                                            32.5%;
                                                                         EMBL; D12477; BAA02044.1; -.
                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                         Matches
 SSSSSEEFFS
                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                     δ
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5

Gaps

6

12; Indels

Length 209;

Score 62.5; DB 1;

32.28; 42.58;

Best Local Similarity 42.5 Matches 17; Conservative

ŏ P

Pred. No. 4.8; 2; Mismatches

· · · ) (POTENTIAL)

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
R -> P (IN REF. 2).

169 198 200 75

22 80 96 140 157 75

DISULFID DISULFID

CARBOHYD SEQUENCE Query Match

CONFLICT

NEUROTROPHIN-5

POTENTIAL.

PRINTS; PR00208; NGF.
ProDom; PD002052; NGF; 1.
SMART; SMO0140; NGF; 1.
PROSITE; PS00248; NGF; 1.
PROSITE; PS00270; NGF\_2; 1.

Growth factor; Signal

SIGNAL PROPEP CHAIN

DR DR DR DR FT FT FT FT SQ

HSSP; P34130; 1B8M. InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1.

DF5112C05C5D5B85 CRC64;

22332 MW;

209 AA;

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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-92212967; PubMed=1313578;
IP N.Y. Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.,
                                                                                                                                                                                                                                                                                                                                         MEDLINE-92075279; PubMed=1742028;
Berkemeter L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                 "Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                     Mammalian neurotrophin-4: structure, chromosomal localization,
                                                                                                                                                                                                                                                                                    tissue distribution, and receptor specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                           209 AA.
                                                                                                         (NT-4) (Neutrophic factor 4). NTF5 OR NTF4 OR NT4
                           STANDARD;
                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                           Neuron 7:857-866(1991).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                    Rosenthal A.;
                        NT5_RAT
RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -I- FUNCTION: THOUGHT TO PLAY A ROLE IN EITHER MITOCHONDRIAL COPPER TRANSPORT OR INSERTION OF COPPER INTO THE ACTIVE SITE OF COX.
-I- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-I- TISSUE SPECIFICITY: UBBIQUITOUS.
-I- TISSUE SPECIFICITY: UBBIQUITOUS.
-I- TISSUE SPECIFICITY: USCQ2 ARE THE CAUSE OF FATAL INFANTILE CARDIOENCEPHALOWYOPATHY WITH COX DEFICIENCY. THIS DISEASE IS CHARACTERIZED BY HYPERTROPHIC CARDIOMYOPATHY, LACTIC ACIDOSIS, AND GLIOSIS. HEART AND SKELETAL MUSCLE SHOW REDUCTIONS IN COX ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20014747; PubMed=10545952;
Papadopoulou L.C., Sue C.M., Davidson M.M., Tanji K., Nishino I., Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Van Coster R., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S., De Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A.; "Fatal infantile cardioencephalomyopathy with COX deficiency and
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Monocytes;
Smink L.J., Burton J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                     SCO2 protein homolog, mitochondrial precursor, SCO2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE SCO1/2 FAMILY.
                                                                                             266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutations in SCO2, a COX assembly gene.";
Nat. Genet. 23:333-337(1999).
                                                                                             PRT;
                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequ
16-OCT-2001 (Rel. 40, Last and
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                   SCO2_HUMAN
043819; Q9UK87;
                                              SCO2_HUMAN
RESULT 5
                                                                                        HER SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND CONTRACTOR SECOND C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR SENSORY AND SYMPATHETIC NEURONS.
-!- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN, HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRYO AND ADDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M86742; AAA41728.1; -. EMBL; S69323; AAB20548.1; -.
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PIR; JH0504; JH0504. PIR; B42687; B42687.

SSUES.

SEQUENCE FROM N.A. (ISOFORM PACE4A-II).

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2;
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT4 HOWAN STANDARD; PRT; 969 AA. P2012; 01509; 015100; 091611; 091612; 091619; 015100; 091611; 091617; 091619; 091612; 015100; 091611; 091617; 091619; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617; 091617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of a second human subtilisin-like protease gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of novel cDNAs encoding human kexin-like protease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                        InterPro; IPR003782; SCO1_SenC.
Pfam; PF02630; SCO1-SenC; 1.
Mitochondrion; Transit peptide; Disease mutation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62.5; DB 1; Length 266; Pred. No. 5.9;
                                                                                                                                                                                                                                                                              MITOCHONDRION (POTENTIAL).
SCO2 PROTEIN HOMOLOG.
R -> P (IN BESNP:140523).
/FTId=vAR_011738.
E -> K (IN FIC).
/FTId=vAR_008874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5.9;
2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LRQWLAARAGGG--GGGGGIEGPTLR-------QWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTId=VAR_008875.
BC2F40E057329BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PACE4 isoforms.";
Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
TISSUE-Hepatoma, and Kidney;
MEDLINE-92075167; PubMed-1741956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 200:943-950(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fes/fps region of chromosome 15.";
Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTIG-VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94235049; PubMed-8179631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95071480; PubMed-7980617;
                                                                              EMBL; AF177385; AAF05313.1; -. EMBL; AL021683; CAA16671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 AA; 29810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.2%;
Best Local Similarity 37.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                         41
266
20
                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                           140
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                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                    MIM; 604272;
                                                                                                                                                             MIM; 604377;
MIM; 220110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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MEDLINE-9440B49; PubMed-9738409;

RA Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,

RA Tsuji A., Matsuda Y.;

RISOSynthetic processing and quaternary interactions of proprotein

RT SONO-frase SPC4 (PACE4).";

RL FEBS Lett. 434:155-159(198).

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED

CONTINUITY RELEASE OF MATURE PROTEINS FROM THEIR

PROPROTEINS BY CLEAVAGE OF RG-XAA-YAA-ARG -1-ZAA BONDS,

WHEREE XAA CAN BE ANY AMINO ACID AND YAS IS ARG OR LYS.

-1- COPACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.

C-1- SUBUNIT: THE PACE4A IS PROBABLY CALCIUM-DEPENDENT.

C-1- SUBUNIT: THE PACE4A IS PROBABLY CALCIUM-DEPENDENT.

C-1- SUBUNIT: THE PACE4A IS PROBABLY CALCIUM-DEPENDENT.

C-1- SUBCELLULAR LOCATION: PACE4A-I BAND MONOMER, SUGGESTING THAT PROPERAME CASE MATURE PACE4A-I EXISTS ONLY AS A WONOMER, SUGGESTING THAT PROPERAME CASE MATOR PACE4A-I EXISTS ONLY AS A WONOMER, SUGGESTING THAT PROPERAME LOCATION: PACE4A-I AND PACE4-AII ARE SECRETED.

C-1- SUBCELLULAR LOCATION: PACEAA-I AND PACE4-AII ARE SECRETED.

C-1- SUBCELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR CASE TERMINUS. PACE4B MIGHT BE SECRETED.

C-1- ALTERNATIVE PRODUCTS: 8 ISOSORMS; PACE4A-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-II AND PACE4E-I
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TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
PLACEMTA, LUNG, SKELETALA MUSCLE, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
                                                                                                                                                                                                                                 MEDIINE-97335942; PubNed-9192737; Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K., Akamatsu T., Nagamune H., Matsuda Y.; Akamatsu T., Nagamune H., Matsuda Y.; Anovel human PACE4 isoform, PACE4E is an active processing protease containing a hydrophobic cluster at the carboxy terminus."; J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), Kexin-like processing endoprotease."; J. Biochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Endopritease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Biochem. J. 339:639-647(1999).
                       TISSUE=Placenta;
Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4A-1; A-II; CS; D; E-I; E-II). MEDLINE-98021085; PubMed-9378725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Functional analysis of human PACB4-A and PACB4-C isoforms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sucic J.F., Moehring J.M., Inocencio N.M., Euchini J.W., Moehring T.J.;
                                                                                                                                   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II)
                                                                                                   "Identification of a novel PACE4 isoform, PACE4E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification of a new PACE4-CS isoform.";
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MEDLINE~99233559; PubMed=10215603;
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                                                                                                                                                                                                                           TISSUE=Cerebellum;
                                                                                 Matsuda Y.;
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                      DOMAIN: THE PROPERTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACE4D LACKS THE PROPEPTIDE DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
         PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
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                                                           SUBTILASE FAMILY.
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D3 (HNF3/FH transcription factor genesis) (Winged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.; "Aberrant cell growth induced by avian winged helix proteins."; Cancer Res. 57:123-129(1997).
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                                                                                                                                                                                                                                                                                                                                DB 1; Length 969;
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-!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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InterPro; IPR001766; Fork_head.
Pfam: PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
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ALTERNATIVE PRODUCTS: 3 ISSORMS; N-OCT 3 (SHOWN HERE), N-OCT 5A
AND N-OCT 5B ARE PRODUCED BY ALTERNATIVE INITIATION.
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE NEUROECTODERMAL
CELL LINEAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ('GCAT') AND ('TAAT'), SEPARATED BY A NONCONSERVED SPACER REGION
OF 0, 2, OR 3 NUCLEOTIDES. POSITIVELY REGULATES THE GENES UNDER
THE CONTROL OF CORTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II
PROMOTERS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -;- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Expression of a large family of POU-domain regulatory genes in mammalian brain development.";
Nature 340:35-42(1989).

1- FUNCTION: TRANSCRIPTION FACTOR THAP BINDS PREFERENTIALLY TO THE RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALE-SITES.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schreiber E., Tobler A., Malipiero U., Schaffner W., Fontana A.; "cDNA cloning of human N-Oct3, a nervous-system specific POU domain transcription factor binding to the octamer DNA motif."; Nucleic Acids Res. 21:253-258(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angus J., Thomson F., Murphy K., Baker E., Sutherland G.R., Angus J., Thomson F., Murphy K., Baker E., Sutherland G.R., Parsons P.G., Sturm R.A.; "The brn-2 gene regulates the melanocytic phenotype and tumorigenic potential of human melanoma cells.";
                                                                                                                                                                                                                                        P2025; Q14960;
01-TEB-1931 (Rel. 17, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-02T-2001 (Rel. 40, Last annotation update)
Nervous-system specific octamer-binding transcription factor N-OCT
Elexal-specific homeobox/POUV domain protein 2) (BRN-2 protein)
Contains: N-OCT 5A; N-OCT 5B).
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           Score 61; DB 1; Length 394;
Pred. No. 12;
                                                   2; Indels
31.4%; Scor.
84.6%; Pred. No. 12.
                                                                                                                                                                                                                          443 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93181199; Pubmed-8441633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 280-404 FROM N.A.
         Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                          STANDARD;
                                                                                         13 RAGGGGGGGIEG 25
                                                                                                                             82 RGGGGGGGGEEG 94
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Rosenfeld M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver
                                                                                                                                                                                                                        OC3N_HUMAN
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PLOC., Natl. Acad. Sci. U.S.A. 89:3280-3284(1992).

-!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREPERBUTIALLY TO THE RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALF-SITES, ('GCAT') AND ('TAAAT'), SEPARATED BY A NONCONSERVED SPACER REGION OF 0, 2, OR 3 NUCLEOTIDES. POSITIVELY REGULATES THE GENES UNDER THE CONTROL OF CORTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II PROMOTERS (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAT.

-!- SISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE NEUROECTODERMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Nervous-system specific octamer-binding transcription factor N-OCT 3
(Brain-specific homeobox/POU domain protein 2) (BRN-2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hara Y., Rovescalli C., Kim Y., Nirenberg M.; "Structure and evolution of four POU domain genes expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                               PROSITE; PS50071; HOMEOBOX_2: 1. DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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A -> G (IN REF. 2).
2CAC852328334A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 13;
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                                                                                                                                                                                                                                                                                                     N-OCT 5A.
N-OCT 5B.
                                                                                                                                                                                                                                                                                                                                                                       POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                            POLY-GLY
                                                                                                                                                                                                                                                                                        N-OCT 3.
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                                                                                                                                                                                                                                                                            Activator; Alternative initiation
                                                                                                                                                          Probon; PD000583; POU; 1.
SMART; SM00389; HOX; 1.
SMART; SM00382; POU; 1.
PROSTIE; PS00027; HOMEOBOX_1; 1.
PROSTIE; PS000035; POU_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                       POU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
                                                                                            InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                                                                                                                                                                                                              46921 MW;
 EMBL; L37868; AAB59611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.78;
                                                                                                                       Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                   PRINTS; PR00028; POUDOMAIN.
                                                                                                                                                                                                                                    POU_2; 1
EMBL; Z11933; CAA77990.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 QWITALSHGGGGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                          PIR; S05043; S05043.
PIR; S29334; S29334.
                                                                  FRANSFAC; T00630; -.
                                                    HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                443 AA;
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    PROSITE; PS00465;
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                                                                               MIM; 600494;
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FAMILY.
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P13645;
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DOMAIN
SEQUENCE
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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Last annotation update)
CAMP-dependent 3',5' cyclic phosphodiesterase (EC 3.1.4.17) (Learning/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
-! - SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
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MEDLINE-87092243; PubMed-3025834;
Chen C.-N., Denome S., Davis R.L.;
"Molecular analysis of cDNA clones and the corresponding genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.4%; Score 61; DB 1; Length 445; 66.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 90 POLY-GLY.
125 149 POLY-GLN.
268 338 POU.
356 415 HOMEOBOX.
445 AA; 47149 MW; 1A47F10950EECE8A CRC64;
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                                                                                                                                                                                                                                                                    HSSP, P14859, 100T.
MGD; MGI:101895; P0u3f2.
InterPro; IPR001356; Homeobox.
InterPro; IPR0001357; P0u.
Pfam; PF00157; Pou; I.
PRINTS; PR00159; Pou; I.
ProDom; PD000583; P0u; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO0027; HOMEOBOX_1; 1.
PROSITE; PSSO017; HOMEOBOX_2; 1.
PROSITE; PSO0035; POU_1; 1.
PROSITE; PSO0465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92085274; PubMed=1660926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster.";
J. Mol. Biol. 222:553-565(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                   EMBL; M88300; AAA39961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              memory process protein).
DUNCE OR DNC.
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SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                       S31224; S31224.
                        TO CLASS-3 POU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNA1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activator.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PART OF CAMP BINDING SITE (BY SIMILARITY TO MAMMALIAN REGULATORY SUBUNIT OF TYPE 2
                                                                                                                                                                                        -!- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE GENERATED BY THE USE OF DIFFERENT TRANSCRIPTION STRAT SITES AND SPLICE PATTERNS.
-!- DISEASE: MUTATION OF DUNCE PRODUCES FEMALE FLIES THAT ARE STERILE.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODISSTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
coding sequences of the Drosophila dunce+ gene, the structural gene
                       for cAMP phosphodiesterase.";
Proc. Natl. Acad. Sci. U.S.A. 83:9313-9317(1986).
-!- CATALITIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)0
ADENOSINE 5'-PHOSPHATE.
-!- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Erraiin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMP DEPENDENT PROTEIN KINASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; CAMP; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THR-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X55170; CAA38960.1; JOINED.
EMBL, X55171; CAA38960.1; JOINED.
EMBL, X55172; CAA38960.1; JOINED.
EMBL, X55173; CAA38960.1; JOINED.
EMBL, X55174; CAA38960.1; JOINED.
EMBL, X55175; CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X55167; CAA38960.1; -.
EMBL; X55168; CAA38960.1; JOINED.
EMBL; X55169; CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, M14978; AAC34201.1; JOINED.
EMBL, M14979; AAC34201.1; JOINED.
EMBL, M14980; AAC34201.1; JOINED.
EMBL, M14981; AAC34201.1; JOINED.
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559 567 G
584 AA; 64875 MW;
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InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0000479; dnc.
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nes 12; Conserv
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MEDLINE-92141228; PubMed-1371013;
Korge B.P., Gan S.-O., McBridge O.W., Mischke D., Steinert P.M.;
"Extensive size polymorphism of the human keratin 10 chain resides, in
the C-terminal V2 subdomain due to variable numbers and sizes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS EHK HIS-156 AND SER-161.
MEDLINE-92376531; PubMed-1380725;
Rothnagel J.A., Dominey A.M., Dempsey L.D., Longley M.A.,
Gareenhalph D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.;
"Mutations in the rod domains of keratins 1 and 10 in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94216497; PubMed-7512983; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; "Genetic mutations in the Kl and KlO genes of patients with epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compton J.G., Bale S.J.; "Preferential sites in keratin 10 that are mutated in epidermolytic
                                                                                                                                                                                     MEDLINE-88122104; PubMed-2448602; Darmon M.Y., Semat A., Darmon M.Y., Vasseur M.; Senat A., Darmon M.C., Vasseur M.; Selected according togeneous of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                            MEDLINE-89125611; PubMed-2464696; Rieger M., Franke W.W.; "Identification of an orthologous mammalian cytokeratin gene. High degree of introm sequence conservation during evolution of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheng J., Syder A.J., Yu Q.-C., Letal A., Paller A.S., Fuchs E.; The genetic basis of epidermolytic hyperkeratosis: a disorder of differentiation-specific epidermal keratin genes."; cell 70:811-819(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126.
                                                                                                                                                                                                                                                                                                                                                                                      Kisselev L.L.; "Exons I and VII of the gene (KerlO) encoding human keratin 10 undergo structural rearrangements within repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
                                                                                                                                                                                                                                                                                                                                                                  rkachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 89:910-914(1992).
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J. Clin. Invest. 93:1533-1542(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93162043; PubMed-1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92386600; PubMed-1381287;
                                                                                                                                                                                                                                                                   expression.";
Mol. Biol. Rep. 12:277-283(1987).
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 197-593 FROM N.A. MEDLINE-92339897; PubMed=1378806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 180-184 AND 577-589.
                                                                                                            cytokeratin 10.";
J. Mol. Biol. 204:841-856(1988).
                                                                                                                                                                       SECUENCE OF 130-593 FROM N.A.
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                  SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. -1- POLYMORPHISH: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN
THE GLY-RICH REGION (POSITIONS 490-560).
THE GLY-RICH REGION (POSITIONS 490-560).

-1- DISEASE: DEFECTS IN RET10 ARE THE CAUSE OF EPIDERMOLYTIC
HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL
CHARACTERIZED BY BLISTERRING AND A MARKED THICKENING OF THE STRATUM
CORNEUM. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH
REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS.
NITHIN A FEW WEEKS, THE ERYTHRODERMA AND BLISTER FORMATION
DIMINISH AND HYPERKERATOSES DEVELOP. TRANSMISSION IS AUTOSOWAL
CONNAMY, BUT MOST CASES ARE SPORADIC.

-1- DISEASE: DEFECTS IN KRY10 ARE THE CAUSE OF ANULAR EPIDERMOLYTIC
CONTACTOR OF THE STRANDOLYTIC
CHYPERKERATOSIS (ABI), A DISTINCT PHENCTYPIC VARIANT OF EPIDERMOLYTIC
HYPERKERATOSIS (ABI), A DISTINCT PHENCTYPIC VARIANT OF EPIDERMOLYTIC
CHYPERKERATOSIS. IT RESEMBLES CLINICAL AND HISTOLOGIC FEATURES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=99215719; PubMed=10201536;
Arin M.J., Longley M.A., Anton-Lamprecht I., Kurze G., Huber M.,
Hohl D., Rothnagel J.A., Roop D.R.;
"A novel substitution in keratin 10 in epidermolytic hyperkeratosis.";
J. Invest. Dermatol. 112:506-508(1999).
                                                                                                                                                                                                                                                                                                                                                                                                               Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.

KERATIN 10 IS GENERALLY ASSOCIATED WITH KERATIN 1.

-:- TISSUE SPECIFICITY: SEEN IN ALL SUPRABASAL CELL LAYERS INCLUDING STRATUM CORNEUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC: 40-55 kDa) [K9 TO K20] AND II (NEUTRAL TO BASIC: 56-70 kDa) [K1 TO K8].
-!- SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
-!- CAUTION: REF 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN
                                                                                                                                                                           MEDLINE-94117870; PubMed-7507152;
McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
VARIANT EHK ASN-160.
BEDLINE-24117868; Pubmed-7507150;
Rothnagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.;
"Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                     "Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and clinical mosaicism in a type of epidermal nevus.";
New Engl. J. Med. 331:1408-1415(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99072665; PubMed=9856845; Suga Y., Duncan K.O., Heald P.W., Roop D.R.; An ovel helix termination mutation in keratin 10 in annular epidermolytic ichthyosis, a variant of bullous congenital ichthyosiform erythroderma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Invest. Dermatol. 111:1220-1223(1998).
                                                                                                               Invest. Dermatol. 102:13-16(1994)
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95059228; PubMed=7526210;
                                                                                                                                                             VARIANTS EHK PRO-156 AND SER-156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT EHK SER-160.
                                                                                                                                                                                                                                                                                                                                                                           VARIANT EHK THR-150.
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                                                                                                                                                                                                                                                              Morley S.M.;
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                                                                                              sequencing.
                                                                                                                                                                                                                                                                                                       congenital
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EMBL; X14487; CAA32649.1; -.

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SEQUENCE FROM N.A.
MEDLINE-88016163; PubMed=3477803;
Jung G., Korn E.D., Hammer J.A. III;
"The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                    PRINTS; PRO1248; TYPEIKERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                           Y -> D (IN EHK; SEVERE PHENOTYPE)
/FTId=VAR_003831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                        /FTId=VAR_003826.

R -> H (IN EHK).

/FTId=VAR_003827.

R -> C (IN EHK).

/FTIG=VAR_003828.

R -> P (IN EHK).
                                                                                                                                                                                                                                                  /FTId=VAR_010505.
M -> R (IN EHK).
/FTId=VAR_010506.
M -> T (IN EHK).
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                    GLY/PHE/SER-RICH.
                                                                                                                                                                                                                                                                                       TIG=VAR_010507.
                                                                                                                                                                                                                                                                                                                                                                 FTIG-VAR_003829
                                                                                                                                                                                                                                                                                                                                                                          R -> S (IN EHK).
/FTId=VAR_003830.
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01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                               GLY/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 17;
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NCBI_TaxID=5755;
                                                                                                                                                                                                   LINKER 12.
                                                                                                                                                                                LINKER 1.
COIL 1B.
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                                                                                                                                                                        1A.
                                                                                                                                                                                                             COIL
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                                                                         InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
                                   PIR; SO2158; KRHUO.
Aarhus/Ghent-2DPAGE; 7405; IEF
M19156; AAA59468.1; -- M77663; AAA59199.1; -- L20218; AAB59438.1; -- L20219; AAB59439.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                         31.4%;
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144
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                                                       MIM; 148080; -
                                                                                                                                  Polymorphism.
DOMAIN
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P10569;
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MEDLINE=90037074; PubMed=2530230;

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MEDLINE=90037074; PubMed=2530230;

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MEDLINE=90037074; PubMed=2530230;

MEDLINE=90037074; PubMed=2530230;

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MEDLINE=90037074; PubMed=2530230;

MEDLINE=90037074; PubMed=2530230;

MEDLINE=90037074; PubMed=2530230;

MEDLINE=90037074; PubMed=2530230;

MEDLINE=90037074; PubMed=2530230;

MEDLINE=90037074; PubMed=2530230;

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PRINTS; PR00422; SH3DOMAIN.
PRODOM; PR000355; myosin_head; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Myosin; ATP-binding; Phosphorylation; Multigene family; SH3 domain.
PARTIAL SEQUENCE FROM N.A.
MEDLINE-86259656; PubMed=3014500;
Hammer J.A. III, Jung G., Korn E.D.;
"Genetic evidence that Acanthamoceba myosin I is a true myosin.";
Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSIN HEAD-LIKE.
TAIL HOMOLOGY REGION 1 (TH.1).
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Interpro; IPR001609; myosin_head.
IFM: PF00063; myosin_head; 1.
Pfam; PF00018; SH3; 1.
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HSSP; P08799; 1LVK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYTOCHTOME B. 13. THE PROTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR FOR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RESPONSES. PER CONTROLS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE INDUCTION OF THOSE RESPONSES. PR CONTROLS THE INDUCTION OF THOSE RESPONSES. PR CONTROLS THE INDUCTION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BROTOCHLOROPHYLLIDE REDUCTASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RESPONSEIN, THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                       Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBDNIT: HOMODIMER (BY SIMILARITY).
-1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-1- SIMILARITY: CONTAINS 2 PAS (PER-ARMT-SIM) DIMERIZATION DOMAINS.
-1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. 58M;
MEDLINE-97198556; PubMed-9046599;
MEDLINE-97198556; PubMed-9046599;
MILIGS K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
MORGAN P.M., Mullet J.E.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                      STRAIN-CV. 58M;
MEDLINE-20188796; PubMed-10723737;
Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.;
A'the phytochrome gene family in tomato and the rapid differential evolution of this family in anglosperms.";
Mol. Biol. Evol. 17:362-373(2000).
16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Phytochrome B.
                                                                                       Sorghum bicolor (Sorghum) (Sorghum vulgare).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00387; HATPASSE_C; 1.
SMART; SM00088; HisKA; 1.
PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PSS0112; PASS; 2.
PROSITE; PSS00125; PHYTOCHROWE 1; 1.
PROSITE; PSS0046; PHYTOCHROWE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR003661; His_kinA.
InterPro; IPR0000014; PAS.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF182394; AAB41398.2; ...
InterPro; IPR003018; GAF.
InterPro; IPR003594; HATPASe_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00360; phytochrome; 1. Pfam; PF00512; signal; 1. PRINTS; PR01033; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 208-1178 FROM N.A.
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Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00065; GAF; 1.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=4558;
                                                                     PHYB OR MA3.
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                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
NTF5 OR NTF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92075279; PubMed=1742028;
Berkemeler L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ip N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R., Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H., Yancopoulos G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-ZAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
MEDLINE=20095835; PubMed=10631974;
Robinson R.C., Radziejewski C., Spraggon G., Greenwald J.,
Kostura M.R., Burtnick L.D., Stuart D.I., Choe S., Jones E.Y.;
"The structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-binding site.";
Protein Sci. 8:2589-2597(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: HIGHEST LEVELS IN PROSTATE, LOWER LEVELS IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC AND ADULT TISSUES.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY SYMPATHETIC NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Neurotrophin-5: a novel neurotrophic factor that activates trk and
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Mammalian neurotrophin-4: structure, chromosomal localization,
                                                                                                                                                                                                                .
0
                                                                                                                                                                         Score 61; DB 1; Length 1178; Pred. No. 31;
                                                                                                                                                                                                                3; Indels
                                                                                                                          CHROMOPHORE (BY SIMILARITY)
                                                                                                                                           129136 MW; C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue distribution, and receptor specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                   PAS 1.
PAS 2.
HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                            PRT; 210 AA.
                                                                                                                                                                                                                   1; Mismatches
                                                                                           POLY-HIS.
                                                                                                           POLY - GLY
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MEDLINE=92212967; PubMed=1313578;
                                                                                                                                                                                31.4%; 75.0%;
                    Repeat; Multigene family DOMAIN 668 739
                                                                                                                                                                                                                   12; Conservative
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                                                                                                                                                                                                                                                                        STANDARD;
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                                                     873
1170
31
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                                                                                                                                             1178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                     802
950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenthal A.;
                                                                                                                                                                                                                                                                                                                                                                              NT5_HUMAN
                                                                                                                                               SEQUENCE
                                                                                                                                                                                  Query Match
                                                     DOMAIN
                                                                                                                              BINDING
                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                             NT5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                         δ
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LAMBDA P2
7E SPLICING.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

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Krolewski J.J., Dalla-Favera R.;
"The ltk gene encodes a novel receptor-type protein tyrosine kinase.";
EMBO J. 10:2911-2919(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toyoshima H., Kozutsumi H., Maru Y., Hagiwara K., Furaya A., Mioh H., Hanai N., Takaku F., Yazaki Y., Hirai H.; "Differently spliced cDNAs of human leukocyte tyrosine kinase receptor tyrosine kinase predict receptor proteins with and without a tyrosine kinase domain and a soluble receptor protein."; proc. Natl. Acad. Sci. U.S.A. 90:5404-5408(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90706632; PubMed-2320375;
MEDLINE-90706632; PubMed-2320375;
Maru V., Hirai H., Takaku F.;
"Human lik: gene Structure and preferential expression in human leukemic cells.";
Oncogene Res. 5:199-204(1990).
-i. FUNCTION: THE EXACT FUNCTION OF THIS PROTEIN IS NOT KNOWN. IT IS PROBABLY A RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last Sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Leukocyte tyrosine kinase receptor precursor (EC 2.7.1.112) (Protein tyrosine kinase-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL). DBC6A30195E139AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                              9.
                                                                                                                                                                                                                                                                                                                                                 Score 60.5; DB 1; Length 210;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               129 GSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRHWVS 168
                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                       3 GPTLRQWL------AARAGGGGGGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                   NEUROTROPHIN-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       864 AA.
                                                                                                                                                                                                                                                                                                                                                               Pred. No. 7.6;
3; Mismatches
or send an email to license@isb-sib.ch),
                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                        PROSITE; PS00248: NGF 1; 1.
PROSITE; PS50270; NGF 2; 1.
Growth factor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=93296146; PubMed=7685902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92007735; PubMed=1655406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                    22426 MW;
                                                                                                                                                                                                                                                                                                                                               31.2%;
35.0%;
                           EMBL; M86528; AAA60154.1; -.
                                                                                                                                   PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
                                                                                                          InterPro; IPR002072; NGF
                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                210
170
199
201
                                                                                                                       Pfam; PF00243; NGF; 1.
                                                                PDB; 1B8M; 09-FEB-99.
PDB; 1B98; 26-FEB-99.
MIM; 162662; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                         PIR; JH0503; JH0503
PIR; A42687; A42687
                                                                                                                                                                                                                                                                                                                    210 AA;
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                            141
158
76
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81
97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLTK_HUMAN
P29376;
                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLTK_HUMAN
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
G -> VAAASGDGAAPAPGARAAWGPGERAFIGAGSPAQRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAPGPRRFPPPLPAG (IN ISOFORM LAMBDA P1).
MISSING (IN ISOFORM LAMBDA P1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> GTKRLAGTVDSRLLLSSELGWVSAAGSRRQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
             tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; LAMBDA P1, LAMBDA P2 (SHOWN HERE) AND LAMBDA P3; ARE PRODUCED BY ALTERNATIVE SPLICIN (SHOWN HERE) AND LAMBDA P3; ARE PRODUCED BY ALTERNATIVE SPLICIN-!- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PS50011, PROTEIN_KINASE_DOM; 1.
Transferase: Tyrosine-Protein kinase; Transmembrane; ATP-binding;
Phosphorylation; Receptor; Glycoprotein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEUKOCYTE TYROSINE KINASE RECEPTOR EXTRACELLULAR (POTENTIAL).
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ک
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V -> GTKRLAGTVDSRLLLSM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.2%; Score 60.5; DB 1; Length 864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2A -> MR (IN REF. 3).
97143DD57684A657 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O -> R (IN REF. 2).
V -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORM LAMBDA P3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 26;
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                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002011; Receptor_tyr_kin_II.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00219; Tyrkc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91653 MW;
                                                                                                                                                                                                                             EMBL; D16105; BAA03679.1; -. EMBL; X60702; CAA43113.1; -. EMBL; X52213; CAA36460.1; -. PIR; S17452.
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334
449
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                                                                                    PROTEIN KINASES.
                                                                                                                                                                                                                                                                                      HSSP; P00523; 2PTK
MIM; 151520; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              864 AA;
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448
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220
274
449
652
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TRANSMEM
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VARSPLIC
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CONFLICT
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
SIGNAL
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JUND_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Ceratitis capitata (Mediterranean fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Tephritoidea, Tephritidae, Ceratitis.
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0043; LEGIZIPPRJUN.
MARRY; SWO0338; BRLE; 1.
PROSITE; PSO0036; BZIE BASIC; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                               -i- SUBDNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A7F6D21A97DBB676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Sex-lethal protein homolog (CCSXL).
         01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; .348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                 Hartl M., Hutchins J.T., Vogt P.K.; "The chicken jund gene and its product."; Oncogene 6:1623-1631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No
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MEDLINE-98171464; Pubmed-9502730;
                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-92019832; PubMed=1923529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S20099; S20099.
HSSP: P05412; 1F0S.
TRANSFAC; T02196; ...
InterPro; IPR002112; Leuzip_Jun.
InterPro; IPR001117; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X60063; CAA42665.1; -.
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                                                           Transcription factor jun-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00170; bZIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 2
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-7213;
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DOMAIN
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061374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                    -:- SUBCELLULAR LOCATION: Nuclear.
-:- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS
A1, A2, A3, A4, AND EMBRYO-SPECIFIC ISOFORMS E1, E2 AND E3 (SHOWN
HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- DEVELOPMENTAL STAGE: EXPRESSED IN BMBRYOS OF BOTH SEXES. ALSO
EXPRESSED IN THE PROGENTROR CELLS OF THE GENALINE.
-:- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
Saccone G., Peluso I., Artiaco D., Giordano E., Bopp D., Polito L.C.; "The Ceratitis capitata homologue of the Drosophila sex-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98337188; PubMed-9674431;
Kloss B., Price J.L., Saez L., Blau J., Rothenfluh A., Wesley C.S.,
Young M.W.;
                                   gene Sex-lethal is structurally conserved, but not sex-specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last amoctation update)
Discs overgrown protein Kinase (EC 2.7.1.-) (Double-time protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The Drosophila clock gene double-time encodes a protein closely related to human casein kinase I epsilon."; Cell 94:97-107(1998).
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                                                                                    -! - FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, ...
SWART; SMO0360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Repeat; Nuclear protein; Alternative splicing.
DOMALN 1 27 GIX/ASN-RICH DOMAIN.
110 188 RNA-BINDING (RRM) 1.
776 RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.9%; Score 60; DB 1; Length 348; 83.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN ISOFORM A1).
CABA3DA5C2C8874A CRC64;
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POLY-GLY.
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                                                                   Development 125:1495-1500(1998)
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF026145; AAC38968.1; -. HSSP; P19339; 1SXL.
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37188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00076; rrm; 2.
PRINTS; PR00961; HUDSXLRNA.
SMART; SM00360; RRM; 2.
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196 2
68 68
95 95
293 3
312 3
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                                                                                                      DETERMINATION.
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NCBI_TaxID=7227;
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                                                      regulated."
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076324;
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VARSPLIC
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                                    MEDLINE=98337187; PubMed=9674430;
Price J.L., Blau J., Rothenfluh A., Abodeely M., Kloss B., Young M.W.;
"Double-time is a novel Drosophila clock gene that regulates PERIOD
                                                                                                                                         FUNCTION: INVOLVED IN CIRCADIAN RHYTHMS, VIABILITY AND MOLECULAR OSCILATIONS OF THE CLOCK GENES PERIOD (PER) AND TIMELESS (TIM). DBT REDUCES THE STABILITY AND THUS THE ACCUMULATION OF MONOMERIC PER PROTEINS, PROBABLY THROUGH PHOSPHORYLATION. NO EVIDENT CIRCADIAN OSCILLATION IS DETECTED IN HEAD.
SUBUNIT: FORMS A COMPLEX WITH PER.
                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: EXPRESSED IN PHOTORECEPTOR CELLS OF THE EYES AS WELL AS IN THE REGION SITUATED BETWEEN THE OPTIC LOBE AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D2 (Forkhead-related protein FKHL17) (Forkhead-related transcription factor 9) (FREAC-9).
                                                                                                                                                                                                                                                                                                                                                      CASEIN KINASE I SUBFAMILY. COULD BE THE ORTHOLOG OF CKI-EPSILON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P->S: IN DBTS; SHORTENS THE BEHAVIORAL
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                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 16;
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POLY-ALA.
POLY-GLN.
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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[2]
MUTAGENESIS, AND FUNCTION
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PROSITE; PS00107; PROTEI)
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                                                                                                  protein accumulation.";
Cell 94:83-95(1998).
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                                                                                                                                                                                                                                                                                                             CENTRAL BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
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060548;
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NP_BIND
BINDING
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DOMAIN
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P02535; P08731;
21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (56 kDa cytokeratin)
(Keratin, type I cytoskeletal 59 kDa).
                                                                                         SEQUENCE FROM N.A.

MEDLINE-S9066765, PubMed-9403061,

Enstisson S., Betz R., Lagercrantz S., Larsson C., Ericksson S.,
Cederberg A., Carlsson P., Enerbaeck S.;
Cloning and characterization of freac-9 (FKHL17), a novel kidney-
expressed human forkhead gene that maps to chromosome 1p32-p34.";
Genomics 46:78-85(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                      REVISIONS.

Enerbaeck S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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FORK - HEAD.
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PRINTS; PR00053; FORKHEAD.
SNART; SM00339; FH; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001766; Fork_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 PTALLROGLKTDAGGGAGGGG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein;
90 94 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PT -- LRQWLAARAGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
250
306
409
426
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T02485; -.
  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442
497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRT10 OR KRT1-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 602211;
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S -> G (IN REF. 2).
WYEKHGNOS -> VNEBRE 2).
WYEKHGNOS -> VVNEBRQLKP (IN REF. 2).
KSDLEM -> QSVLEL (IN REF. 2).
H -> L (IN REF. 2).
ECRYCY -> VESLLR (IN REF. 2).
GGSHGGS -> CGGRGGG (IN REF. 2).
                                                                                                                                                  MEDLINE-83192464; PubMed-6188955; Stainer P.M., Rice R.H., Roop D.R., Trus B.L., Steven A.C.; Stainert P.M., Rice R.H., Roop O.R., Trus B.L., Steven A.C.; Complete amino acid sequence of a mouse epidermal keratin subunit and implications for the structure of intermediate filaments.";
                                                                                                                                                                                                            Nature 302:794-800(1983).

-!- SUBUNT: HFFEROMETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.

-!- SUBUNT: HFFERALLY SOSCIATED WITH KERATIN 1.

-!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND

MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)

(40-55 AND 56-70 KILLDDALFONS, RESPECTIVELY).

-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                           MEDLINE-85207552; PubMed-2581944;
Krieg T.W., Schafer M.P., Cheng C.K., Filpula D., Flaherty P.,
Steinert P.M., Roop D.R.;
"Organization of a type I keratin gene. Evidence for evolution of
                                                                                       intermediate filaments from a common ancestral gene.";
J. Biol. Chem. 260:5867-5870(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S -> C (IN REF. 2).
S -> F (IN REF. 2).
S -> F (IN REF. 2).
Y -> L (IN REF. 2).
E -> G (IN REF. 2).
AG -> G (IN REF. 2).
MISSING (IN REF. 2).
SY -> GC (IN REF. 2).
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H -> R (IN REF. 2).
S -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam. PF00038; filament; 1.
PRINTS; PR01248; TYPEIKERATIN.
PROSITE; PS0226; IF; 1.
Intermediate filament; Coiled coil; Keratin.
INIT_MET 0 0 0
DOMAIN 1 142 HEAD.
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COIL 1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L00193; AAA39391.1; -.
EMBL; M10081; AAA39391.1; JOINED.
EMBL; V00830; CAA24214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P10968; IWGC.
MGD; MGI:96685; Krtl.10.
InterPro: IPR001664; IF.
InterPro: IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02940; KRMSE1.
PIR; S07330; S07330.
            SEQUENCE FROM N.A.
                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-9215335; PubbMed-1662793; Haase V.H., Snijders A.J., Cooke S.M., Teng M.N., Kaul D., Haase V.H., Snijders A.J., Cooke S.M., Teng M.N., Kaul D., Ie Beau M.M., Bruns G.A., Bernards A.; Alternatively spliced ltk mRNA in neurons predicts a receptor with a larger putative extracellular domain."; Oncogene 6:2319-2325(1991).
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Leukocytes express a novel gene encoding a putative transmembrane protein-kinase devoid of an extracellular domain.";
Nature 33:672-676(1988).
-!- FUNCTION: THE EXACT FUNCTION OF THIS PROTEIN IS NOT KNOW, IT IS PROBABLY A RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE SPLICING
-!- ALTERNATIVE SPLICING
-!- PRODUCES VARIANTS WITH SHORTER EXTRACELLULAR DOMAIN.
-!- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernards A., de la Monte S.; "The ltk receptor tyrosine kinase is expressed in pre-B lymphocytes and cerebral neurons and uses a non-AUG translational initiator."; EMBO J. 9:2279-2287(1990).
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                               DB 1; Length 569
                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Snijders A.J., Haase V.H., Bernards A.; Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
 S -> G (IN REF. 2).

GQ -> RR (IN REF. 2).

KS -> SGT (IN REF. 2).

; EEC59D4D8FFE484D CRC64;
                                                                                                                                                                                                                                                                                 888 AA.
                                                                                                     Pred. No. 21;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 217-270 AND 332-888 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 252-270 AND 332-888 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 252-270 AND 332-888 FROM N.A.
                                                                                      Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88232962; PubMed=2836739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90291994; PubMed=2357970;
                                                                                                                                                           7 ROWLAARAGGGGGGGGGIEGPTLR 29
                                                                                                                                                                             : |: ::|:||||||| : : |
9 KQFSSSRSGGGGGGGGVRVSSTR 31
543 S
548 GQ
556 KS
57711 MW;
                                                                                     30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ben-Neriah Y., Bauskin A.R.;
                                                                                                        Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
 543
547
555
569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C
                                                                                                                                                                                                                                                                             KLTK_MOUSE
P08923;
                   CONFLICT
 CONFLICT
                                                      SEQUENCE
                                                                                          Query Match
                                                                                                                                                                                                                                                                KLTK_MOUSE
                                                                                                                                                                                                                                                RESULT 21
                                                                                                                                                                                             qq
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1;
                                                                                                                                                                                                                                                             Phosphorylation; Receptor; Glycoprotein; Signal; Alternative splicing... SIGNAL 1 16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidaa; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91117256; PubMed-1703632; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T., "The Drosophila suppressor of sable gene encodes a polypeptide with regions similar to those of RNA-binding proteins."; Mol. Cell. Biol. 11:894-905(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE=91169252; PubMed=1963868; Voelker R.A., Graves J.P., Gibson W., Eisenberg M.T.; Mobile element insertions causing mutations in the Drosophila suppressor of sable locus occur in DNase I hypersensitive subregions
                                                                                                                                                                                      PROSITE; PSOU107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSOU109; PROTEIN_KINASE_TYR; 1.
PROSITE; PSOU2039; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PSSOU11; PROFEIN_KINASE_DOM; 1.
Transferase; Tyrosine protein kinase; Transmembrane; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                             LEUKOCYTE TYROSINE KINASE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB 1; Length 888; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3FFCA80AB4863C55 CRC64;
                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
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Q -> H (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                   MGD; MGI:96840; Ltk.
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR002011; Receptor_tyr_kin_II.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                   (BY
EMBL; M90470; AAA39451.1; -...EMBL; X52621; CAA36848.1; ALT_SEQ. EMBL; X07984; CAA30793.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 PGWRRW----AGGGGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%;
                                                                                                                                       Pfam: PF00069; prinase; 1.
PRINTS; PR00109; TYRKINASE.
SMART; SM00219; TYRK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suppressor of sable protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PTLRQWLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-9 FROM N.A.
                                              S00904; S00904.
S12792; S12792.
                                            PIR; S00904; S00904
PIR; S12792; S12792
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991
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01-NOV-1997
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TRANSMEM
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MOD_RES
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
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DOMAIN
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SUS_DROME
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                                                                                              -i- DEVELOPMENTAL STAGE: AT ALL STAGES.
-i- SIMILARITY: HAS REGIONS SIMILAR TO THOSE OF RNA-BINDING PROTEINS.
of 5'-transcribed nontranslated sequences.";
Genetics 126:1071-1082(1990).
-!- FUNCTION: AFFECTS THE TRANSCRIPT LEVELS OF THOSE ALLELES THAT IT
SUPPRESSES. MAY BE INVOLVED IN RNA METABOLISM.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M., Obris D., Rastan S., Stevanovic M., Goodfellow P.N., Lovell-Badge R.; "A comparison of the properties of Sox-3 with Sry and two related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes, Sox-1 and Sox-2.";
Development 122:509-520(1996).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!TISSUE SPECIFICITY: MAINLY IN THE DEVELOPING CENTRAL NERVOUS SYSTEM. EXPRESSED IN DEVELOPING UROGENITAL RIDGE.
-!- SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB 1; Length 1322; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 GLN-RICH (OPA-REPEAT).
62 RNA-BINDING (BY SIMILARITY).
143555 MW; D5FS34EB5702EA08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGHLY CHARGED DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
01-077-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96189340; PubMed=8625802;
                                                                                                                                                                                                                                                                                                                                                             Flybase; FBgn0003575; su(s).
InterPro; IPR000571; zf-CCCH.
Pfam; pF00642; zf-CCCH; 2.
RNA-binding; Nuclear protein.
BOMAIN
                                                                                                                                                                                                                                                                                                      EMBL; M57889; AAA28920.1; -.
EMBL; X59364; CAA42010.1; -.
PIR; A39612; A39612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1159 GGGGGGGVVLPNLSQ 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1087
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SOX1 OR SOX-1.
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Query Match
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                                                                                                                                                                                                                          Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulator of BETR2 and MyOD-helix protein, can act as a negative regulator of BETR2 and MyOD-responsive genes.";

Mol. Cell. Biol. 16.626-63(1996).

• FUNCTION: INHIBITS DNA BINDING OF TCF3 (E47) HOWODIMERS AND TCF3 (E47) / NEURODIMERS AND ACTS AS A STRONG REPRESSOR OF NEURODIAND MYOD-RESPONSIVE GENES, PROBABLY BY HETERODIMERIZATION WITH CLASS A BASIC HELIX-LOOP-HELIX FACTORS. DESPITE THE PRESENCE OF NITH CLASS A BASIC DOMAIN, DOES NOT BIND TO DNA.

• SUBUNT: HETERODIMER WITH OTHER BHILH PROTEINS, LIKE TCF3 (E47).

• SUBCELLULAR LOCATION: Nuclear (Potential).

• SUBCELLULAR EDCATION: TRIDNEY, LUNG, BARIN AND PANCREAS (INSULINOMA).

• ITRILABILY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBEAMILY.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BEDLINE-90140430; PubMed-8552091;
Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
ISAI M.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                          5;
                                                                                                                                                                                                 Score 59.5; DB 1; Length 391;
Pred. No. 17;
                                                                                                                                                                                                                          Indels
                                                                                                                                                              POLY-ALA.
9F81ED667F947C05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00353; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
NUClear protein; Transcription regulation; Repressor.
DOMAIN 11 14 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         367 AA.
                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     BETA3 protein.
Mesocricetus auratus (Golden hamster).
                                                                                                                        POLY-ALA.
POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                               Pred. No.
                                                                                                               POLY-GLY
                                                                                                  HMG BOX
                   MGD; MGT:98357; SOX1.
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG, box; 1.
SMART; SM00398; HMG; 1.
DNA-binding; Nuclear protein.
DOMAIN 30 43 POLY-(
                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                         22 LSGPA----GARGGGGGGGG 38
                                                                                                                                                                          39237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003015; HIH Myc.
InterPro; IPR001092; HIH Myc.
Pfam; PF00010; HIH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S80870; AAB50691.1; -.
                                                                                                                                                                                                30.7%;
ilarity 54.5%;
Conservative
                                                                                                                                                                                                                                                   1 IEGPTLROWLAARAGGGGGGG
 EMBL; X94126; CAA63846.1;
HSSP; Q05066; 1HRY.
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                          391 AA;
                                                                                                                                                                                                            Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                        BET3_MESAU
009029;
                                                                                                   DNA_BIND
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                    Query Match
                                                                                                                          DOMAIN
                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                               HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-Dinding; Nuclear protein; Transcription regulation.
DOMAIN 39 48 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                Score 59; DB 1; Length 367;
                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0006AEAD71D594FE CRC64;
                                                                                                                6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      401 AA.
                                                                                                                                                                                   Mismatches
                                                                  BASIC DOMAIN.
                                                                                                                                                                 Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY - ALA.
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                                 POLY-GLY.
                                               POLY-GLY
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                                                                                                    POLY-ALA
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Placenta;
MEDLINE=94327547; PubMed=7914194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U07663; AAB60647.1; -...EMBL; U07663; AAB60647.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
Pfam; PF000046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
SWART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40932 MW;
                                                                                                                  35905 MW;
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                                                                                                                                                     30.4%;
                                                                                                                                                                 61.1%;
                                                                                                                                                                                                                                      11 AARAGGGGGGGGTEGPTL 28
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
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135
177
301
325
62
99
1179
217
240
282
319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                367 AA;
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 142994; -
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                                                                                                                                                   Query Match
Best Local Simi
Matches 11;
                                                                                                                                                                                                                                                                                                                                      HB9_HUMAN
P50219;
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DOMAIN
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                                                                  DNA_BIND
                                                                                                                  SEQUENCE
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                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                       RESULT 25
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14 AGGGGGGGGIEGPT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
One cut domain family member 2 (ONECUT-2 transcription factor) (OC-2).
                                                                                                                                                                                                                                MEDLINE-99115605; PubMed-9915796;
MEDLINE-99115605; PubMed-9915796;
Jacquemin P., Lannoy V., Rousseau G.G., Lemaigre F.P.;
"OC-2, a novel mammalian member of the ONECUT class of homeodomain transcription factors whose function in liver partially overlaps with that of hepatocyte nuclear factor-6.";
J. Biol. Chem. 274:2665-2671(1999).
--- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. ACTIVATES THE TRANSCRIPTION OF A NUMBER OF LIVER GENES SUCH AS HNF3B.
--- SUBCELLOLAR LOCATION: Nuclear.
--- SIMILARITY: DELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
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0
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              Indels
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             5
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                                                                                                           485 AA.
   Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA
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                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro; IPR003350; CUT.
InterPro; IPR001356; Homeobox.
Pfam; PF02376; CUT; 1.
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y18198; CAB38253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GGGGGGGIEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 GGGGGGGGGCPGHEOELLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.4%;
                                                    37 ASGTGGGGGGGGASGGT 53
                                11 AARAGGGGGGGGIEGPT 27
            11; Conservative
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466
37
66
82
165
303
                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSFAC; T03259; -.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 604894;
                                                                                                         ONC2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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DOMAIN
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                                                                                                                    095948;
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                                                                                               ONC2_HUMAN
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            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE STRIATIN FAMILY OF WD-REPEAT PROTEINS.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
-!- CAUTION: The name "Zinedin" probably originates from the name of the famous soccer player from Marseille (Zinedine Zidane)!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS CALMODULIN IN A CALCIUM DEPRINENT MANNER. MAY FUNCTION AS SCAFFOLDING OR SIGNALING PROTEIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-BOUND (BY
                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20347911; Pubmed=10748158;
Castets F., Rakitina T., Gaillard S., Mogrich A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                              "Zinedin, SGZNA, and striatin are calmodulin-binding, WD repeat proteins principally expressed in the brain."; J. Biol. Chem. 275:19970-19977(2000).
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SMART; SM00320; WD40; 6.
PROSITE: PS50082; WD_REPEATS_1; 1.
PROSITE: PS50082; WD_REPEATS_2; 4.
PROSITE: PS50294; WD_REPEATS_2; 4.
Calmodulin-binding; Repeat; WD_repeat; Coiled coil.
DOMAIN 165 186 COILED COIL (POTENTIAL).
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WD 3.
WD 4.
WD 5.
WD 6.
WD 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAD -> GTR (IN REF. 2).
4DA016A8FF7EDB5E CRC64;
                                        01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80581 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 402-753 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.4%;
78.6%;
  STANDARD;
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                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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4436
4489
542
587
635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Muscle;
ZIN_HUMAN
                                                                                                                     Zinedin.
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                    09NRL3;
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3 GPTLRQWLAARAGGGGGGG
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                                                                                                                                                                                                                                                                                                                                    STRAIN-21GR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SOURCE STATE TETTET TETTET SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                         Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Peterygota: Neoptera: Endopterygota: Diptera: Brachycera; Muscomorpha;
Ocstroidea; Calliphoridae; Lucilia.
NCBI_TaxID-7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; NOLLEAR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORMONE-BINDING (POTENTIAL).
C1511452ED37D359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MODULATING (POTENTIAL).
NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 4499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83075 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U75355; AABB1130.1; -. HSSP; P20393; 1A6Y.
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Best Local Similarity 76.9
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                                                                                          STANDARD;
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366
321
361
674
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   44 AGKGGGGGGSPGPT 57
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301
337
454
657 AA;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NR1 SUBFAMILY.
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039610;
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DOMAIN
SEQUENCE
                                                                                        ECR_LUCCU
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain genes.";
J. Cell Sci. 107:635-644(1994).

- I. Cell Sci. 107:635-644(1994).

- I. FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

DYNEIN HAS ATPASE ACTIVITY.

- I. SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

- I. SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                      MEDLINE-97329535; PubMed-9186009;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas reinhardtii flagellar alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50194; FILAMIN_REPEAT; 1. Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
ATP (POTENTIAL).
MW: 319AC7FD30F1591A CRC64;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
LoCT-2001 (Rel. 40, Last annotation update)
Dynein alpha chain, flagellar outer arm (DHC alpha).
ODAll OR ODA-11.
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Motil. Cytoskeleton 37:120-126(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILAMIN.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003593; AAA.
Interpro; IPR001298; Filamin.
Interpro; IPR001298; Filamin.
Interpro; IPR001798; Kelch.
Interpro; IPR001798; PLD.
Pfam; PF00630; Filamin; 1.
Pfam; PF001344; Kelch; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1142-4499 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2655 2688
3003 3023
310 3262
348 3515
1716 1723
2019 2026
2717 2754
4499 AA; 503606 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L26049; AAA57316.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00382; AAA; 3.
SMART; SM00429; IPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1334
1450
1864
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Matches 12; Conserv
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4194 GETLFKTVVEVAGGGGGGG 4213

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morelli F., Stornaluolo A., Nigro V., Simeone A., Migliaccio E., Morelli F., Stornaluolo A., Nigro V., Simeone A., Boncinelli E.; Nucleic Acids Res. 17:10385-10402(1989).

-i- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Spinal cord;
TISSUE-2097538; PubMed=1756725;
Zappavigna V. Renucci A., Izpisua-Belmonte J.-C., Urier G., Peschle C., Duboule D.;
"HOX4 genes encode transcription factors with potential auto- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Nuclear.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LIMB BUDS.
-i- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complementary homeo protein gradients in developing limb buds."; Genes Dev. 3:641-650(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00024; HOMEOBOX.
SMART; SMORISHS; HOX.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA binding; Developmental protein; Nuclear protein;
DOMAIN 115 1149.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 264-342 FROM N.A.
BDLINE-89306602; PubMed-2268311;
Oliver G., Sidell N., Fiske N., Heinzmann C., Mohandas T.,
Sparkes R.S., de Robertis E.M.;
                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Homeobox protein Hox-D9 (Hox-4C) (Hox-5.2).
HOXD9 OR HOX4C.
 342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
SER/THR-RICH.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 275-340 FROM N.A.
MEDLINE=90098876; PubMed=2574852;
                                                                                                                                                                                                                                                                                                                          cross-regulatory capacities."; EMBO J. 10:4177-4187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X59372; CAA42016.1; -. EMBL; X15506; CAA33528.1; -.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S18649; S18649.
PIR; S05958; S05958.
PIR; A32830; A32830.
HSSP; P02834; 1B81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSFAC; T01424; -
                                                                                                                                                                            NCBI_TaxID=9606;
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HXD9_HUMAN P28356;
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DOMAIN

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Gaps
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                                            30.2%; Score 58.5; DB 1; Length 342; 44.8%; Pred. No. 19;
                                                                     9; Indels
            266 266 E -> A (IN REF. 2).
342 AA; 35580 MW; 731981FE25C5ACD7 CRC64;
                                                     44.8%; Pred No. -
                                                                                                                                                    October 9, 2002, 09:00:10
                                                                                                         3 GPTLRQWLAARAG-----GGGGGGGIEGP 26
                                                       Best Local Similarity 44.8
Matches 13; Conservative
334
                                                                                                                                                    Search completed: Octo
DNA_BIND
CONFLICT
                       SEQUENCE
                                               Query Match
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HOMEOBOX

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:52:16; Search time 12.8993 Seconds (without alignments) 482.803 Million cell updates/sec Run on:

US-09-422-838C-24

194 1 IEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 36 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_19:\* Database

sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_bacteriap:\*
sp\_archeap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_organelle:\*sp\_phage:\* sp\_rvirus:\* sp\_rodent:\* sp\_plant:\* sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æР (				
Kesult		Query				
No.	Score	Match	Match Length DB	DB	OI.	Description
1	74	38.1		10	63PGC6	Q91qc9 oryza sativ
7	73.5	37.9		13	O9PVG9	O9pvq9 coturnix co
3	71	36.6		10	Q943K0	
4	70	36.1		10	Q9SDK6	
S	69	35.6	200	S	019476	Q19476 caenorhabdi
9	68.5	35.3		16	000060	Q9ccc0 mycobacteri
7	68.5	35.3		7	049843	Q49843 mycobacteri
80	99	35.1		10	Q9LWC8	Q91wc8 oryza sativ
σ	89	35.1		٣	Q9HEA4	O9hea4 neurospora
10	29	34.5		'n	Q9W033	Q9w033 drosophila
11	99	34.3		10	Q9FTZ5	Q9ftz5 oryza sativ
12	66.5	34.3		16	033230	033230 mycobacteri
13	66.5	34.3		7	Q9AD76	Q9ad76 streptomyce
14	99	34.0		13	Q9YHD0	Q9yhd0 petromyzon
15	99	34.0		10	Q9ASE5	Q9ase5 oryza sativ
16	99	34.0		4	Q9P270	09p270 homo sapien

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431 AA.

PRT;

PRELIMINARY;

RESULT 2 Q9PVG9 ID Q9PVG9

Q9aii5 mycobacteri Q9pux6 gadus morhu Q9jkb4 mus musculu Q9ld54 oryza sativ Q93h33 streptomyce Q9pud8 lampetra fl Q9nec7 leishmania	3 013	165 286 334 540 642 642	0.00000	0000000	0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Q9c0il homo sapien Q9afi5 mycobacteri	2 Q9AFI5	775 165		62.5 62.5	. B G
Oryz	0	752	00		36
Q9byd8 homo sapien 096iq7 homo sapien	4 Q9BYD8 4 Q96JG7	688 689	9.0	03 03	34 35
Q96sq2 homo sapien O04270 chlamydomon		474 490	9.5	63 63	32 33
Q9m699 catharanthu Q942r8 oryza sativ	10 Q9M699 10 Q942R8	160 186		63 63	30 31
Q91bc5 spodoptera Q9m6al catharanthu	12 Q91BC5 10 Q9M6A1	66 137	9.5	63 63	28 29
Q94iw9 oryza sativ Q91i16 oryza sativ		207 584	32.7 32.7	63.5 63.5	26 27
Q9u2i0 caenorhabdi O96755 branchiosto	5 Q9U2IO 5 Q96755	333 422	. m	64 64	24 25
Q9vv01 drosophila Q9u2i1 caenorhabdi		309 331	 m m	64 64	22 23
$\infty$	J	447	n m	65 65	20
Q9nyw9 homo sapien Q9y566 homo sapien	4 Q9NYW9 4 Q9Y566 13 Q73628	1548	 	65.5 65.5	8 6 6
Q9ar44 oryza sativ	10 Q9AR44	243	۳. ش	65.5	17

## ALIGNMENTS

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0; Gaps
                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
Sasakl I., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P046AH08";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003525; BAB07996.1; -.
InterPro; IPR00571; Zf-CCCH.
Pfam; PF00421; Zf-CCCH, 4.
SEQUENCE 360 AA; 37368 MW; 5105598D7EIC77B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%; Score 74; DB 10; Length 360; 56.0%; Pred. No. 1.4; tive 2; Mismatches 9; Indels
                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE ZINC FINGER PROTEIN.
00 Stativa (Rice)
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 LEGPMWRMGLGGGGGGGGGGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 14; Conservative
                           PRELIMINARY;
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Best Local Similarity
                             629760
RESULT 1
                091.GC9
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80 GPTVGVRVAYRAGAGGGGGGPRGFALK 106

RESULT 4

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                                                                           Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
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42.9%; Pred. No. 1.9;
ive 2; Mismatches 5; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0039A07."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.6%; Score 71; DB 10; Length 253; 55.6%; Pred. No. 2.1; tive 3; Mismatches 9; Indels
                                                                                                                                                                          SEQUENCE FROM N.A.

Liu Y., Xue J.X., Zhang W., Fu D.C., He R.Q., Xue Z.G.;

"garain-2, a POU-box gene expressed in quail embryos.";

submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003235; BAB64100.1; - SEQUENCE 253 AA; 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDC47E53F9ACC7D5 CRC64;
          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 QWLAARA------GGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 OWIAALSHGGPGGGGGGGGGGGGGGGGGGEAP----WAAAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTLRQWLAARAGGGGGGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                            HSSP; P14859; 10CT.
InterPro: IPR001356; Homeobox.
InterPro: IPR001327; POU.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; POU. 1.
PRINTS; PR00028; POUDOWAIN.
ProDom; PD000583; POU; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PSS0071; HOMEOBOX_2; 1.
PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 AA; 43722 MW;
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Best Local Similarity 55.6<sup>†</sup>
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 42.9 nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                              POU-BOX PROTEIN BRAIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P0039A07.6 PROTEIN.
P0039A07.6.
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                                                                                                                                           NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DEC-2001
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                           Oryza sativa (Rice).
Sukaryota, Vitálplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza satiya nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                             36.1%; Score 70; DB 10; Length 439; 34.0%; Pred. No. 4.6; Live 2; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGG------IEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                39 LHAPLLRLWPLGGGGGGGGGGGGGGGGERVGAVGGAVRGEEARSQRAAEA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 5; Length 500; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                           Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 278013; CAB01420.1; -.
EMBL, 278013; CAB01420.1; -.
InterPro; IPR001254; Trypsin.
PROSITE; PS50240; TryPsin. DOM; 1.
Hydrolase; Serine Protesse.
SEQUENCE 500 AA; 53946 WW; 1416327086FE7CF6 CRC64;
                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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           439 AA
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 GSMLGRFLSNRGGGGGGGGGGGG 451
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56.5%;
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nes 13; Conservative
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           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.
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                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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                                                                                                                                                                                                                                clone:P0705D01
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                           09SDK6;
            Q9SDK6
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99SDK6
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4 PTLRQW-----LAARAGGGGGGGGIEGP 26
                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                             HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                clone:P0483F08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B11A5.200.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09HEA4;
                                                                                           Q9LWC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9HEA4
                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                              O9LWC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HEA4
                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ϊ;
                                                                                                                                                                                                                          MEDLINE=21129732; Pubmed=11234002; James K.D., Thomson N.R., Webline=21129732; Pubmed=11234002; Gole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                              Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00019; AAA17274.1; -.
SEQUENCE 518 AA; 56001 MW; 6641916CC84F374B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 AA; 52800 MW; 188918856F9774AA CRC64;
                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-GCT-2001 (TrEMBLrel. 18, Last annotation update)
POSSIBLE APP/GTP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.3%; Score 68.5; DB 2;
46.7%; Pred. No. 7.8;
ative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583920; CAC31378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68.5; Di
Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PTLRQW-----LAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000765; GTP1_OBG.
PRINTS; PR00326; GTP10BG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.73
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 488 AA;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Leproma; ML0997;
                                                                                                                                                                                      NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                        RESULT 6
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                                   022260
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SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.1%; Score 68; DB 10; Length 125; 42.9%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.1%; Score 68; DB 3; Length 776; 57.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002094; BAA96216.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AL451109; CAC18624.2; -.
Hypothetical protein.
SEQUENCE 776 Aa; 82771 MW; C9BEA870D94A37DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C609D8D0B07BC505 CRC64;
                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EGPTLRQWLAARA-------GGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  776 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                           125
219 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GGGGGGGI---EG-PTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 125 AA; 13396 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 42.9
Matches 18; Conservative
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Matches 15; Conservative
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PRELIMINARY;

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Q9FTZ5
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RADILINE-20196006; Pubmed=10731132;

RADILINE-20196006; Pubmed=10731132;

RADILINE-20196006; Pubmed=10731132;

RADILINE-20196006; Pubmed=10731132;

RADILINE-20196006; ROLLER S.E. RICHARGS S.A. Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthan J. R., Yandell M.D., Ashburner M., Henderson S.N., Radindor G.G., Worthan J. R., Yandell M.D., Rahburner M., Henderson S.N., Man K.H., Doyle C., Bazel K., Helt G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Deaven A., Den B.P., Bhandari D., Bolshakov S., Ra Ballew R.M., Cavley B. Burtis R., Bouck J., Brokstehn P., Brottler P., Rottler P., Chandre R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandre I., Radieu S., Delson W.Y., Bernan B.P., Bhandari D., Bolshakov S., Achtry J.M., Cavleys S., Dalnkov B.C., Doun P., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Re Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Re Pablos B., Delcher A., Herman B.Y., Hernandez J.R., Houck J., Rosley R. Gorfell J.H., Garg N.S., Gelbart W.M., Glasser K., Alandri M., Kalush F., Karpen G.H., Kavitz S., Kulp D., Lal Z., Harris M., Housh D., Lel Y., Helman T.J., Hernandez J.R., Houck J., Housh D., Laskop P., Lel Y., Leltsky A.A., Lil J., Wellow D., Laskop D., Lel Y., Mortis D., Waller B., Mollockh T.C., Mortis J., Mosherson D., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L., Rabing D.M., Natchi B., Mollockh T.C., Mortis J., Mosherson D., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L., Rabington K.A., Nixon K., Nusskern D.R., Pecleber F., Shen H., Spier E., Spradling A.C., Stapleton M., Stupsk M., Sheng K., Sheng E., Spradling A.C., Stapleton M., Stupsk M., Sheng K., Sheng E., Spradling A.C., Stapleton M., Stupsk M., Sheng K., Sheng E., Spradling R.W., Stupsk M., Sheng K., Rangelence of Drosophila melanogaster.", 2 Nav Starker S., Schence Stocker Stroke Starker Starker Star
                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.5%; Score 67; DB 5; Length 170; 50.0%; Pred. No. 3.7; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01228; EGGSHELL.
GERHINGE 170 AA; 19099 MW; 477D79D55ADF4CE5 CRC64;
                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG13807 PROTEIN.
                                   170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EGPTLRQWLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE0034/4; AAF4/627.1; ~.
FlyBase; FBgn0035323; CG13807.
InterPro; IPR002952; Eggshell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003474; AAF47627
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                      Q9W033;
                                   O9W033
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Q9FTZ5
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 RESULT 10
                  Q9W033
                                                    Q
O
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McDiangle 2023937; Fully Full J., Garnier T., Churcher C., Harris D., Role S.T., Brosch R., Gas S., Barry C.E. III, Tekala F., Baccok K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Centles S., Hamiln N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A., Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., T., Taylor K., Whitehead S., Barrell B.G., Moule Sequence.";

Rutter S., Segor K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., T., Taylor R., Whitehead S., Barrell B.G., Moule Sequence.";

Rutter S., Scoger K., Skelton S., Squares R., Sulston J.E., Taylor R., Whitehead S., Barrell B.G., T., Taylor R., Whitehead S., Barrell B.G., T., Taylor R., Whochacterium tuberculosis from the Nature 393:537-544(1998).

REMBL, 298209; Cahl0901.1; -.

Ruberculist, RV27255.

Ruberculist, RV27255.

Ruberculist, RV27255.

Ruberculist, RV27255.

Ruberculist, RV27255.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBL_TaxID=1773;
                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 202;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0436E04.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AP002818; BAB16319.1; -- SEQUENCE 202 AA; 19763 MW; BFC2520037F8E274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                             Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 VVSPSCRROTAGRHGGCGGGRWMAAAGGRDGGGCRRWWAA 134
                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.3%; Score 66.5; DB 10; 39.0%; Pred. No. 5; Live 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGGGG-----GGIEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 PRLRGWGESMSRQAGGRAGGSGGGVGLRGP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PTLRQW-----LAARAGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last segu 01-DEC-2001 (TrEMBLrel. 19, Last ann
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                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL 53.3 KDA PROTEIN. HFLX OR RV2725C OR MTCY154.05C.
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                                                         01-MAR-2001 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.
                            (TrEMBLrel.
                                                                                                                                                                                      Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 16; Conserv
                                                                                                                         P0436E04.1 PROTEIN.
P0436E04.1.
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4530;
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Q9FTZ5;
01-MAR-2001
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DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 377 AA; 37998 MW; C2DBC19402D3A172 CRC64;
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Tomsa J.M., Langeland J.A.;

Tot expression during lamprey embryogenesis provides insights into flow evolution of the vertebrate head and jaw.";

Dev. Biol. 0:0-0(1998).

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.

EMBL; AF099746; AAC82470.1;

ENSE; PO6601; IFIL.

BITTEPRO: IPR001355; Homeobox.

Pfam; PF00046; homeobox.

SMART; SM00389; HOX; 1.
                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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                                                                                                                                                                                                                                                                                                                                                                                       Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                        STRAIN-A3(2);
Seeger K.J., Harris D.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 AA
                                    496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 PTLOAQLGGGAGGGGGGGGGGGGGGGP 439
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                                                                     (TrEMBLrel. 17, Created)
                                    PRT;
                                                                                                                        PUTATIVE INTEGRAL MEMBRANE PROTEIN
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46.9%;
                                                                                       (TrEMBLrel. 17, (TrEMBLrel. 18,
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Matches 15; Conservative
                                 PRELIMINARY;
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                                                                                                                                                                 Streptomyces coelicolor
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                  09AD76;
01-JUN-2001 (
01-JUN-2001 (
01-OCT-2001 (
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                                 09AD76
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RESULT 13
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Q9YHD0
               09AD76
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MEDLINE-20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikwa K., Hirosawa M., Ohara O.;
Negases T., Kikuno R., Ishikwa K., Hirosawa M., Ohara O.;
Nediction of the coding sequences of unidentified human genes.XVII.The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
NNA Res. 7:143-150(2000).
NNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0456F08.";
34.0%; Score 66; DB 13; Length 377; 48.1%; Pred. No. 11; 12 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.0%; Score 66; DB 10; Length 529; 68.4%; Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002901; BAB39414.1; -InterPro; IPR002937; Amino_oxidase. InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0A5DA55CDD076D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 AA; 65593 MW; 9AA4061D21E1E9FD CRC64;
                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUCT-2001 (TrEMBLrel. 18, Last annotation update)
P0456F08.14 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Last Sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) KIAA1458 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                             529 AA.
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2; Mismatches
                                                                                                                                   265 QGYTAASYYGVECGGGGGGGGGGGFYL 291
                                                                                                     2 EGPILRQWLAARAGGGGGGGGGTEGPTL 28
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                                                                                                                                                                                                                                                                                             PRT;
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SEQUENCE 529 AA; 55981 MW; (
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Query Match 34.09
Best Local Similarity 48.19
Matches 13; Conservative
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Best Local Similarity 68.4%
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4 PTLRQWLAARAGG-----
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Matches 16; Conserv
SEQUENCE FROM N.A.
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                                                                                                                                                                                          Receptor.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0498A12.";
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOSTATIN RECEPTOR-INTERACTING PROTEIN SPLICE VARIANT B.
                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P0498A12.7 PROTEIN (OSJNBA0004B13.18 PROTEIN) (P0581F09.21
 Score 66; DB 4; Length 612;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Graza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0581F09.";
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:OSSUNBA004B13.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                        7; Indels
                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.8%; Score 65.5; DB 10; 52.2%; Pred. No. 7.7;
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                                                                                                                                  243 AA
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3; Mismatches
                        1; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 VRTPDORRW---RRGGGGGGG 47
                                                4 PTLRQWLAARAGGGGGGGGIEG 25
                                                              34.0%;
63.6%;
                                                                                                                                                                                                      PROTEIN).
P0498A12.7 OR P0581F09.21.
  Query Match 34.0%
Best Local Similarity 63.6%
Matches 14; Conservative
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                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
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                                                                                                             RESULT 17
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Zitzer H., Hoenck H.-H., Richter D., Kreienkamp H.-J.;
Zitzer H., Hoenck H.-H., Richter D., Kreienkamp H.-J.;
Zitzer H., Hoenck H.-H., Richter D., Kreienkamp H.-J.;
The somatostatin receptor instracting protein (SSTRIP) defines a novel family of multidomain postsynaptic density proteins.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF163302, AAD45121.1;
HSSP; PG6241; 1SHF.
InterPro; IPR002110; ANK.
InterPro; IPR001478; PDZ.
MEDLINE=20020275; PubMed=10551867;
Zitzer H., Honck H.H., Bachner D., Richter D., Kreienkamp H.J.;
"Somatostatin receptor interacting protein defines a novel family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 1548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
somarostatin RECEPTOR INTERACTING PROTEIN SPLICE VARIANT A.
                                                                                                                                                                              SEQUENCE FROM N.A.

Zitzer H., Hoenck H., Baechner D., Richter D., Kreienkamp I Zitzer H., Hoenck H., Baechner D., Richter D., Kreienkamp I Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF225728; AAF33887.1; -.

InterPro; IPR001478; PDZ.

InterPro; IPR001660; SAM.
                                                                            multidomain proteins present in human and rodent brain.";
J. Biol. Chem. 274:32997-33001(1999).
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SEQUENCE 2161 AA; 225019 MW; 5FEFC969CBE98701 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1548 AA; 158854 MW; 8E5209F785A04D73 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%; Score 65.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%;
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InterPro; IPR001452; SH3.
Pfam; PP00023; ank; 6.
Pfam; PP00595; PD2; 1.
Pfam; PP00536; SAM; 1.
Pfam; PP00018; SH3; 1.
SMART; SM00248; ANK; 3.
SMART; SM00248; ANK; 3.
SMART; SM00248; SAM; 1.
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Matches 16; Conservative
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-----GGGGGGGIEGPTLR 29

SEQUENCE Query Match CG13055 09VV01 Matches RESULT 22 09VV01 δλ g 0 Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Gaps MEDLINE-20196006; PubMed-10731132; Admis M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., MEDLINE=97475689; PubMed=9335144;
Makachi Y., Hayakawa T., Oota H., Sumiyama K., Wang L., Ueda S.;
Nakleotide compositional constraints on genomes generate alanine-,
"Nucleotide compositional constraints on genomes generate alanine-,
glycline-, and prolline-rich structures in transcription factors.";
Mol. Biol. Evol. 14:1042-1049(1997).
-!- SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
EMBL; AB001869; BAA28666.1; -HSSP; P14859; LOCT. Anolis carolinensis (Green anole) (American chameleon).
Wataryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
NCBI\_TaxID=28377; . 0 Score 65; DB 13; Length 447; Pred. No. 16; Indels 47160 MW; AFA362894FCBC419 CRC64; 1:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | : 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update) Brain; DNA-binding; Homeobox; Nuclear protein. 447 AA 452 AA 2; Mismatches PRT; PRT; PROSITE; PS00027; HOMEOBOX\_1; 1. PROSITE; PS50071; HOMEOBOX\_2; 1. PROSITE; PS00035; POU\_1; 1. PROSITE; PS00465; POU\_2; 1. InterPro; IPR001356; Homeobox. InterPro; IPR000327; POU. 33.5%; 73.38; Pfam; PF00046; homeobox; 1. Pfam; PF00157; pou; 1. PRINTS; PR00028; POUDOMAIN. ProDom; PD000583; POU; 1. Local Similarity 73.3 nes 11; Conservative PRELIMINARY; PRELIMINARY; 8 QWLAARAGGGGGGG 22 ||:|| : ||||||| | 56 QWIAALSHGGGGGGG 70 SMART; SM00389; HOX; 1. SMART; SM00352; POU; 1. 447 AA; SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-BERKELEY; NCBI\_TaxID=7227; CG5953 PROTEIN. BRAIN-2 GENE SEQUENCE Query Match 073628 073628; O9VJK4 Q9VJK4 CG5953 Best Loca Matches RESULT 20 RESULT 21 **09VJK4** 셤 g õ

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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxerer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Beasley E.M.,
RA Berson K.Y., Bernan B.P., Barnandari D., Beasley E.M.,
RA Borkova D., Botchan M.R., Boutck J., Brokstein P., Brottier P.,
RA Borkova D., Dalcher A., Deng E., Davnel P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Codek A., Gong Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
A Gabrielian A.E., Gorrell J.H., Gu Z., Guan P., Harris M.
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
A Jalall M., Kallen F., Karpen G.H., Ke Z., Kenlson J.A.,
RA Liu X., Mattel B., Morincoh T.C., Kravitz S., Kullp D., Lai Z.,
RA Liu X., Mattel B., Morincoh T.C., Kravitz S., Kullp D., Lai Z.,
RA Liu X., Mattel B., Morincoh T.C., McLeod M.P., Mosbrerson D.,
RA Netson D.R., Nelson K.A., Nixon K., Nosherson D.R., Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puti V., Resee M.G.,
RA Shire B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shire E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstelbard J., Puti W. D., Yang S., Yao Q.A.,
RA Wallom S.A., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.W., Robert J.C., Shen H.,
R. Schene S., Sylenene S., Subner S., Shirk S., Shirk S., Shith M., Shine S., Shirk S., Shirk S., Shith M., Shine S., Shirk S., Shirk S., Shirk S., Shirk 
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Last annotation update)
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MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBqn0032587; CG5953.
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EMBL; AE003651; AAF53541.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Berkon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkordan M.R., Bouck J., Broketlen P., Brottler P., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W., Roller S.M., Gariellan R.B., Garg M., S., Galbart W.M., Glasser K., A. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Mandrus M., Mandrus M., Murphy B., Murphy L., Morberson D., Mandrus M., Murphy B., Murphy D., Musskern D.R., Purl V., Reese M.G., Shen H., Rainert K., Remington K., Saunders R.D., Saith T., Ranger M., Wang X., Wassaman D.A., Walson K., Wang X., Wassaman D.A., Wang X.-Y., Wassaman D.A., Wang X., Wang X., Wassaman D.A., Wang X., Wang X., Wang X., Zhon M., Zhou X., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon M., Zhou X., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G., Zhon G.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.0%; Score 64; DB 5; Length 309; 57.9%; Pred. No. 14; 1; Live 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9DAEB67784852A93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0036583; CG13055.
SEQUENCE 309 AA; 33224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|:|||| |||: | ||::
94 SRSGGGGGGGGVAGVTLQE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 ARAGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001871; bZIP.
InterPro; IPR003102; pKID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y41C4A.4A.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Rhabditidae; Peloderinae; Caenorhabditis.
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Eukaryota; Matazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                    0;
                                                                                        33.0%; Score 64; DB 5; Length 331; ilarity 76.9%; Pred. No. 15; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 5; Length 333;
Pred. No. 15;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Nuclear protein.
SEOUENCE 331 Aa; 34985 MW; A414C19D4ADCC91E CRC64;
                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERMEDIATE FILAMENT PROTEIN E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
-!- SUBCELLIAR LOCATION: NUCLEAR (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 AA.
                                                                                                                                                                                                                                          333 AA
                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
Pfam; PF00170; bZIP; 1.
Pfam; PF02173; pKID; 1.
SMART; SM00338; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL032627; CAB54382.1; -. InterPro; IPR001871; bZIP. InterPro; IPR003102; pKID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.0%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 76.9
nes 10; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                        167 GGGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 GGGGGGGVPGPS 181
                                                                                                                                              15 GGGGGGGGIEGPT 27
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                                                                                                     Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           Y41C4A.4B PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                Steward C.A.;
                                                                                                                                                                                                                                                                                                                      Y41C4A.4B.
                                                                  · SEQUENCE
                                                                                            Query Match
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Matches
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Matches
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                                                                                                                                                                                                                             090210
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[1]
SEQUENCE FROM N.A.
                                                    clone: P0708G02.
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                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                         RESULT 28
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                               Karabinos A., Riemer D., Erber A., Weber K.;
"Homologues of vertebrate type I, II and III intermediate filament
(IF) proteins in an invertebrate: the IF multigene family of the
cephalochordate Branchiostoma.";
FEBS Lett. 437:15-18(1980).
EMBL, AJ010294; CAA09068.1;
InterPro; IPR001552; Eggshell.
InterPro; IPR001564; IF.
InterPro; IPR001564; IF.
InterPro; IPR001489; Ribosomal_S30.
                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 32.7%; Score 63.5; DB 10; Length 207; I Similarity 45.5%; Pred. No. 11; Tonservative 4; Mismatches 5; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                      Length 422;
                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:P0037C04.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003233; BAB55526.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1233; BAB55526.1; -. 207 AA; 21266 MW; F514ABC36A6DC403 CRC64;
                                                                                                                                                          PRINTS; PR01228; EGGSHELL.
PRINTS; PR01248; TYPE1KERATIN.
SEQUENCE 422 AA; 44892 MW; 85FE742F07751B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                      33.0%; Score 64; DB 5; 61.9%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                              207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AARAGGGGG-----GGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                PRT;
                         MEDLINE=99019308; PubMed=9804163;
                                                                                                                                                                                                                                                                         92 GGGGGGGISGMWIEEKPTMR 112
                                                                                                                                                                                                                                                  15 GGGGGGGIEG-----PTLR 29
                                                                                                                                                Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                61.9%;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                   P0037C04.13 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                SECUENCE FROM N.A.
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q9LI16;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                  DB 10; Length 584;
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 63; DB 12; Length 66;
Pred. No. 3.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu 7. Wang L., Hu X., Pang Y.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, 787325155, AAL01786.1; -. Hypothetical protein. SEQUENCE 66 AA; 6998 MW; C5626A8FFA9C9E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                               Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001539; BAA92923.1; -.
HSSP; P00950; 5PGM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Analysis of the Spodoptera litura Multicapsid
                                                                                                                                                                                                                                                63515 MW; 351C684C8BBBD9CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 7.0 KDA PROTEIN.
Spodoptera litura nucleopolyhedrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                     32.7%; Score 63.5; 1
48.3%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ROWLAARA-----GGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21425398; PubMed=11531416;
                                                                                                                                                                      InterPro; IPR001345; PG_mutase.
Pfam; PF00300; PGAM; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleopolyhedrovirus Genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.5%;
68.8%;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                        Query Match 32.7
Best Local Similarity 48.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 RSGGGGGGGGVVGAML 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                     584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Veau B., Oudin A., Courtois M., Chenieux J.-C., Hamdi S., Rideau M., Clastre M.;

Clastre M.;

"Cloning of two CDNAs encoding crGRP2 and crGRP3 (Accession Nos. AF200323 and AF200322), the first members of the RRM-GRP family in Catharanthus roseus (PGR00-049).";

Plant Physiol. 122:1459-1459(2000).

EMBL: AF200323; AAF31404.1;

HSSP: P09651; IRA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                          Vedu B., Oudin A., Clastre M., Chenieux J.C., Rideau M., Hamdi S.; Vienes encoding glycine-rich Catharanthus roseus proteins with RNA-binding motifs.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
BEMBL: AF200321; AAF31402.1;
HSSP; P09651; HHA.
InterPro: IPR000564; RRW.
PFam; PF00076; rrm: 1.
PROSTIE: P550102; RRM; 1.
PROSTIE: P550102; RRM; 1.
PROSTIE: P550103; RRM_RNP_1; 1.
PROSTIE: P550103; RRM_RNP_1; 1.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; sterides; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae; Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentlanales; Apocynaceae; Rauvolfioideae;
Vinceae; Catharanthus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%; Score 63; DB 10; Length 160; 50.0%; Pred. No. 9.4; ive 4; Mismatches 7; Indels
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PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 160 AA; 16264 MW; DCDC9F63C983F5F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0EC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA-BINDING PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 160 AA.
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InterPro; IPR000504; RRM.
Pfam; PF000706; rrm; 1.
PRINTS; PR01228; EGGSHELL.
SMART; SM00360; RRM; 1.
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Best Local Similarity
                                                                                SEQUENCE FROM N.A.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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147.5	152	156	156	156	156	156	156	171	171	183		Score		
80.6	83.1	85.2	85.2	85.2	85.2	85.2	85.2	93.4	93.4	100.0		Match	Query	æ
31	268	269	42	42	42	41	32	32	32	34		Match Length DB		
21	21	21	21	21	21	21	21	21	. 21	21	1	DB		
AAB17288	AAB16959	AAY96531	AAY96530	AAB17308	AAB17281	AAY96528	AAB17289	AAY96520	AAB17297	AAY96527		ID		COMMINICIES
TPO-mimetic peptid	FC-TMP-TMP protein	Human IgG1 Fc TMP	Thrombopoietin mim	Synthetic TMP-TMP	TPO-mimetic pentid	Thrombonoiet in mim	TPO-mimetic pentid	Thrombopoietin mim	TPO-mimetic peptid	Thrombopoietin mim		Description		

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118	118	118	120.5	120.5	127.5	133.5	133.5	133.5	134	140.5	141	142	142.5	142.5	143	143.5	14	144	144	144	144	144	144	144	144	144	144	144.5	145	145	145	145.5	147	
64.5			.5	.51	9	ω.	ω.	ω.	ω.	6	7.	77.6	7.	7.	8	78.4	8	78.7	78.7	78.7	78.7	78.7	78.7	8		8	8	9.	9.	9.	9.	79.5	0	
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<b></b> -																	TMP-TMP-Fc protein	Synthetic TMP-TMP-	TPO-mimetic peptid		Thrombopoietin mim	_						TPO-mimetic pentic	7				TPO-mimetic peptid	

## AAY96527 standard; peptide; 34 AA. ALIGNMENTS

04-SEP-2000 (first entry)

AAY96527;

Thrombopoietin mimetic peptide compound 8.

Thrombopoietin; mimetic; TMP; TPO; platelet; anti-human immunodeficiency virus; anti-HIV; immunosuppressive; anti-inflammatory; linker. megakaryocyte; production; anti-anemic; dermatological;

Synthetic.

RESULT 1
AAAY96527
ID AAAY96527
ID AAAY96527
AC AAAY9
AC AAAY9
XX Thrc
XX Thrc
XX Thrc
XX Inm
XX Inm
XX Syn
XX Eff Moc
FT Pe
FT Pe
FT Pe
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FT Pe
FT Pe
FT Pe
XX XX
PN WC
XX XX
PN Q
XX 2
PF 2
XX 2
PF 2
XX 2 23-OCT-1998; 04-MAY-2000. 22-OCT-1999; W0200024770-A2. Peptide Peptide Peptide Modified-site 98US-0105348 99WO-US24834. /label= TMP\_2 /label= linker 21..34 /label= TMP\_1 17..20 Location/Qualifiers note= "optionally linked to an Fc molecule"

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A compound which binds to an mpl receptor comprising a thrombopoletin commetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least composition to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_1-X_1_2, X_1-X_1_2, X_1-X_1_2, X_1-X_1_2, X_1-X_1_2, X_1-X_1_3, and composition (X_2-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and composition (X_1-X_1-4, X_1-1, X_1-X_1-1, X_1-X_1-3, and composition (X_1-X_1-4, X_1-1, X_1-X_1-1, X_1-X_1-3, and composition (X_1-X_1-4, X_1-1, X_1-X_1-2, X_1-X_1-3, and composition (X_1-X_1-1) = X_1, Y_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1 = X_1, Y_2-1, Y_3-1, Y_3-1 = X_1, Y_2-1, Y_3-1, Y_3-1 = X_1, Y_2-1, Y_3-1, Y_3-1, Y_3-1 = X_1, Y_2-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_3-1, Y_
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 64; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II.; TNF; antagonist; MMP; inhibitor; erythropoleth; thrombopoleth; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17297 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
  Feige U, Liu C,
                                                                                                     23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                                  W0200024782-A2
                                               (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGIEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGIEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                  98US-0105371.
99US-0428082.
                                                                                                                                                                                  99WO-US25044.
  Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 183;
Pred. No. 1
       Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 3
AAY96520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC (X1)a-F1-(X2)), where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-F1-(X2)), where: F1 = an Fc domain; X1 and X2 = are each CC (x1)a-F1-(X2)), where: F1 = an Fc domain; X1 and X2 = are each CC (x1)a-F1-(X2)d-P2-(X3)e-P3-3, or -(X1)c-P1-(X2)d-P2-(X3)e-P3-(X4)f-P4 (X2)d-P2-(X3)e-P3-(X3)e-P3-3, or -(X1)c-P1-(X2)d-P2-(X3)e-P3-(X4)f-P4 (X2)d-P2-(X3)e-P3-(X4)f-P4 (X2)d-P2-(X3)e-P3-(X4)f-P4 (X2)d-P2-(X3)e-P3-(X4)f-P4 (X3)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)e-P3-(X4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96520 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin mimetic peptide compound 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2000 (first entry)
                                                                 04-MAY-2000.
                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                          Peptide
                     22-OCT-1999;
                                                                                                                WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                     99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                  /label= linker
19..32
                                                                                                                                                                                                                                                                              /label= TMP_1
15..18
                                                                                                                                                                 /note= "optionally linked to
                                                                                                                                                                                                               'label- TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.4%; Score 171; DB 21; 100.0%; Pred. No. 5.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                     an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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is:
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Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A compound which binds to an mpl receptor comprising a thrombopoietin c mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], c is new TMP_1 and TMP_2 are amino acid sequences varying from at least c 10 to 14 residues in length comprising X_2 X_1_0, X_2-X_1_1, X_2-X_1_2, C X_2-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and c X_1-X_1_4, X_1=1, A, V, L, S or R; X_2=E, D, K or V; X_3=G or A; C X_4=P; X_5=T or S; X_6=L, I, V, A, or F; X_7=R or K; X_8=Q, N, C C L, F, S, T, K, H, or E; X_1_2=A, I, V, L, F, G, S, or O; X_1_3=R, K, C C T, V, N, O or G; X_1_4=A, I, V, L, F, G, S, or G; L, 1=1 inker c comprising 1 to 20 amino acids; and n=0 or 1. The compounds bind to and c activate the c-Mpl receptor which mediates the activity of endogenous c thrombopoietin. The TMPs are useful for increasing the production of c is useful for treatment of diseases which involve thombocytopenia, e.g. c c virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
(AMGE-) AMGEN INC
                                                                                                                                                                                                                   MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                  22-OCT-1999;
                                                                                                                                                W0200024782-A2
                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF, immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain;
                                                23-OCT-1998;
                                                                                25-OCT-1999;
                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:345.
                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17289 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLROWLAARAGPNGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                              98US-0105371.
99US-0428082.
                                                                              99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 171; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
5.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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AAY96528
ID AAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The present invention describes composition of matter (I) comprising an CC (X1)a-FI-(X2)b, where: F1 = an FC domain; X1 and X2 = are each CC (X1)a-FI-(X2)b, where: F1 = an FC domain; X1 and X2 = are each CC independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2. (L4)f-P2 -(L3)e-P3. (CC -(L1)C-P1-(L2)d-P2-(L3)e-P3. (CC -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (CC where P1, P2, P3, and P4 = are each independently sequences of CC pharmacologically active peptides; L1, L2, L3, and L4 = are each independently composition can CC independently linkers; and a, b, C, d, e, and f = are each independently CC (O or 1, provided that at least 1 of a and b Is 1. The composition can CC have cytostatic, antiasthmatic, thrombosity and immunosuppressive CC activities. DNAs, vectors and host cells from the present invention can CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases. CT he use of an Fc domain (rather than a Fab domain) can provide a longer CC half-life or incorporate functions such as Fc receptor binding, protein CC A binding, complement fixation, and possibly placental transfer. AAA69443 CC sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                04-MAY-2000.
                                                                                 WO200024770-A2.
                                                                                                                                                                                                                                                                                                      Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                Peptide
                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96528 standard; peptide; 41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLROWLAARAGGGGIEGPTLROWLAARA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                              20.
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                             /label= TMP_2
                                                                                                                                              /label= linker
                                                                                                                                                                            /label= TMP_1
                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.2%;
93.8%;
                                                                                                                                                                                                        "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 156; DB 21,
Pred. No. 7.1e-15;
""Gmatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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22-OCT-1999;

99WO-US24834

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cc mimetic peptide (TMP) dimer joined by a linker [TMP]-(L_1)_nTMP_2], cc mimetic peptide (TMP) dimer joined by a linker [TMP]-(L_1)_nTMP_2], cc is new. TMP_1 and TMP_2 are amino acid sequences varying from at least cc 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, cc X_1-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_2, and cc X_1-X_1_4, X_1=1, A, V, L, S or R; X_2=E, D, K or V; X_3=G or A; cc X_4=P; X_5=T or S; X_6=L, I, V, A or F; X_7=R or K; X_8=Q, N, cc X_4=P; X_5=T or S; X_6=L, I, V, A, F, M, or K; X_1=A, I, V, C or E; X_9=W, Y or E; X_1_0=L, I, V, A, F, M, or K; X_1=A, I, V, C c L, F, S, T, K, H, or E; X_1_2=A, I, V, L, F, G, S, or Q; X_1_3=R, K, C C L, F, S, T, K, H, or E; X_1_4=A, I, V, L, F, T, K, E, or G; L_1=linker cc comprising 1 to 20 amino acids; and n=0 or 1. The compounds bind to and cc activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which cc is useful for treatment of diseases which involve thombocytopenia, e.g. cc virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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   PAR YEAR OF A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 65; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17281 standard; Peptide; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                                                           W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune
(AMGE-) AMGEN INC.
                                                                  23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGIEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105348.
                                                                      98US-0105371
99US-0428082
                                                                                                                                                                         99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 156; DB 21;
Pred. No. 9.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
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The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (Independently selected from -(In)c-F1-(In)c-F1-(In)d-F2-(In)e-F3-(In)c-F1-(In)d-F2-(In)e-F3-(In)c-F1-(In)d-F2-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-(In)e-F3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멍
AAB17308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U,
                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17308 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000
                   (AMGE-) AMGEN INC
                                                                                                                                                                                                                                   WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
                                                                  23-OCT-1998;
22-OCT-1999;
                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                       04-MAY-2000
                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGIEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGIEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                  98US-0105371.
99US-0428082.
                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 156; DB 21;
Pred. No. 9.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC Fc domain, pharmacologically active peptides, and linkers. Where [I] is:

CC (X1)a-F1-(X2)b. where: FI = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1-(L2)d-P2,

CC (L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of

CC pharmacologically active peptides; L1, L2, L3, and L4 = are each

CC independently linkers; and a, b, c, d, e, and f = are each independently

CC 0 or 1, provided that at least 1 of a and b is 1. The composition can

CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

CC activities. DNAs, vectors and host cells from the present invention can

CC activities. DNAs, vectors and host cells from the present inventions are

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC The use of an Fc domain (rather than a Fab domain) can provide a longer

CC abinding, complement fixation, and possibly placental transfer. AAA69443

CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid

CX sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment \boldsymbol{\varepsilon}
                                                          WPI; 2000-365108/31.
N-PSDB; AAA29225.
                                                                                                                                         (AMGE-) AMGEN INC
                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                         22-OCT-1999;
                                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                         WO200024770-A2
                                                                                                                                                                                                                                                                                                                                          anti-anaemic;
                                                                                                                                                                                                                                                                                                                                                      megakaryocyte;
                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96530 standard; Protein; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes composition of matter (I) comprising an is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                     dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                        98US-0105348
                                                                                                                                                                                                                                                                                                                                               ; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; production; anti-human immunodeficiency virus; anti-HIV
                                                                                                                                                                                                      99WO-US24834.
                                                                                                         Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 156; DB 21;
Pred. No. 9.6e-15;
                                                                                                                                                                                                                                                                                                                                  immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                 anti-HIV;
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PR
PA
PI
                                                                                                                                                               Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                           Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
Example 2A; Page 49-50; 91pp; English
                                                                                                                                                                                                                             Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                    diseases which involve thombocytopenia
                                                             N-PSDB; AAA29229
                                                                      WPI; 2000-365108/31.
                                                                                        Liu C, Feige U,
                                                                                                                                  23-OCT-1998;
                                                                                                                                                                         04-MAY-2000.
                                                                                                             (AMGE-) AMGEN INC
                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                            W0200024770-A2
                                                                                                                                                                                                                                                                                              04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                     AAY96531;
                                                                                                                                                                                                                                                                                                                                      AAY96531 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Overlapping oligonucleotides were used to construct a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2A; Page 48; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                         1 GGIEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                       GGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                            FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                         TMP fusion protein.
                                                                                                                                98US-0105348
                                                                                                                                                    99WO-US24834.
                                                                                          Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                        85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 156; DB 21;
Pred. No. 9.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                           for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB16959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiasthmatic; thrombolytic; vEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist; MMP; inhibitor; erythropoiettin; thrombopoiettin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          AAB16959 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                           WO200024782-A2
                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                  Fc-TMP-TMP protein sequence SEQ ID NO:8
The present invention describes composition
                                             Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                           N-PSDB; AAA69445
                                                                                                      Feige U, Liu C, Cheetham J,
                                                                                                                                                     23-OCT-1998;
                   Example 2;
                                      autoimmune diseases -
                                                                                                                         (AMGE-)
                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                      232 GGIEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGIEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                     2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                          AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA;
                  Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                     98US-0105371
                                                                                                                                             99US-0428082
                                                                                                                                                                        99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.2%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.6e-14;
                                                                                                        Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                               Fc domain and
for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                          269
  of matter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
  (I) comprising
                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3 (C1)c-P1-(L2)d-P2-(L3)e-P3) or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (C2) where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of C2 independently linkers; and a, b, c, d, e, and f = are each independently can can cativities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are cuseful for treating cancer, asthma, thrombosis, or autoimmune diseases. C7 The use of an Fc domain (rather than a Fab domain) can provide a longer C8 alf-life or incorporate functions such as Fc receptor binding, protein C9 AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid C9 composition and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17288 standard; Peptide; 31 AA
                                                                                              autoimmune diseases
                                                                                                             Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                           23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                          04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:344.
                                                             Example 1; Page 316; 608pp; English
                                                                                                                                                               WPI; 2000-350702/30
                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 GGIEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGIEGPTLRQWLAARA----GPNGIEGPTLRQWLAAR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                             98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                               Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.1%;
                                                                                                                                                                                               ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 152; DB 21;
Pred. No. 2.7e-13;
                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; tumour necrosis factor;
                                                                                                                                  Fc domain and
                                                                                                                  for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Fc domain, pharmacologically active peptides, and (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and

The present invention describes composition of matter (I) comprising

linkers. Where (I) X2 = are each

is:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     independently selected from -(L1)c-P1, -(L1)d-P2-(L3)d-P2,
-(L1)c-P1-(L2)d-P2-(L3)e-P-3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(C) where P1, P2, P3, and P4 = are each independently sequences of
-(C) pharmacologically active peptides; L1, L2, L3, and L4 = are each
-(C) or 1, provided that at least 1 of a and b is 1. The composition can
-(C) or 1, provided that at least 1 of a and b is 1. The composition can
-(C) or 1, provided that at least 1 of a and b is 1. The composition can
-(C) or 2, provided that at least 1 of a minumosuppressive
-(C) cativities. DNAs, vectors and host cells from the present invention can
-(C) be used for producing pharmaceutical compositions. The compositions are
-(C) useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
-(C) The use of an Fc domain (rather than a Fab domain) can provide a longer
-(C) half-life or incorporate functions such as Fc receptor binding, protein
-(C) A binding, complement fixation, and possibly placental transfer. AAA69443
-(C) CC AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
-(C) creating complement fixation of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
        Fc domain, pharmacologically active peptides, and linkers. Where (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
                                            The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VECF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; immunosuppressive; erythropoietin; thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                             Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                       Example 1; Page 315-316; 608pp; English
                                                                                                                                                   autoimmune diseases
                                                                                                                                                                                                                                                                    Feige U,
                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17287 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAG-GGIEGPTLRQWLAARA 31
                                                                                                                                                                                                                            2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEGPTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide sequence SEQ ID NO:343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                           99US-0428082
                                                                                                                                                                                                                                                                                                                                                               98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044
                                                                                                                                                                                                                                                                Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.6%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 147.5; DB Pred. No. 1e-13;
                                                                                                                                                                                                                                                              Boone TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                               Fc domain and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                 and
                                                                                                                                                                 cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
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-(L1)c-P1-(L2)d-P2-(L3)e-P^3,

or

-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2, -(L3)e-P3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each
                                                                                          The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                    Novel composition of matter comprising an FC domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                          Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VF
                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17290 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; vEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                     Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                99US-0428082.
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                                                                                                                                                                                                                                                                                                          Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.3%;
93.8%;
                                                                                                                                                                                                                                                                                                        J,
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ω
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Pred. No. 1.2e-13;
                                                                                                                                                                                                                                                                                                        Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a rab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA66925 to AAA69255 and AAB16055 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
FC domain, pharmacologically active peptides, and linkers where (1) is:
(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L1)c-P2-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(L1)c-P1-(L2)d-P2-(L3)e-P3-(D1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
o or 1, provided that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17291 standard; Peptide; 34 AA
                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T cell lymphocyte antigen 4;
                                                                                                                                                                                                                                 autoimmune diseases
                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating
                                                                                                                                                                                                                                                                                                                                              Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2
                                                                                                                                                      The present invention describes composition of matter (I) comprising
                                                                                                                                                                                         Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist MAP; inhibitor; erythropoietin; thrombopoletin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 IEGPTLRQWLAARA-GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                              Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 145.5; DB 2
Pred. No. 2.1e-13;
                                                                                                                                                                                                                                                                                                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                       cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
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       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
0 or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17306 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis;
                                                                                                                                                                             The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                              Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                   autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IEGPTLRQWLAARA--GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 145;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ
                                                                                                                                                                                                                                                                                                                                                                                Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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AAY96526
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1 · (L_1)_nTML_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 - x_1 -
                                                                                                                                                                                                                                                            Claim 16; Page 62;
                                                                                                                                                                                                                                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                        diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; anti-human immunodeficiency virus; anti-HIV; immunosuppressive; anti-inflammatory; linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96526 standard; peptide; 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= linker
19..32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheetham J;
                                                                                                                                                                                                                                                    91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "optionally linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    megakaryocyte; production;
anti-anemic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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Best Local
          FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2. (L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L, F, S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, T, V, N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. applastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                             Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                      The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                            Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                   autoimmune diseases
                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; anta;
                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor; erythropoietin; thrombopoietin; interleukin 1;
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vectors and host cells from the present invention
                                                                                                                                                                                                                                                                                                                                                       Cheetham
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83.3%;
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Pred.
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No. 2.8e-13;
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                     The present invention describes composition, and linkers. Where (I) is: FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P3-(L4)f-P4 -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 -(L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 -(L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 -(L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 -(L1)c-P1-(L3)d-P3-(L4)f-P4 -(L3)c-P1-(L3)d-P3-(L4)f-P4 -(L1)c-P1-(L3)d-P3-(L4)f-P4 (L3)d-P3-(L1)c-P1-(L3)d-P3-(L1)c-P1-(L3)d-P3-(L1)c-P1-(L3)c-P1-(L3)d-P3-(L1)c-P1-(L3)c-P1-(L3)c-P1-(L3)c-P1-(L3)c-P1-(L3)c-P1-(L3)c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB16963 standard; Protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 190; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   untoimmune disease; cytostatic; antiasthmatic; thrombol; mmunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEGPTLROWLAARA---GPNGIEGPTLROWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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99US-0428082.
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85.7%;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombolytic; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antagonist;
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treating

asthma,

thrombosis, or autoimmune diseases

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     RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69436 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                   FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activitles. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; anta MMP; inhibitor; erythropoietin; thrombopoietin; interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17293 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular endothelial growth factor; matrix metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain;
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein
                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                          Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                               autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105371.
99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.7%;
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Pred. No. 3.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RESULT 20
AAB17301
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 where PI, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6944.
                                                                                                                                                                                                        independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                                                                                                                                                        The present
                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                             Fc domain, pharmacologically active peptides, and linkers. Where (X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each
                                                                                                                                                                                                                                                                                                                      Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17301 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in the exemplification of the present invention
                                                                                                                                                                                                                                                              invention describes composition of matter (I) comprising tharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 144; DB 21; Pred. No. 3.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matrix metalloproteinase;
represent nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TC;
                                                                                                                                                                                                                                                                                                                                                                  Fc domain and for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
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The present annual court was compositions, and linkers where (I) is:

C (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

C independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L4)f-P4

C (L1)c-P1-(L2)d-P2-(L3)a-P-3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

C where P1, P2, P3, and P4 = are each independently sequences of

C pharmacologically active peptides; L1, L2, L3, and L4 = are each

C independently linkers; and a, b, c, d, e, and f = are each independently

C or 1, provided that at least 1 of a and b is 1. The composition can

C have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

C activities. DNAs, vectors and host cells from the present invention can

C useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

C The use of an Fc domain (rather than a Fab domain) can provide a longer

C a binding comporate functions such as Fc receptor binding, protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                       A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
              sequences used
                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMP; inhibitor; erythropoietin; thrombopoietin; interleukin cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17303 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
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            the
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83.3%;
            exemplification of
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           the present invention
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.8e-13;
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                                                                                   The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-F1-(X2)d-P2-(X1)c-P1, -(X1)c-P1, -(X1)c-P1-(X1)d-P2.

CC independently selected from -(X1)c-P1, -(X1)c-P1-(X1)d-P2.

CC where P1, P2, P3, and P4 = are each independently sequences of CC pharmacologically active peptides; I1, I2, I3, and I4 = are each independently sequences of CC independently linkers; and a, b, c, d, e, and f = are each independently CC 0 or 1, provided that at least 1 of a and b is 1. The composition can CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC activities. DNAs, vectors and host cells from the present invention sare CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases. CC The use of an Fc domain (rather than a Fab domain) can provide a longer CC abinding, complement fixation, and possibly placental transfer. AAA69443 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid component services are the examplification of the present invention acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid components of the present nucleotide and mino acid componen
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 324; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the stat
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                                                                    sequences used in
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                                                                               the exemplification of the present invention.
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83.3%;
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Pred. No. 3.8e-13;
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             minetic peptide (TMP) dimer joined by a linker [TMP]1-(L_1)_nTMP_2], and the strict peptide (TMP) dimer joined by a linker [TMP]1-(L_1)_nTMP_2], is new. TMP]1 and TMP 2 are amino acid sequences varying from at least to the strict peptide of the sequences varying from at least to the strict peptide of the sequences varying from at least to the strict peptide of the sequences varying from at least to the strict peptide of the sequences varying from at least to the strict peptide of the sequences varying from at least to the sequences varying from at least to the sequences varying from at least to the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences varying from the sequences
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin mimetic peptide compound 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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                                                                                                                                                                                                                                                                                                    A compound which binds to an mpl receptor comprising a thrombopoletin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],
                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 62; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
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  anaemia,
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immunodeficiency virus; anti-HIV; anti-anemic; dermatologica
ressive; anti-inflammatory; linker; cyclic; linear.
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15..22
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83.3%;
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    thrombocytopenia
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RESULT 24
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Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                    Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatologica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus associated ITP,
                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                 22-OCT-1999;
                                                                                                                                                                                                                                                WO200024770-A2
                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96524 standard; peptide;
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive; anti-inflammatory; linker; cyclic; linear.
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                                                                                                                                                                   Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        mimetic peptide compound
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                                                                                                                                                                                                                                                                                       /note= "optional"
15..22
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             /label= TMP_1
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83.3%;
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Pred.
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.8e-13;
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                                                                                                                                                                                                                                                                                                                            an Fc molecule"
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Best Local S
Matches 30
Thrombopoietic peptides which activate mpl receptors and increase production of platelets or platelet precursors, useful for treatmediseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelets or platelet precursors (e.g. megakaryocytes) in a mammal, whi is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                             Claim 16; Page 62; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; anti-human immunodeficiency virus; anti-HIV; anti-anemic; duimmunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal,
                                                                                                                                                           WPI; 2000-365108/31.
                                                                                                                                                                              Liu C,
                                                                                                                                                                                                   (AMGE-) AMGEN INC
                                                                                                                                                                                                                        23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin mimetic peptide compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                   /label= TMP_2
32
                                                                                                                                                                                                                                                                                                                                      /label= linker
19..32
                                                                                                                                                                                                                                                                                                                                                           /label= TMP_1
15..18
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83.3%;
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                                                                                            English.
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Pred. No. 3.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Best 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L, F, S, T, K, H, Or E; X_1 = A, I, V, L, F, G, S, or Q; X_1 = A, R, K, T, V, N, Q or G; X_1 = A, A, I, V, L, F, T, R, E, or G; X_1 = A = 1.1nker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                        autoimmune
                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an pharmacologically active peptides, useful autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17282 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                          diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                       Page 313; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144;
No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                        domain and
                                                                                                                                                                                                                                                                                                                                                                                 treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                 cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
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RESULT 27
AAB17311
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   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
FC domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-FI-(X2)b, where: FI = an FC domain; XI and XZ = are each independently selected from -(L1)c-PI-(L1)c-PI-(L2)d-P2.

-(L1)c-PI-(L2)d-P2-(L3)e-P^3, or -(L1)c-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, C, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; LL-1; TWE; anta MMF; inhibitor; erythropoietin; thrombopoietin; interleukin cytotoxic T cell lymphocyte antiqen 4; tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                              The
                                                                                                                                                                                                                                          pharmacologically active autoimmune diseases -
                                                                                                                                                                                                                                                       Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17311 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences used in the exemplification of the present invention.
                                                                                                                                                                                                            Example 2; Page 331; 608pp; English.
                                                                                                                                                                                                                                                                                                                                        Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            väscular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                       (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLROWLAARAGGGGGGGGIEGPTLROWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                          2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                         AMGEN INC.
                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocyte antigen 4; tumour necrosis factor lial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic agent;
                                                                                                                                                                                                                                                                                                                                         Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.7%;
83.3%;
                                                                                                                                                                              describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                        'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                         Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion;
                                                                                                                                                                                                                                                                                                                                         TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                                          Fc domain and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 42
                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonist;
ıkin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA69443
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                                                                                                                                                            is:
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RESULT 28
AAB16960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
         The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L3)e-P3, (L4)f-P4, -(L1)c-P1-(L2)d-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3 (L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of considerable independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAS, vectors and host cells from the present invention can activities. DNAS, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an pharmacologically active peptides, useful autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thrombol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB16960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB16960 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA694 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                               Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTOIMMUNE disease; cytostatic; antiasthmatic; thrombolytic; VEGF; Limunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                  AAA69446
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                         Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.7%;
83.3%;
pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 144; DB 21;
Pred. No. 6.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                         Boone TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
 compositions.
                                                                                                                                                                                                                                                                                                  Fc domain and for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
   compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA69443
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                            Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA65526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
useful for treating cancer, asthma, thrombosis, or autoimmune diseases The use of an Fc domain (rather than a Fab domain) can provide a longe:
                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EFO; TFO; CTLA4; mimetic; IL-1; TWF; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating cancer, asthma, thrombosis, or autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 IEGPTLRQWLAARA----GPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 144; DB 21;
Pred. No. 3.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
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                                                                                                                                                                                                                                                                                                                                                is:
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                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L12, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each indep
                                     activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein
A binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an pharmacologically active peptides, useful
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                          30; Conservative
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Search completed: October Job time: 15.2881 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
     231628 seqs, 24425594 residues
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US-09-244-298A-13
US-09-516-704-193
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US-08-764-640-17
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37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	39.9	39.9	39.9	39.9
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Sequence 200, App	-	`	Sequence 209, App	•	•	`	•	•	Sequence 195, App	•	•	•	Sequence 195, App	•	Sequence 194, App	Sequence 18, Appl	Sequence 232, App

## ALIGNMENTS

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RESULT 1
US-08-764-640-231
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Patent No. 5869451 5837683
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                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: I
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                             REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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FEATURE:
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                               STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                 TELEPHONE:
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ZIP: 27709
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                                                                             LENGTH:
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                                                                             25 amino acids
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Balasubramanian, Palaniappan
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Sequence

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                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 231, Application US/09244298A
                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                         FEATURE:
                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RECEPTOR
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LOCATION: 13
OTHER INFORMATION: /product= "Ava"
                                                                                                       LOCATION: 13
OTHER INFORMATION: /product= "Ava"
                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                Local
                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                   LENGTH:
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 4 EGPTLRQWLAARAGPNGIEGPTLRQWLA 31
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                                 13;
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Five Moore Drive, P.O. Research Triangle Park
                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                     25 amino acids
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Hendren, Richard W.
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Cwirla, Steven E.
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                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glaxo Wellcome
                                                                                                                                                                                        linear
                                                                                                                                                                      peptide
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                                              42.9%;
46.4%;
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                                                                                                                                                                                                                                                                                                               PK3281
                                              Score 78.5; DB 3; Pred. No. 0.00033;
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                                 Mismatches
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                                                             DB 3;
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US-08-764-640-13

Sequence 13 Application U

Patent No. 5869451

Patent No. 5869451 5837683
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US-09-516-704-231
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                                                                              RESULT 4
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GENERAL INFORMATION:
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                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 231: SEQUENCE CHARACTERISTICS:
                                                                                                                                     4 EGPTLROWLAARAGPNGIEGPTLROWLA 31
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DGPTLREWISFXA-----DGPTLREWIS 24
                                                                                                                                                                                                                                Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARAE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704

ETILING DATE: 01-Mar-2000

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /
SEQUENCE DESCRIPTION: SEQ
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 25 amino acids
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                                        Application US/08764640
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                                                                                                                                                                                                                  Conservative
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Balasubramanian, Palaniappan
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Cwirla, Steven E.
Gates, Christian
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46.4%;
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                                                                                                                                                                                                                                  Score 78.5; DB 4;
Pred. No. 0.00033;
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) ID NO: 231:
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US-08-764-640-193
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                                                                                                                                                                                                                   Patent No. 5869451
Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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APPLICANT:
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APPLICANT:
APPLICANT:
 TITLE OF INVENTION:
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                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                           3 IEGPTLRQWLAARA 16
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REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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Five Moore Drive, P.O. Box 13398
                             Yin, Qun
                                                                          Wagstrom, Christopher R. Hendren, Richard W.
                                                                                                                        Gates, Christian
Schatz, Peter J.
                                                                                                                                                     Barrett, Ronald W. Cwirla, Steven E.
                                                                                                                                                                                    Dower, William J.
                                           Podduturi, Surekha
                                                            Deprince, Randolph B.
                                                                                                        Balasubramanian, Palaniappan
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Balasubramanian, Palaniappan
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Cwirla, Steven E.
Gates, Christian
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PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                   39.9%; Score 73; DB 2; Lo 100.0%; Pred. No. 0.00089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13:
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RESULT 6
US-08-973-225-13
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                             Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J
                                                                                                                                                  COUNTRY:
                                                                                                                                   ZIP: 27709
APPLICATION NUMBER: US/08/973,225A
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9 SEO ID NO: 193:
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Mattheakis, Larry C.
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100.0%; Pred. No. 0.00089;
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US-08-973-225-193
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GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 193:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION MUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J
MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: 9
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                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                              NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PK3065USW
                                          TOPOLOGY: linear
                                                                                                      LENGTH: 14 amino acids
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Cwirla, Steven E.
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    SEQ ID NO: 193:
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Pred. No. 0.00089;
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GENERAL INFORMATION:
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                                                            Matches
                                                                                        Query Match
                                                                          Best
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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ADDRESSEE: Glaxo Wellcome
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                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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NAME: Hrubiec, Robert T.
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                                                                                                                                    MOLECULE TYPE:
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                                                                        Local
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                 NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,
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                                                                        Similarity
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                                                                                                                                                                                                 14 amino acids
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Hendren, Richard W.
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SYSTEM: PC-DOS/MS-DOS
                                                            Conservative
                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                    peptide
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100.0%; Pred. No. 0.00089;
                                                        39.9%; Score 73; DB 3; L
100.0%; Pred. No. 0.00089;
tive 0; Mismatches 0;
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US-09-244-298A-193; Sequence 193, Application US/09244298A

RESULT 9

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US-09-516-704-13
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                                                                                                                                                                                                              Sequence 13, Application Patent No. 6251864
GENERAL INFORMATION:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             Match 39.9%; Score 73; DB 3; L
Local Similarity 100.0%; Pred. No. 0.00089;
                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                             3 IEGPTLRQWLAARA 16
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
                                                                                                                                                                                               APPLICANT: Dower, William J
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                                                                                                                                                                                                                                                  Application US/09516704
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Wagstrom, Christopher R.
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                                                                                                                                            Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                          Schatz, Peter J.
Balasubramanian, Palaniappan
                                   Deprince, Randolph B. Podduturi, Surekha
                                                                      Wagstrom, Christopher R. Hendren, Richard W.
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 Mismatches

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NAME: HTUBIEC, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193, Applicat Patent No. 6251864 GENERAL INFORMATION:
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Best Local Similarity
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CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: -Unknown>
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COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                         NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                       COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STRANDEDNESS: <Unknown>
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                                                                                                                                                                         STATE: NC
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Cwirla, Steven E.
Gates, Christian
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Wagstrom, Christopher R.
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100.0%; Pred. No. 0.00089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ronald W.
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 Mismatches

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RESULT 12
US-08-764-640-17
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APPLICANT: Dower, William J.
                                    INFORMATION FOR SEQ ID NO:
                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764,640
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
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APPLICANT:
                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                  NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 11-DEC
                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 27709
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
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T: Five Moore Drive, P.O.
Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                        NO
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15 amino acids
                                                                                                                                                                                                                                                                                                                        USA
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Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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Hendren, Richard W.
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                                                                                                                                                        11-DEC-1996
N: 514
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: 244
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QУ
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; MOLECULE TYPE: peptide
US-08-764-640-185
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                                                    Query Match
Best Local :
                                 Matches
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Patent No. 5869451 5837683
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                                                                                                                                                                                                                   TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.0%; Pred. No. 0.00096;
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                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: RECEPTOR
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                                               Local Similarity
                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/O
FILING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
3 IEGPTLRQWLAARA 16
                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Five Moore Drive, P.O. Box 13398
CTITY: Research Triangle Park
                                                                                                                                                                                 ENGTH:
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                               14;
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C
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                               Conservative
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                        39.9%; Score 73; DB 2; L
100.0%; Pred. No. 0.00096;
tive 0; Mismatches 0;
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                                                           Length 15;
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                          0; Gaps
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2 IEGPTLRQWLAARA 15

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US-08-973-225-185
; Sequence 185, Application US/08973225A
; Patent no. 6083913
; GENERAL INFORMATION:
APPLICANT: Dower, William J.
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US-08-973-225-17
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GENERAL INFORMATION:
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARA 14
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NAME: HTUBLEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PERTIDES AND COMPOUNDS THAT BIND TO A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids
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                                                     Duffin, David J. Gates, Christian
               Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                           Cwirla, Steven E.
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Mattheakis, Larry C.
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Schatz, Peter J
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100.0%; Pred. No. 0.00096;
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                                                                                                               Ronald W.
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RESULT 16
US-09-244-298A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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APPLICANT:
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APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICANT:
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                                       COUNTRY: U:
ZIP: 27709
                                                                                            ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
                                                                            STATE:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 15 amino acids
TYPE: amino acid
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO THROMBOPOIETIN RECEPTOR
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COUNTRY: U
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                                                                            NC
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                                                          USA
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                                                                                                                                                                                                                                                                                                                                            Gates, Christian
Schatz, Peter J.
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Cwirla, Steven E.
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244
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                                                                                                                                                                                                          PEPTIDES AND COMPOUNDS THAT BIND TO
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Pred. No. 0.00096;
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                                                                                                                 Box 13398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 185,
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
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APPLICANT:
                               REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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ZIP: 27709
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TOPOLOGY: li
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Wagstrom, Christopher R.
Hendren, Richard W.
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                   919-248-1000
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                                                                                                                                                      US/09/244,298A
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Pred. No. 0.00096;
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US-09-516-704-17
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                                                                                                 US-09-516-704-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17,
                                                               Query Match
                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 17:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                 Local Similarity
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3 IEGPTLRQWLAARA 16
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                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 27709
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/516,704 FILING DATE: 01-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398
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                                 Conservative
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Wagstrom, Christopher R.
Hendren, Richard W.
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Cwirla, Steven E.
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                                               100.0%;
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                                                                 39.98;
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                                 0;
                                                 Score 73; DB 4; Length 15; 
; Pred. No. 0.00096;
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Pred. No.
                                 Mismatches
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                               Indels
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Sequence 18, Application US, Patent No. 5869451 5837683; Patent No. 5869451 5837683; GENERAL INFORMATION: APPLICANT: Dower APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid; STRANDENNESS: <Unknown>; TOPOLOGY: Linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 185: US-09-516-704-185
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GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
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US-09-516-704-185
; Sequence 185, A
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           Match 39.9%; Score 73; DB 4; Length 15; Local Similarity 100.0%; Pred. No. 0.00096; Indels 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/516,704 FILING DATE: 01-Mar-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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ADDRESSEE: Glaxo Wellcome
7---- Moore Drive, P.O. Box 13398
                                                                                                                                                                 Application US/08764640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 amino acids
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deprince, Randolph B. Podduturi, Surekha
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RESULT 21
US-08-764-640-194
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                                                                                                                                                                                                                                           Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                              Sequence 194,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
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APPLICANT: Deprince,
APPLICANT: Podduturi
APPLICANT: Yin, Qun
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                              APPLICANT:
               APPLICANT: Yin, Qur
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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APPLICANT:
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NUMBER OF SEQUENCES:
                                                                APPLICANT:
                                                                                                               APPLICANT:
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OTHER INFORMATION: /product= "Beta-ala"
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STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 amino acids
                                                          Deprince, Randolph B. Podduturi, Surekha
                                                                                            Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                           Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                           Barrett, Ronald W. Cwirla, Steven E. Gates, Christian
                                              Yin, Qun
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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: 244
             PEPTIDES AND COMPOUNDS THAT BIND TO RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         39.9%; Score 73; DB 2; 100.0%; Pred. No. 0.001;
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US-08-764-640-232
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Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Dower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 16 amino acids
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               TITLE OF INVENTION: PEPTIDES TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
                                                                                                                                                  CITY:
                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Glaxo Wellcome STREET: Five Moore Drive, P.O. Box 13398
             SOFTWARE:
                                                                                                               COUNTRY:
                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%;
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                                                                                                                                                              Five Moore Drive, P.O.
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                                                                                                               USA
                                                                                                                                                                                                                                                                           Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R. Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                               Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                               Dower, William J
               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                               Glaxo Wellcome
                                                                                                                                                                                                                                                PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                               Box 13398
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-232
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US-08-973-225-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6083913
GENERAL INFORMATION:
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                                                                                           INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
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                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                 REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
MOLECULE TYPE: peptide
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6083913
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                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
                 STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NC
                                                                           LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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Cwirla, Steven E.
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Wagstrom, Christopher R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
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Pred. No. 0.001;
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TOPOLOGY: Innear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-973-225-194
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GENERAL INFORMATION:
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                                                                   Matches
                                                                                                 Query Match
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Local Similarity 100.0%;
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                                                                                 Local Similarity
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OTHER INFORMATION: /product= "Beta-ala"
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 N
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                IEGPTLRQWLAARA 16
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STREET: Five Moore Drive, P.O.
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Research Triangle Park
                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                           LENGTH: 16 amino acids
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                                                                   Conservative
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Mattheakis, Larry C.
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                                                                                   39.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ronald W.
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                                                                                   Score 73; DB 3; Pred. No. 0.001;
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US-08-973-225-220
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US-09-244-298A-18
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GENERAL INFORMATION:
                                                                                                                                                                                 Sequence 18, Application US/09244298A Patent No. 6121238
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                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                        APPLICANT:
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   APPLICANT:
                                  APPLICANT:
                                                       APPLICANT:
                                                                           APPLICANT:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 220:
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ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Glaxo Wellcome STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                        Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                           Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duffin, David J. Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrett, Ronald W
Cwirla, Steven E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert T
                                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB 3; pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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RESULT 27
US-09-244-298A-194
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                                                                                                                                                                                                                                                                                                                                Sequence 194, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                APPLICANT:
                                                                                             TITLE OF INVENTION: PEPTIDES
                                                              CORRESPONDENCE ADDRESS
                                                                                                                                 APPLICANT:
                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
TECRMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: US/09/244,298A APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 APPLICANT:
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
STATE:
                 CITY:
                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
LOCATION: 15
COTHER INFORMATION: /product= "Beta-ala"
                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARA 14
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             Research Triangle Park
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Hrubiec, Robert T.
Hrubiec, Robert T.
NUMBER: 36,392
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                         E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                Yin, Qun
                                                                                                                                             Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                              Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                              PEPTIDES AND COMPOUNDS THAT BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.9%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Releacuration DATA:
CURRENT APPLICATION UMBER: US/(
FILING DATE: 11-DEC-199(
CLASSIFICATION: 514
                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                   STREET: Five Moore Drive, F. CITY: Research Triangle Park
                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                            ZIP:
NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 39.9%; Score 73; DB 3; Local Similarity 100.0%; Pred. No. 0.001; les 14; Conservative 0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 27709
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o. 6121238
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Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-09-516-704-18
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; MOLECULE TYPE: peptide
US-09-244-298A-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application Patent No. 6251864
GENERAL INFORMATION:
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                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNknown>
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dower, William J
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                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T
REGISTRATION NUMBER: 36,392
                  OTHER INFORMATION:
                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    NAME/KEY:
                                                                                                       TOPOLOGY: linear
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Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
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Tr NO: 232:
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                                                                                      peptide
                                   Modified-site
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US-09-516-704-194
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US-09-516-704-194
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                      Local Similarity es 14; Conserv
                                                                                                                                                              3 IEGPTLROWLAARA 16
2 IEGPTLRQWLAARA 15
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETERS OF THE PARAMETE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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Search completed: October Job time: 5.6534 secs

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Result
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 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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## ALIGNMENTS

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R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770
A;Accession: B71325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein TP0421 - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999 C;Accession: B71325
                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F58B3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain Nichols C; Genetics:
                                       A;Map position: 4
A;Introns: 68/1
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-683 <COL>
A;Cross-references: GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65409.1; PID:g332
                                                                                                                                                                                                                                                                              A; Reference number: Z19633
A; Accession: T22896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                  A; Gene: CESP: F58B3.3
                                                                                                                                                               A; Experimental source: clone F58B3
                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-214 <WIL>
                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                 R; Harris,
                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T22896
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                                                                                                                                                                                          EMBL: Z73427; PIDN: CAA97801.1; GSPDB: GN00022; CESP: F58B3.3
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Pred. No.
    Score 58;
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Length 214;
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sorbitol oxidase (EC 1.-.-) -
C; Species: Streptomyces sp.
                                                                                                                   Вb
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                                                                                                                                                                                                                                                                    A; Gene: STY2145
C; Superfamily: tyrosine-specific transport protein
                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple of A; Reference number: AB0502; PMID:11677608
A; Accession: AD0748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine-specific transport protein STY2145 [imported] - Salmonella enterica subsp. enter; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C;Accession: AD0748
                                        JW0076
                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL513382; PIDN:CAD05687.1; PID:g16503181; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-403 < PAR>
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J. th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 *sequence_revision 20-Apr-2001 *text_change 20-Apr-2001
C;Accession: F87286
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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A; Residues: 1-361 <STO>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connerton, P.; Cronii
oule, S.; O'Gaora, P.
                                                                                                                                                    1 GGIEGPTLRQWLAARAGPNGI 21
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              Streptomyces
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A; Residues: 1-346 <STO>
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A; Residues: 1-440 <MAT>
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A; Residues: 1-420 <HIR>
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                              unknown protein encoded within prophage CP-933U [imported] - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Matsumoto, A.; Matsumoto, R.; Fujiwara, Y. Eur. J. Biochem. 230, 337-343, 1995
A;Title: Molecular cloning of human cDNA with a A;Reference number: S65358; MUID:95324544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 *sequence_revision 13-Mar-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hiraga, K.; Eto, T.; Yoshioka, I.; Oda, Biosci. Biotechnol. Biochem. 62, 347-353, A;Title: Wolecular cloning and expression A;Reference number: JW0076; MUID:98193986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 24-Oct-2000
C;Accession: JW0076
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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Ar Arntelo. 2001
                                                                                                                   A;Cross-references: GB:AE005174; NID:g12516109; PIDN:AAG57008.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                  A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551
    Conservative
                      29.5%;
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                    Score 54;
Pred. No.
    Mismatches
                      20;
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  Gaps
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GDGIRQAMLARAGFENVEKDNAYNGMTLREW 32

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A;Cross-references: GB:J03464; NID:g179595; PIDN:AAB59374.1; PID:g179596 R;Kuivaniemi, H.; Tromp, G.; Chu, M.L.; Prockop, D.J. Biochem. J. 252, 633-640, 1988 Biochem. J. 252, 633-640, 1988 A;Title: Structure of a full-length cDNA clone for the prepro-alpha-2(I) chain A;Reference number: S00824; MUID:88339824 A;Accession: S00824
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Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA, A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 1-275,'A',277-332,'V',334-337,'A',339-482,'A',484-548,'D',550-765 <KUI A;Residues: EMBL:Y00724; NID:g30022; PIDN:CAA68709.1; PID:g30023 R;Dickson, L.A.; de Wet, W.; di Liberto, M.; Weil, D.; Ramirez, F. Nucleic Acids Res. 13, 3427-3438, 1985 Nucleic Acids Res. 13, 3427-3438, 1985 A;Tile: Analysis of the promoter region and the N-propeptide domain of the human A;Reference number: S09176; MUID:85242047
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A;Title: Organization of the human pro-alpha-2(I) collagen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
C;Date: 30-Jun-1989 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
C;Accession: A28500; S00824; S09176; I55311; A58111; A28472; A42165; A34405; 9005; A02865
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A;Residues: 1-1095 <STO>
A;Cross-references: GB:AE004569; GB:AE004091; NID:g9947339; PIDN:AAG04789.1; GSPDB:GN001
                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-23;33-58, 'P',60-93 <DIC>
A; Residues: 1-23;33-58, 'P',60-93 <DIC>
A; Cross-references: EMBL:X02488; NID:g30098; PIDN:CAA26320.1; PID:g30099
A; Weil, D.; D'Alessio, M.; Ramirez, F.; Eyre, D.R.
J. Biol. Chem. 265, 16007-16011, 1990
A; Title: Structural and functional characterization of a splicing mutation
A; Title: Structural and functional characterization of a splicing mutation
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A; Residues: 1-248, 'N', 250-1366 <DEW>
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A; Accession: A28500
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N;Alternate names: procollagen alpha 2(I) chain
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C; Species: Pseudomonas aeruginosa
                                                                                          A; Reference number: I55311; MUID:90368825
A; Accession: I55311
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                                                             A; Status: translated from GB/EMBL/DDBJ
                     A; Molecule type:
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R; Fietzek, P.P.; Furthmayr, H.; Ku
Eur. J. Biochem. 47, 257-261, 1974
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A;Molecule type: protein
A;Residues: 'Z',81'B',83-96;417-447 <CLI>
A;Residues: 'Z',81'B',83-96;417-447 <CLI>
A;Rote: the compositions of peptides CNBr1, CNBr0, and CNBr2 were determined;
R;Kuivaniemi, H.; Sabol, C.; Tromp, G.; Sippola-Thiele, M.; Prockop, D.J.
J. Biol. Chem. 263, 11407-11413, 1988
A;Title: A 19-base pair deletion in the pro-alpha 2(I) gene of type I procolla
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J. Biol. Chem. 267, 6361-6369, 1992
A;Title: A base substitution at the splice acceptor site of intron 5 of s-Danlos syndrome type VII.
A;Reference number: A42165; MUID:92210617
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A;Title: Ehlers-Danlos syndrome type VIIB. Deletion of 18 amino acids comprising the A;Reference number: A28472; MUID:88059013
                                                                                                                                                        A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 163-181,200-213 <CH2>
A;Cross-references: GB:S41099; NID:9252702; PIDN:AAB22761.1; PID:9252703
A;Note: mutant sequence from a patient with osteogenesis imperfecta type
R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A;Title: Comparative study of glycopeptides derived from selected vertebr
A;Reference number: A92069; MUID:71001508
A;Accession: B92069
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A; Residues: 32-75,94-111 <WIR>
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A; Residues: 23-75,94-96 <WEI2>
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A;Note: single base mutation in intron leads to abnormal splicing of mRNA
R;Chipman, S.D.; Shapiro, J.R.; McKinstry, M.B.; Stover, M.L.; Branson, P.; Rowe, D.W
J. Bone Miner. Res. 7, 793-805, 1992
A;Title: Expression of mutant alpha (I)-procollagen in osteoblast and fibroblast cult
A;Reference number: I55485; MUID:92351816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Isolation and characterization of the cyanogen bromide peptides from the A;Reference number: A90567; MUID:71038625 A;Accession: A90567
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A;Title: Temperature-dependent expression of a collagen splicing defect in the fibrob
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A; Residues: 50-126 <CHI>
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A; Experimental source: skin A; Note: attachment of 2-0-alpha-D-glucosyl-0-beta-D-galactose to 5-hydroxylysine
                                                                                A; Molecule type: protein A; Residues: 175-180 < MOR>
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A;Experimental source: fibroblast cell culture R;Myers, J.C.; Chu, M.L.; Faro, S.H.; Clark, W.J.; Prockop, D.J.; Proc. Natl. Acad. Sci. U.S.A. 78, 3516-3520, 1981
A;Title: Cloning a cDNA for the pro-alpha2 chain of human type I chair R;Reference number: A18855; MUID:81273090
                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 960-1021, 'L',1023-1188,'D',1190-1197,'S',1199-1356 <MAE>
A;Cross-references: EMBL:X55525; NID:g30101; PIDN:CAA39142.1; PID:g3
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A; Residues: 672-675, 'V',677,'P',679-681 <BAT>
A; Residues: 672-675, 'V',677,'P',679-681 <BAT>
A; Cross-references: GB:S39878; NID:g1679911; PIDN:AAB19314.1; PID:g232761
A; Note: sequence extracted from NCBI backbone (NCBIN:39878, NCBIP:39886)
A; Note: mutant sequence of patient with osteogenesis imperfecta type IV;
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A.Residues: 665-666, 'D', 668-670 <NIY>
A.Residues: 665-666, 'D', 668-670 NID:g180888; PIDN:AAB59384.1; PID:g180889
A.Cross-references: GBL00613; NID:g180888; PIDN:AAB59384.1; PID:g180889
A.Note: mutant sequence from a patient with osteogenesis imperfecta
R.Bateman, J.F.; Hannagan, M.; Chan, D.; Cole, W.G.
Biochem. J. 276, 765-770, 1991
A.Title: Characterization of a type I collagen alpha 2(I) glycine-586 to valine
                                                                                                       A;Title: Cloning a cDNA for A;Reference number: A18855; A;Accession: A18855
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Biochim. Biophys. Acta 1049, 171-176, 1990
A;Title: Growth-dependent modulation of type I collagen
A;Reference number: S10768; MUID:90304220
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J. Biol. Chem. 267, 23108-23112, 1992
A:Title: Incorporation of type I collagen molecules that contain a mutant alpha A:Reference number: 153369; MUID:93054637
                                           A; Molecule type: mRNA
A; Residues: 964-979,'
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A; Title: Severe (type III) osteogenesis imperfecta due A; Reference number: I54365; MUID:95187161
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A;Molecule type: mRNA
A;Residues: 623-742, A',744-764,'X',766-827,'A',829-830,'p',832-836,'p',838-1097,'L',109
A;Cross-references: GB:J00115; GB:V00503; NID:g30123; PIDN:CAA23761.1; PID:g825646
A;Experimental source: skin fibroblast cells
A;Experimental source: skin fibroblast cells
A;Fortino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes
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A;Cross-references: GB:M21353; NID:g180881; PIDN:AAA52053.1; PID:g180882
A;Note: single base mutation in intron leads to splicing out of exon 28
A;Bernard, M.P.; Myers, J.C.; Chu, M.L.; Ramirez, F.; Eikenberry, E.F.; Prockop,
Biochemistry 22, 1139-1145, 1983
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A;Cross references: GB:147668; NID:91009095; PIDN.AAB59577.1; PID:91009096
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A; Accession: S09174
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A;Accession: I59125
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A; Accession: A91224
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A;Residues: 520-573 ·
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A; Residues: 418-447 <FIE>
                    Cross-references:
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      'V',981-1018,'Q',1020 < GB:J00114; NID:g180393;
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      PID:g180394
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.; Lory, S.; Olson, M.V.
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A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337
                                                                  .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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C;Accession: F83487
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A.Note: sequence extracted from NCBI backbone (NCBIP:111965) C:Superfamily: unassigned collagens; fibrillar collagen carboxyl-terminal F:48-106/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen alpha 2 fibrillar chain precursor - sea urchin (Strongylocentrotus C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999 C;Accession: A43426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M22817; NID:g179606; PIDN:AAA51846.1; PID:g179607 A;NOte: mutant sequence from a patient with osteogenesis imperfecta type IN R;Myers J.C.; Dickson, L.A.; de Wet, W.J.; Bernard, M.P.; Chu, M.L.; di L.J. Biol. Chem. 258, 10128-10135, 1983
A;Title: Analysis of the 3'end of the human pro-alpha-2(I) collagen gene.
                                                                                                                                                                                                                            F;2978-3198/Domain: fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: nucleic acid A; Residues: 1-3198 < EXP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Novel amino-terminal propeptide configuration A;Reference number: A43426; MUID:92381062 A;Accession: A43426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Exposito, J.Y.; D'Alessio, M.; Ramirez, J. Biol. Chem. 267, 17404-17408, 1992
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R; Wenstrup, R.J.; Cohn, D.H.; Cohen, T.; Byers,
J. Biol. Chem. 263, 7734-7740, 1988
A;Title: Arginine for glycine substitution in th
A; Reference number: I55285; MUID: 88227975
A; Accession: I55285
                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: M92041; NID: g161448; PIDN: AAA30040.1; PID: g161449
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A; Accession: S09175
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A; Residues: 1090-1101, 'R', 1103-1107 <WEN2>
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A; Residues: 1090-1107 <WEN1>
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                                                     2 GIEGPTLRQWLA-----ARAGPNGIEGP 24
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GMVGPPGRPGLAGSVGYHGRRGPNGLSGP 1871
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Pred. No. 2
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                                                                                                                                                                      DB 2;
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Coulter,

A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas,

P.; Hickey, A.; Larbig,

PAO1,

an

opportunistic

#text\_change 31-Dec-2000

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A; Experimental source: strain PAO1 C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AG0147
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A; Residues: 1-371 <STO>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                   probable UV damage endonuclease - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #text_change 31-Mar-2000
C;Date: 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: C75350
C;Accession: C75350
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
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                                                                                                                                                                                                                                                                                                                                                      M.; Shen, M.; Vamathevan, J.J.; Lam, P.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
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                                                                                                                                                                         A;Cross-references: GB:AE002022; GB:AE000513; NID:g6459590; PIDN:AAF11370.1; PID:g645959
A;Experimental source: strain R1
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A; Residues: 1-326 <WHI>
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A; Status: preliminary
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A; Residues: 1-296 <KUR>
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A; Reference number: AB0001; MUID:21470413; PMID:11586360
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Query Match
Best Local Similarity
Matches 15; Conserv
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                                                         Length 326;
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collagen alpha 2(1) chain precursor - mouse
C; Species: Mus musculus (house mouse)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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C; Species: Chandipura virus
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R;Phillips, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J.
Genomics 13, 1345-1346, 1992
A;Title: Sequence analysis of a full length cDNA for the murine pro alpha 2(I) collag
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A; Residues: 1-524 <MAS>
                                                                                                                    C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homolo C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F;1145-1373/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence extracted from NCBI backbone (NCBIP:112027)
R;Phillips, C.L.; Lever, L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J.
J. Invest. Dermatol. 97, 980-984, 1991
A;Title: Construction of a full-length murine Proalpha2(I) collagen cDNA by the polym
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-110 < PH2>
                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A54328; MUID:92084969 A;Accession: A54328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1373 < PHI>
A; Cross-references: GB: X58251; NID: g50488; PIDN: CAA41205.1; PID: g50489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A43291; MUID: 92372043
A; Accession: A43291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;184,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                               A; Gene: COL1A2
                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
Matches
                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 IDGPVLKEPKGKRESPSGISSDIWTQW 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity hes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 EGPTLRQW-LAARAG------PNGIEGPTLRQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IEGPTLRQWLAARAGPNGIEGPTLRQW 29
                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDPSVREWVLRARATWOPPEWQVVHLSNGIEGPQDRR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.S.; Bella, R.S.; Butcher, M.; Patel, B.; Ghosh, H.P.; Banerjee, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A32443
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:J04350; NID:g323376; PIDN:AAA42916.1; PID:g323377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.0%;
37.0%;
                             29.0%;
52.2%;
1.
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                             Score 53; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 524, 42;
                                                          Length 1373;
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2 GIEGPTLRQWLAARAGPNGIEGP 24

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757

GIVGPTGSVGAAGPSGPNGPPGP 779

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RESULT 18
T22892
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C;Date: 21
C;Accessio
R;Herren,
       hypothetical protein F58B3.1 - C; Species: Caenorhabditis elega
                                                                                                                                                      밁
                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                     F;420-503/Domain: disintegrin homology <DIS>F;348,352,358/Binding site: zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: articular chondrocyte C; Comment: This protein is a membrane bound protein and involved C; Superfamily: mouse meltrin alpha; disintegrin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:MCKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell, Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAN A;Reference number: PC4263; MUID:97168971
A;Accession: PC4263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 17
G02390
                                                                                                                                                                                                                                                                                                                                 F;349/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: hydrolase; metalloproteinase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-461 < MCK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Reference number: H01157
A;Accession: G02390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
A46053
A46053
bullous pemphigoid antigen, BPAG2, type XVII collagen alpha 1-chain - mouse C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 21-Sep-1993 #text_change 05-Nov-1999
C:Accession: A46053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: U46005; NID: g1335871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from A;Molecule type: mRNA
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A;Cross-references: GB:L08407; NID:g309182; PIDN:AAA37443.1; PID:g309183
A;Note: sequence extracted from NCBI backbone (NCBIN:129627, NCBIP:129628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;L1, K.; Tamai, K.; Tan, E.M.L.; Uitto, J.
J. Biol. Chem. 268, 8825-8834, 1993
A;Title: Cloning of type XVII collagen. Complementary and genomic DNA sequences of mountain and unusual features in the 5'-end of the gene and the 3'-untranslated region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-814 <HER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1433 <L
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                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                        Query Match
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Herren, B.; Raines, E.W.; Ross,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
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                                                                                                                                                 728 LKGPTC-QYRAAQSGPSERPGPPQRALLA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 GMEGPIGQRGLAGPMGPRGEPGP
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                            3 IEGPTLRQWLAARAGPNGIEGPTLRQWLA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GIEGPTLRQWLAARAGPNGIEGP 24
                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                28.7%;
            elegans
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                               Caenorhabditis elegans
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                                                                                                                                                                                                                                                              Score 52.5;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644
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                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                      DB
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                                                                                                                                                                                                                                                                                   Length 814;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g1335872
B.; Graham,
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                                                                   A; Molecule type: DNA
A; Residues: 1-396 <OLI>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                          conserved hypothetical protein SC5F2A.12c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 18-
                          C; Genetics:
                                                                                                                                                                                                        R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
  A; Gene:
                                           A; Experimental source: strain
                                                                                                                                     A; Status: preliminary; translated from
                                                                                                                                                             A; Accession: T35254
                                                                                                                                                                                A; Reference number: Z21573
                                                                                                                                                                                                                                                      C; Accession: T35254
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SCOEDB:SC5F2A.12c
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A;Map position: 4
C;Superfamily: Caenorhabditis elegans hypothetical protein F58B3
                                                                                                                                                                                                                                                                                                                                                                                        A;Description: The sequence of A;Reference number: Z21262 A;Accession: T32999
                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, Februa A:Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F17E9.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 68/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F58B3
                                                                                                                                                                                                                                                      A; Gene: CESP:F17E9.11
                                                                                                                                                                                                                                                                                           A; Experimental source: strain Bristol
                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AF047656; PIDN:AAC05110.1; GSPDB:GN00022; CESP:F17E9.11
                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-230 <WOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Woessner, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-214 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data A; Reference number: Z19633 A; Accession: T22892
                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone F58B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: 273427; PIDN: CAA97797.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                    Matches
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                          Genetics
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                                                      202 GGWKKPTIHQWHGTTKGPCGV 222
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20
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                                                                                           1 GGIEGPTLRQWLAARAGPNGI 21
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9; Conser
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9; Conserv
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                                                                                                                                  Conservative
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42.9%;
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                                                                                                                                                  Pred.
                                                                                                                                                                      Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB Pred. No. 22;
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                                                                                                                                                                                                                                                                                        clone F17E9
                                                                                                                                                                                                                                                                                                                                                                                                                             cosmid F17E9
                                                                                                                                                                      DB 2;
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                                                                                                                                                                      Length 230;
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                                                                                                                                Gaps
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EMBL: AL049587; PIDN: CAB40679.1; GSPDB: GN00070; SCOEDB: SC5F2A.12c

GB/EMBL/DDBJ

J.; Barrell,

B.G.; Rajandream,

М .

#text\_change 18-Aug-2000

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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AF3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitric-oxide reductase cytochrome c chain (EC 1.7.99.7) [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb_2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-150 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL54241.1; PID:g17985213; GSPDB:GN00191
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                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000019; PIDN:BAB75314.1; PID:g17132748; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: all3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AH2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein all3615 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
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A; Residues: 1-621 <KUR>
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A;Accession: AH2257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakazaki, N.; Shimpo, S.
DNA Res. 8, 205-213, 2001
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
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RESULT
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Best Local
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                                                                    403 GMFGEIYTRWYEARAGRDVIEVP---DWLA 429
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                                                                                                                                                                                       Local
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                                                                                                                2 GIEGPTLRQWLAARAGPNGIEGPTLRQWLA 31
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Pred. No. 18;
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                                                                                                                                                                                         Score 51.5; No. 77;
                                                                                                                                                                   Mismatches
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hypothetical protein F58B3.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 C;Accession: T22B95
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C; Superfamily:
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A; Residues: 1-215 <WIL>
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A; Accession: T22895
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                                                R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
A;Accession: G72680
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C;Accession: AH0190
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                                                                                                                                                                                                                           C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: G72680
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A; Residues: 1-246 < KUR>
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C; Species: Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL590842; PIDN:CAC90387.1; PID:g15979605; GSPDB:GN00175
A; Molecule type: DNA
                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                               hypothetical protein APE0867 - Aeropyrum pernix (strain K1)
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Best Local Similarity
Trahes 9; Conserv
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Pred. No.
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DDBJ:AP000060; NID:g5104188; PIDN:BAA79847.1; PID:d1043633; PID:g510

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A; Introns: 12/2
C; Superfamily: collagen
                                                                                                                                                                  A; Gene: CESP:C50F7.2
                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 1-589 < JOH>
                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C50F7
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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C;Keywords:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: D70601
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C;Accession: D70601
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Connor, R.; Davies, R.; Devlin, K.; Seeger, K.; Skelton, S.; Squares, (
                                                                                                                                                                                                                                                                                           A; Reference number: Z20601
A; Accession: T29299
                                                                                                                                                                                                                                                                                                                                                                            R;Johnson,
                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C50F7.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA7984
A;Cross-references: Strain K1
C;GenetLcs:
A;Gene: APE0867
C;Superfamily: Aeropyrum pernix hypothetical protein APE0867
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                                                                                   Query Match
                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                             ; Accession:
                                          Best Local Similarity Matches 9; Conserv
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9; Conserv
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                                          Conservative
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                                                                                                                                                                                                     EMBL: U41557; PIDN: AAA83307.1; CESP: C50F7.2
                                                                                                                        alpha 1(VIII) chain;
                                                            27.9%;
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                                                            Score 51; DB Pred. No. 84;
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Pred. No. 43;
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                                                                                                               complement Clq carboxyl-terminal homology
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conserved hypothetical protein SMa0937 [imported] - Sinorhizobium meliloti (strain
                                  B95325
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WLGLPSAANGSQGPLLMKW 396

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 2-11; 435-449, X', 451-452, 'X', 454-459; 634-649 <JEN2>
C; Superfamily: SITS-binding protein sp105
C; Keywords: disulfide bond; glycoprotein; homodimer; transmembrane
F; 2-697/Product: SITS-binding protein #status experimental <MAT>
F; 30-50/Domain: transmembrane #status predicted <TMI>
F; 30-50/Domain: transmembrane #status predicted <TMI>
F; 30-50/Domain: transmembrane #status predicted <TMI>
F; 30-50/Domain: transmembrane #status predicted <TMI>
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F; 30-50/Domain: transmembrane #status predicted <TMI>
F; 30-50/Domain: transmembrane #status predicted <TMI
                                                                                                                                                                                  F;25,112,134,162,386,405,470,568/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                            F;503-521/Domain: transmembrane #status predicted <TM2>F;542-562/Domain: transmembrane #status predicted <TM3>
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C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Primary structure of a novel 4-acetamido-4'-isothiocyanostilbene-2,2'-disulp A; Reference number: S04987; MUID:89374082
A; Accession: S04987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITS-binding protein sp105 - Pacific electric ray
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #t
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R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-697 < JEN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Jentsch, T.J.; Garcia, A.M.; Lodish, H.F. Biochem. J. 261, 155-166, 1989
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C83221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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11 WLAARAGPNGIEGPTLRQW 29
                                                                      Local Similarity
les 8; Conserv
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                                                                      Conservative
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                                                                                              27.9%;
42.1%;
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52.9%;
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                                                                                                                              Score 51;
                                                                                                  Pred. No.
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A.; Larbig, K.; L
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A; Molecule type: DNA
A; Residues: 1-719 < KUR>
A; Cross-references: GB: AE006469; PIDN: AAK65164.1; PID: g14523607; GSPDB: GN00165
A; Experimental source: strain 1021, megaplasmid pSymA
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
E.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
A; Aithors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Fitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
A; Contents: annotation
C; Genetics: SMA0937
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B95325
R;Barnett, M.J: Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95325
A;Status: preliminary
Search completed: October Job time: 8.64403 secs
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Matches
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                                                                                                                         71 LDDPEVRQWLTAKQAAAPAAATTPAGLASQWIA 103
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                        2002, 09:05:04
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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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the pro-alpha 2(I) collagen gene of an Ehlers-Danlos type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
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ient.";
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              11-10
                                                                                               J.F., Moeller I.,
                                                                                                                             II-IO
                                                                                                                                                                                                                                                                                                                                                                                OI-II ARG-784
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                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 266:2590-2594(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       terminus destabilizes the v
Chem. 264:3002-3006(1989).
                                        Gly to Arg substitution NA sequence mismatch."; 1:55-62(1992).
                                                                                                                                                                                                                            Constantinou
                                                                                                                         ARG-547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265:16007-16011(1990).
                                                                                 osteogenesis
                                                                                                             PubMed=1284475;
                                                                                                                                                     osteogenesis
Sci. U.S.A. 8
                                                                                                                                                                                                                                         PubMed=2052622;
PubMed=1385413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2777764;
1 H.-H.M., Cole W.
                                                                                                Hannagan
                                                                                                                                                                                                                           C
                                                                                                                                                                  evidence for p
                                                                                                                                                                                                                         .D.,
                                                                                                                                                      88:5423-5427(1991).
                                                                                 agan M., Ch
imperfecta
                                                                                                                                                                                                                                                                                                                                                                                                                                      distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lever L.W.,
                                                                      detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for glycine substitutions within
                                                                                                                                                                         for phenotypic
                                                                 Chan D., Cole W.G.; cta due to a type I collagen ected by chemical cleavage of
                                                                                                                                                                                                                         ۲.,
                                                                                                                                                                                               (COL1A2)
                                                                                                                                                                                                                         Ganguly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phillips
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a type IV. Detect
ical cleavage met
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VII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             043819; Q9UK87;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
SCO2 protein homolog, mitochondrial precursor
                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Fatal infantile cardioencephalomyopathy with COX deficiency mutations in SCO2, a COX assembly gene.";
Nat. Genet. 23:333-337(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20014747; PubMed=10545952;
Papadopoulou L.C., Sue C.M., Davidson M.M., Tanji K., Nishin Sadalock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Van Coster R., Lyon G., Scalais E., Lebel R., Kaplan P., Sha De Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A.;
                                                                                                                                                                                                                 EMBL; AF177385; AAF05313.1; EMBL; AL021683; CAA16671.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: THOUGHT TO PLAY A ROLE IN EITHER MITOCHONDRIAL COPPER TRANSPORT OR INSERTION OF COPPER INTO THE ACTIVE SITE OF COX.
-i- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-i- TISSUE SPECIFICITY: UBUIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smink L.J., Burton J.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                  VARIANT
                                                                  VARIANT
                                                                                                   TRANSIT
                                                                                                                  Mitochondrion;
                                                                                                                                Pfam; PF02630; SCO1-SenC;
                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Monocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCO2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751 GVVGPTGPVGAAGPAGPNGPPGP 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GIEGPTLRQWLAARAGPNGIEGP 24
                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: DEFECTS IN SCO2 ARE THE CAUSE OF FATAL INFANTILE CARDIOENCEPHALOMYORATHY WITH COX DEFICIENCY. THIS DISEASE IS CHARACTERIZED BY HYPERTROPHIC CARDIOMYOPATHY, LACTIC ACIDOSIS, GLIOSIS. HEART AND SKELETAL MUSCLE SHOW REDUCTIONS IN COX ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX
                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                  DEFICIENCIES
                                                                                                                                                                                  604377; -
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                                                                                                                                               IPR003782; SC01_SenC.
 225
                                  140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                              Transit peptide; Disease mutation; Polymorphism.

MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               BELONGS TO THE SCO1/2 FAMILY.
                                  140
                                                               266
20
 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND VARIANTS FIC LYS-140 AND PHE-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                              R -> P (IN DBSNP:140523).
/FTId=VAR_011738.
E -> K (IN FIC).
/FTId=VAR_008874.
S -> F (IN FIC).
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                                                                                PROTEIN HOMOLOG
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No.
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34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shanske S.,
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RESULT 3
VGLG_CHAV
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990
01-JAN-1990
15-JUL-1999
                                                                                                                                                                Signal.
SIGNAL
                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage hy non-profit institutions as long as its content is in no entitites requires a license arron-
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                                         SEQUENCE
                                                                   LIPID
                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89299473; PubMed=2741347;
Masters P.S., Bhella R.S., Butche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                   CARBOHYD
                                                                                              CARBOHYD
                                                                                                              DOMAIN
                                                                                                                                       DOMAIN
                                                                                                                                                     CHAIN
                                                                                                                                                                                             Transmembrane; Envelope
                                                                                                                                                                                                          Pfam; PF00974; Rhabd
                                                                                                                                                                                                                                   EMBL; J04350; AAA42916.1; PIR; A32443; VGVNCV.
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 171:285-290(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Banerjee A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=11273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabdoviridae; Vesiculovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandipura virus (strain I653514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spike glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P13180;
                                                        LIPID
                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Structure and expression of the glycoprotein gene of Chandipura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 LRSWLLSRQGPAETGGQGQPQGPGLRTRLLITGLFGAGLGGAWLALRA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                       POSITION 479 OR 484. SIMILARITY: 39% IDENTITY TO THE G PROTEINS OF VSV.
                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: TRIMERS IN THE ENDOPLASMIC RETICULUM.
PTM: THIS PROTEIN IS MODIFIED BY THE COVALENT ADDITION OF PALMITIC
ACID VIA A THIOETHER LINKAGE TO A CYSTEINE. IT COULD BE EITHER ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.
IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE
HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL.
THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION
AND THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASMIC
FRACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRUS BUDDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _CHAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                         IPR001903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 13, Created)
(Rel. 13, Last sequence up
(Rel. 38, Last annotation
                                                                                   1
22
22
473
497
184
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                                                                   524
472
496
524
184
184
479
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                                         58826 MW;
29.0%;
                                                                                                                                                                                                         _glycop;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.S., Butcher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%;
                                                                                                                                                                                                                   Rhabd_glycop.
                                                                                                                                                                                          protein; Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
Score 53;
Pred. No.
                                                     N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
PALMITATE (POTENTIAL).
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53.5;
Pred. No. 7.
                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_008875.
BC2F40E057329BF3 CRC64;
                                                                                                                          POTENTIAL
                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                     SPIKE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                         A84AF0A5FFFB73CD CRC64;
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            DB 1;
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           Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 266;
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                                                                                (POTENTIAL)
                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                                        for commercial
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RESULT 4
CA21_MOUSE
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Q01149;
Q1-APR-1993
                                                                                                entities
or send a
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions are long as its content modified and this statement is not removed. Usage by and
                                        EMBL;
                                                                     EMBL;
                                                                                                                                                                                                                                                                                                  "Identification of a cell-specific transcriptional enhancer in first intron of the mouse alpha 2 (type I) collagen gene."; proc. Natl. Acad. Sci. U.S.A. 84:5590-5594(1987).
-i- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN (FIBRILIAR FORMING COLLAGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagen alpha 2(I) chain precursor COL1A2 OR COLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips C.L., Morgan A.L., Lever L.W., Wenstrup R.J.; "Sequence analysis of a full-length cDNA for the murine pro alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92084969; PubMed=1748823;
Phillips C.L., Lever L.W., Pinnell S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Calvaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Calvaria;
                                                                                                                                                                                                                                                                                                                                                                             Rossi P., de Crombrugghe B.;
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87289650;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-23 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Construction of a full-length murine the polymerase chain reaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wenstrup R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-110 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92372043; PubMed=1505972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359
                                                                                                tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 IEGPTLRQWLAARAGPNGIEGPTLRQW
                                                                                                                                                                                                                                                                          SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS. TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
                                                                                                                                                                                                                  UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS
                                                                                                                                                                                                                                                 HYDROXYAPATITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen chain: comparison of the derived n pro alpha 2(I) collagen."; mics 13:1345-1346(1992).
                            A43291; A43291
             MGI:88468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDGPVLKEPKGKRESPSGISSDIWTQW
                                                                     X58251; CAA41205.1; -.
                                        K01832; AAA37331.1;
                                                      BC007158; AAH07158.1;
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                                                                                                                                                                                                                                 PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
 IPR000087;
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             Colla2
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Rodentia;
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97:980-984(1991).
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase admain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
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Pfam; PF01410; COLFI; 1
Pfam; PF01391; Collagen; 18.
ProDom; PD002078; Fib_collagen_C; 1
SMART; SM00038; COLFI; 1.
Zhang X.P., Kamata T., Yokoyama K., Puzon-McLaughlin W., T
"Specific interaction of the recombinant disintegrin-like
MDC-15 (metargidin, ADAM-15) with integrin alphavbeta3.";
J. Biol. Chem. 273:7345-7350(1998).
-i- FUNCTION: MAY BE INVOLVED IN CELL-SURFACE PROTEOLYSIS,
ADHESION OR INTRACELLULAR PROTEIN MATURATION.
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                                                                                                                                                                                                                            cells and in vivo."; FASEB J. 11:173-180(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Kraetzschmar J., Lum L., Blobel C.P.;
"Metargidin, a membrane-anchored metalloprotease-disintegrin protein
with an RGD integrin binding sequence.";
J. Biol. Chem. 271:4593-4596(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Breast carcinoma; MEDLINE=96214870; PubMed=8617717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Metargidin).
ADAM15 OR MDC15
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                                                                                                                                                 MEDLINE=98184837; PubMed=9516430;
                                                                                                                                                                                                                                                                                                   Herren B., Raines E.W., Ross
                                                                                                                                                                                                                                                                                                                             MEDLINE=97192141; PubMed=9039960;
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Umbilical vein;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                         "Expression of a disintegrin-like
cells and in vivo.";
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                                                                                                                                                                              NTERACTION WITH INTEGRIN ALPHAV-BETA3
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Pred. No.
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InterPro; IPR000561; EGF-like.
InterPro; IPR001818; Watrixin.
InterPro; IPR002870; Pep_M12B_propep.
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DISULFID
            DISULFID
                         METAL
                                     METAL
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                                                                                                                                                                                                                                                          dydrolase;
                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                              ransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBGUIT: INTERACTS WITH INTEGRIN ALPHAV-BETA3, ENDOPHILIN I AND SORTING NEXIN 9. PREFERENTIALLY BIND THE PRECURSOR BUT NOT THE PROCESSED FORM OF ADAM15, SUGGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN SORTING NEXIN 9 (BY SIMILARITY).

DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHAY-BETA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. OVEREXPRESSED IN ARTHEROSSCLEROTIC LESIONS. CONSTITUTIVELY EXPRESSED IN CULTERED ENDOTHELIUM AND SMOOTH MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605548;
                                                                                                                                                                                                                                                                                                                                                                                              PF01421;
                                                                                                                                                                                                                                                                                                                                                                                                       PF00200; disintegrin; PF01562; Pep_M12B_prop
                                                                                                                                                                                                                                                                 E; PS50215; ADAM_MEPRO; 1.

E; PS00427; DISINTEGRIN_1; FALSE_NEG.
E; PS00214; DISINTEGRIN_2; 1.
E; PS00022; EGF_1; FALSE_NEG.
E; PS00126; EGF_2; 1.
E; PS01186; EGF_2; 1.
E; PS00142; ZINC_PROTEASE; 1.
E; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                               PD000664; Disintegrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long as its content is in no wast and this statement is not removed. Usage by and for commercial an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE PRECURSOR IS CLEAVED
                                                                                                                                                                                                                                                          Metalloprotease;
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AAC50404.1; -.
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S 1 EGF-LIKE DOMAIN.
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          CELL ATTACHMENT S
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BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
BY SIMILARITY.
                                                                                                                                                                                                                                                         Zinc;
                                                     CYSTEINE SWITCH.
CELL ATTACHMENT SITE
ZINC (CATALYTIC) (BY
                                                                                                                                 DISINTEGRIN-LIKE. CYS-RICH.
                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                            ADAM 15. EXTRACELLULAR (POTENTIAL).
                                                                                                SH3-BINDING
                                                                                                           SH3-BINDING
POTENTIAL
                                                                                                                                                            METALLOPROTEASE
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                                                                                                          (POTENTIAL).
                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                         Glycoprotein; Zymogen;
                       (BY SIMILARITY)
(BY SIMILARITY)
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SIMILARITY).
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                                                                                                                MEDLINE-73049496; PubMed=4636752; Fietzek P.P., Kell I., Kuehn K.; "The covalent structure of collagen. terminal region of alpha 2-CB4 from FEBS Lett. 26:66-68(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P02466; Q9R1E8; 21-JUL-1986 (Rel. 01, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Collagen alpha 2(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _RAT
                                                                                                                                                                                                    "Isolation and characterization of the cyanogen bromide peptides from the alpha 2 chain of rat skin collagen."; Biochemistry 8:2129-2133(1969).
                                                                                                                                                                                                                                                                                                             MEDLINE=67162268; PubMed=5337886;
Kang A.H., Bornstein P., Piez K.A.;
"The amino acid sequence of peptides from the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA21_RAT
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                                        Highberger J.H., Kang A.H., Gross J.; "Comparative studies on the amino acid sequence of the peptides from chick and rat skin collagens.";
                                                                                                                                                                                                                                                                                                                                                                              Guenther D., Seibold Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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 TISSUE=Skin;
                                                                        MEDLINE=71115216; PubMed=5544653;
                                                                                                                                                                       TISSUE-Skin;
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            SEQUENCE OF 453-501
                                                                                     TISSUE-Skin;
                                                                                               SEQUENCE OF
                                                                                                                                                                                  SEQUENCE OF 102-144
                                                                                                                                                                                                                                      Fietzek P.P., Piez K.A.;
                                                                                                                                                                                                                                                 MEDLINE=69206881; PubMed=5785232;
                                                                                                                                                                                                                                                                      SEQUENCE OF 99-102.
                                                                                                                                                                                                                                                                                                     rat skin collagen
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                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                               3iochemistry 10:610-616(1971).
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Rodentia;
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the EMBL/GenBank/DDBJ databases
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N-LINKED (GLCNAC...
G'> S (IN REF. 2).
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Pred. No. 31;
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N-LINKED (GLCNAC. ...
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                              . Amino acid sequence of the calf and rat skin collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                               cross-linking region
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The order of the CNBr peptides from the alpha 2 chain of Biochem. Biophys. Res. Commun. 38:703-708(1970).
-i- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGE (FIBRILLAR FORMING COLLAGE).
                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02867; CGRT2S.
InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The covalent structure of collagen: amino acid sequence of the terminal region of alpha 2-CB5 from rat skin collagen."; FEBS Lett. 36:289-291(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fietzek P.P., Kuehn K.;
"The covalent structure of collagen: amino acid sequence terminal region of alpha2-CB3 from rat skin collagen and from calf skin collagen.";
                                                                                                                                                                                                                                                                                                                                                                            SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; PF01391; Collagen; 18.
proDom; PD002078; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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Vuust J., Lane J.M., Fietzek P.P.,
                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                    MOD_RES
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[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular matrix; Connective tissue; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 791-836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS A BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
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                      Similarity
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N-LINKED (GLCNAC...) (POT

T -> P (IN REF. 4).

S -> P (IN REF. 4).

MISSING (IN REF. 4).

ST -> TS (IN REF. 5).

E -> Z (IN REF. 6).

N -> A (IN REF. 6).
1;
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COLLAGEN ALPHA 2(I) CHAIN.
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01-FEB-1991 (Rel. 17,
01-FEB-1991 (Rel. 17,
16-OCT-2001 (Rel. 40,
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Pfam; PF01055; Glyco_hydro_31;
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Torpedo californica (Pacific electric ray).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondricht
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
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Biochem. J. 261:155-166(1989)
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ULLPHONIC ACID (SITS), AN INHIBITOR OF A VARIETY OF ANION TRANSPORT
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TISSUE SPECIFICITY: ELECTROPLAX TISSUE, BRAIN
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and this statement is not removed. Usage by an
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                          01-FEB-1991 (Rel. 17, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(V) chain precursor.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Chorioamniotic membrane;
MEDLINE-94237164; PubMed-8181482;
Moradi-Ameli M., Rousseau J.C., Kleman J.P., Champliaud M.F.,
Boutillon M.M., Bernillon J., Wallach J.M., van der Rest M.;
Boutilion M.M., Bernillon J., Wallach J.M., van der Rest M.;
"Diversity in the processing events at the N-terminus of type-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of the alpha 3-chain of human type V characterization by partial sequencing."; Biol. Chem. Hoppe-Seyler 373:69-75(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yaoi Y., Hashimoto K., Koitabashi H., Takahara
"Primary structure of the heparin-binding site
Biochim. Biophys. Acta 1035:139-145(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyanogen bromide-derived peptides from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89227189; PubMed=2496661; Seyer J.M., Kang A.H.;
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                                                                                                                                                                                                                                                    de Paepe A., Nuytinck L., Hausser I., Anton-Lamprecht I., Naeyaert J.-M.; "Mutations in the COLSAl gene are causal in the Ehlers-Danlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92239022; PubMed=1571108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 823-950, AND HEPARIN-BINDING. MEDLINE-90366601; PubMed-2203476;
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MEDLINE=97195540; PubMed=9042913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 565-576; 756-772; 1012-1029; 1219-1232 AND 1465-1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Covalent structure of collagen: amino acid sequence of three cyanogen bromide-derived peptides from human alpha 1(V) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete primary structure of human collagen alpha 1 (V) chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 556-571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. 271:120-129(1989).
                                                                                                                                                                                                                                                                                                                                                   Biochem.
                                                                                                                                                                                                                                                                                     Nuytinck L., Hausser I., Anton-Lamprecht I.,
   VELVETY, STRETCHABLE, BRUISABLE SKIN THAT HEALS 'CIGARETTE-PAPER' SCARS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266:13124-13129(1991).
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ProDom; PD002078; Fib_collagen_C;
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DNA polymerase I (EC 2.7.7.7) (POL I)
POLA OR RV1629 OR MT1665 OR MTCY01B2.21.
            Mizrahi V., Huberts P., Dawes S.S., Dude
"A PCR method for the sequence analysis
gene segments from mycobacteria.";
Gene 136:287-290(1993).
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L -> P (IN REF 2).
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P -> L (IN REF 2).
D -> A (IN REF 2).
D -> N (IN REF 2).
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> D (IN REF. 3).
7D58239C0D77BDAE CRC64;
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                                                                the
                                                                                       L.R.;
                                                           gyrA, polA and
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1 GGIEGP-TLRQWLAARAGPNGIEGPTL 26

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Query Match
Best Local
    Matches
                                                                                                                      PROSITE; PS00447; DNA POLYMERASE A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 904 AA; 98471 MW; 1C8E560FE5F74323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L11920; AAB46393.1; --
EMBL; 295554; CAB08882.1; --
EMBL; AE007030; AAK45935.1;
HSSP; P19821; 1BGX.
TIGR; MT1665; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.

-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002562;
                                                                                                                                                                                                                                                                                                                                                                              TubercuList;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
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SUBUNIT: SI
    l Similarity
13; Conser
    Conservative
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); 3_5_exonuclease.

5, DNA_polI.

8; DNA_pol_A.
                27.6%;
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                Score
Pred.
 Mismatches
           2 50.5; L
                              DB 1;
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 Indels
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Gaps
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TONB_PASHA
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                                                                                                                            Matches
                                                                                                                                        Query Match
Best Local
P72204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A human homolog of bacterial peptide deformylases.";
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
-i- FUNCTION: Removes the formyl group from the N-terminal Met of newly synthesized proteins (By similarity).
-i- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)0 = formate
          TONB_PASHA
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giglione C., Serero A., Pierre M., Boisson B., Meinnel T.;
"Identification of eukaryotic peptide deformylases reveals
"Identification of N-terminal protein processing mechanisms.";
                                                                                                                                                                                                                    METAL
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                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                   ProDom;
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                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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MEDLINE=20514156; PubMed=11060042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           PRANSIT
                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lonetto M.A., Zhu Y., Li X., Southan C., "A human homolog of bacterial peptide de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 19:5916-5929(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Polypeptide deformylase). PDF1A OR PDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide deformylase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                         Local Similarity
nes 8; Conserv
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                                                                                               13 AARAGPNGIEGPTLRQ 28
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                                                                        SSTAAPDGVEGPALRR 46
                                                                                                                                                                                                                                                                                                PF01327
                                                                                                                                                                                                                                                                                                                       AF322879;
                                                                                                                                                                                                                                                                    biosynthesis;
                                                                                                                                                                                                                                                                           PD003844; Pep_deformylase; 1.
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243 /
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         STANDARD;
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50.0%;
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                                                                                                                                                                                                                                                                Hydrolase; Iron; Mitochondrion; Transit peptide
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                                                                                                                                    Score 50; DB
Pred. No. 19;
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                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                      MITOCHONDRION (POTENTIAL).
PEPTIDE DEFORMYLASE.
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        PRT;
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      246 AA
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                                                                                                                                                DB 1; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                              as its content
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Best Local
Burns G., Brown T., Hatter K., Idriss J., Jones G. Brown T., Hatter K., Idriss J., Jones G. Brown T., Hatter K., Idriss J., Jones G., Jones G., Similarity of the El subunits of branched-chain-oxoacid dehydrogenase from Pseudomonas putida to the corresponding subunits of mammalian
                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4)
chain alpha-keto acid dehydrogenase component alpha chain
                                           MEDLINE-88329084; PubMed-3416875;
Burns G., Brown T., Hatter K., Idriss J., Sokatch J.R.;
                                                                                       STRAIN-PPG2
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                        ODBA_PSEPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998
16-OCT-2001
                                                                                                                                       NCBI_TaxID=303;
                                                                                                                                                                                        Pseudomonas putida
                                                                                                                                                                                                                                                                                                                          P09060;
                                                                                                                                                                                                                      (BCKDH E1-alpha).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Protein transport; Inner membrane; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U62565; AAB09530.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY EDPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPTLRQWLAARAGPNGIEG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERIPLASM (BY SIMILARITY)
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                          STANDARD;
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37,
40,
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27785 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%;
47.4%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERIPLASMIC (POTENTIAL).
C9582F619FCBA5B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                      component alpha chain (E1))
                                                                                                                                                                                                                                                                                                                                        410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, SPANS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 246;
                                                                                                                                                                                                                                                  (Branched-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 13
       QΥ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             architecture of 2-oxo acid dehydrogenase multienzyme complexes.";
Nat. Struct. Biol. 6:785-792(1999).

-i- FUNCTION: THE BRANCHED-CHAIN ALPHA-KETO DEHYDROGENASE COMPLEX
CATALYZES THE OVERALL CONVERSION OF ALPHA-KETO ACIDS TO ACYL-COA
AND CO(2). IT CONTAINS MULTIPLE COPIES OF 3 ENZYMATIC COMPONENTS:
BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE (E1), LIPOAMIDE
BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE (E1), LIPOAMIDE
ACYLTRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E3).

-i- CATALYTIC ACTIVITY: 3-methyl-2-oxobutanoate + lipoamide = S-(2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                branched-chain-oxoacid and pyruvate dehydrogenases.";
Eur. J. Biochem. 176:311-317(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aevarsson A., Seger K., Turley S., Sokatch J.R., Hol W.G.J., "Crystal structure of 2-oxoisovalerate and dehydrogenase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           putida branched-chain keto acid dehydrogenase operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madhusudhan K.T., Huang G., Burns G., Sokatch J.R.; "Transcriptional analysis of the promoter region of the Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99356017; PubMed=10426958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91008935; PubMed=2211503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-17 FROM N.A.
                                                                                                                                                                                                         Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                             SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                     Brown D., Churcher C.M., Submitted (SEP-1997) to t
                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
                                                                                                                                                                                                                                                                                                        TRMU_SCHPO 013947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Flavoprotéin; Thiamine pyrophosphate; 3D-structure.
SEQUENCE 410 AA; 45268 MW; 0C998460CCFB9CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001017; E1_dh.
Pfam; PF00676; E1_dehydrog; 1.
                                                                            SEQUENCE FROM N.A.
                                                                                                                                              Schizosaccharomycetales;
                                                                                                                                                                                                     SPAC23H4.04
                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                             298 GPSLIEWVTYRAGPH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 172:5655-5663(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GPTLRQWLAARAGPN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methylpropanoyl)dihydrolipoamide + CO(2). COFACTOR: THIAMINE PYROPHOSPHATE.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%;
       , Barrell B.G., Rajandream M.A., Wood V.;
the EMBL/GenBank/DDBJ databases.
S-adenosyl-L-methionine + tRNA = S-adeno
                                                                                                                                                  Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. NO. 52,
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50;
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                            415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 410;
            + tRNA = S-adenosyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 14
PSBC_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chisholm D., Williams J.G.K.;
"Nucleotide sequence of psbC, the
a-binding protein of photosystem
Synechocystis 6803.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-NOV-1990 (Rel. 16, Last seq
16-OCT-2001 (Rel. 40, Last ann
Photosystem II 44 kDa reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Methyltransferase; tRNA processing. 
SEQUENCE 415 AA; 47626 MW; D2B604335B7A935F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                          Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kir
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naru
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroccoccales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P09193; P73749, 
01-MAR-1989 (R6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNY3
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Pfam; PF03054; tRNA_Me_trans; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 298977; CAB11659.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSBC OR SLL0851
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1148;
This SWISS-PROT entry is copyright.
                                                                                                                              EMBO
                                                                                                                               procedure.
EMBO J. 7:
                                                                                                                                                              Dzelzkalns V.A., Bogorad L.;
Dzelzkalns V.A., Bogorad L.;
"Molecular analysis of a mutant defective in photosynthetic oxygen
"Molecular analysis of a complementing clone by a novel screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 10:293-301(1988).
                                    -i- SIMILARITY: BELONGS TO THE PSBB / PSBC FAMILY.
                                                                        PHOTOSYSTEM II. IT IS A CHLOROPHYLL BING -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                                                                                       SEQUENCE OF 1-300 FROM N.A. MEDLINE=88211542; PubMed=3130247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IEGPTLROWLAARAGPNGIEGPTLROW 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TRMU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thiouridylate
                                                                                                            FUNCTION: THE 43 kDa PROTEIN (P6) IS A COMPONENT OF THE CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGVFMRNWLDEDSAPSGC--PAERDW 82
                                                         THYLAKOID MEMBRANE.
                                                                                                                              7:333-338(1988).
                                                                                                                                                                                                                                                                               3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         KOtani H., Tanaka A., Asamizu E., Nakamura
wa M., Sugiura M., Sasamoto S., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reaction center protein (P6 protein) (CP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
                                                                                             CHLOROPHYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene encoding the CP-43 chlorophyll II, in the cyanobacterium
     It is produced through
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                                                                                                                                                                                                                                                                                                                   Sequence determination of the
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                                                                                               BINDING
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       a collaboration
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                             IE18_PRVKA
P33479;
                                                                                                                     enhancer regions.";
Virology 179:365-377(1990).

-i- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.

-i- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.

-i- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
PIR; §
          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as loss as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                               Vlcek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.; "Pseudorabies virus immediate-early gene overlaps with an oppositely oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                           Alphaherpesvirinae; Varicellovirus NCBI_TaxID=33703;
                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M21538;
                                                                                                   -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Pseudorabies virus (strain Kaplan) (PRV)
                                                                                                                                                                                                                                                                                                                                                          Immediate-early protein IE180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Photosynthesis; Photosystem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000932; PSII.
                                                                                                                                                                                                                                                        MEDLINE=91021039; PubMed=2171211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 GETMRFWDFRGPWLEPLRGPNGLDLDKLRNDIQPWQVRRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GPTLR-----QWLAARAGPNGIEGPTLRQ----WLAARA 34
                                                                                                                PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; D90909; BAA17799.1; -. x07018; CAA30071.1; -. S06469; S06469. S02380.
                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                             the Swiss Institute of Bioinformatics and the
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107
160
202
237
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423
423
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162
472 AA;
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(Rel. 28, Last sequence update)
(Rel. 28, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
 6
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291
license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteome
                                                                                                                                                                                                                                                                                                                     RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II; Thylakoid; Chlorophyll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50;
Pred. No.
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NI ) N <-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            1446 AA
                                                                                                                                                                                                                                                                                                                                                                         update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                              EMBL
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                                                              outstation
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Вb

187 GSPGPSAAPRRWSPARGDPVGEPGPAAR 214

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IE18_PRVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                           Matches
                                                  Query Match
                                                                                                                                                      EMBL;
                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudorabies virus (strain Indiana-Funkhauser Viruses; dsDNA viruses, no RNA stage; Herpesvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Phosphorylation; Nuclear protein DOMAIN 347 354 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M34651; AAA47470.1; -. PIR; A45344; A45344.
                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=89315207; PubMed=2546124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alphaherpesvirinae; Varicellovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IE18_PRVIF P11675;
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                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                            Cheung A.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31523;
                                                                                           DOMAIN
                                                                                                       DOMAIN
                                                                                                                  DNA-binding; Phosphorylation; Nuclear protein
                                                                                                                              Early protein;
                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                pseudorabies virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DNA nucleotide sequence analysis of the immediate-early gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immediate-early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 GSPGPSAAPRRWSPARGDPVGEPGPAAR 206
                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GIEGPTL -- RQWLAARAGPNGIEGPTLR 27
                                                                                                                                                                                                                                                                                                               OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION.
                                                                                                                                            S04713;
  GIEGPTL -- RQWLAARAGPNGIEGPTLR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                           X15120;
                           12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1446 AA;
                                                                             1461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 12, Created)
(Rel. 14, Last sequence update)
(Rel. 28, Last annotation update)
                                                                                            958
                                                                                                        390
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                            Conservative
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                                                                                                                                                        CAA33214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Trans-acting factor;
                                                                                                                              Transcription regulation; Trans-acting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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                                      27.3%;
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                                                                              149833 MW;
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Pred. No.
                           2
                                        Pred.
                                                   Score 50;
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                                                                                           POLY-SER
                                                                                                       POLY-SER.
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                            Mismatches
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                                                                              7F31E7ABE403B208 CRC64;
                                          NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1461 AA
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                                                     Length 1461;
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RESULT 16
SETA_ECOLI
ID SETA_ECOLI STANUA...
AC P31675; P75639;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last seque
DT 16-OCT-2001 (Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z22705; CAA80406.1; -.
EMBL; X17252; -; NOT_ANNOTATED_CDS.
PIR; S13578; S13578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RuBisCO operon transcriptional regulator CBBR OR CFXO.
Xanthobacter flavus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                    Transcription regulation; Activator; DNA-binding.
DNA_BIND 22 41 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94012468; PubMed=8407781;
van den Bergh E., Dijkhulzen L., Meijer W.G.;
"CbbR, a Lyskr-type transcriptional activator, is required for
expression of the autotrophic CO2 fixation enzymes of xanthobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and organization of carbon xanthobacter flavus H4-14.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meijer W.G., Arnberg A.C.,
Dijkhuizen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-H4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBBR_XANFL
                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91172133; PubMed=1900916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-150 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hyphomicrobium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                               interPro;
                                                                                                                                                                                         264
                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                        3 IEG-PTLRQWLAARA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 175:6097-6104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE CBB OPER FOR RUBISCO AND OTHER CALVIN CYCLE GENES. BINDS SPEC TWO BINDING SITES IN THE CBBR-CBBL INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                       VEGLPVVRQWLAVRA 278
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                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                   PF00126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genet. 225:320-330(1991)
                                                                                                                                                                                                                                                                                                                                                                              IPR000847; HTH_LysR.
                                                                                                                                                                                                                                                                                                        333 AA;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                HTH_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                         36003 MW;
                                                                                                                                                                                                                                                             27.0%;
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                                                     sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enequist H.G., Terpstra P., Lidstrom M.E.,
                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                               Score 49.5;
Pred. No. 3
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                         9B375B4FB2D1EE73 CRC64;
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SPECIFICALLY TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                   EMBL; D10483; -; NOT_ANNOTATED_CDS. EMBL; AE000117; AAC73181.1; -.
                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION. MEDLINE-99367417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99226230; PubMed=10209755;
Liu J.Y., Miller P.F., Gosink M., Olson E.R.;
"The identification of a new family of sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yura T., Mori H.,
Isono K., Mizobuc
                                                                                                                                    Complete
                                                                                                                                                 Transport;
                                                                                                                                                            Pfam; PF00083; sugar_tr;
                                                                                                                                                                                        EcoGene;
                                                                                                                                                                                                                                                                                                                                               (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   efflux transporters."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugar efflux
SETA OR B0070
  TRANSMEN
                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional and biochemical characterization of Escherichia coli sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu J.Y., Miller P.F., Willard J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 274:22977-22984
FUNCTION: INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                     SPECIFICITY, WITH PREFERENCES FOR GLUCOSIDES ALKYL OR ARYL SUBSTITUENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: INVOLVED IN THE EFFLUX OF SUGARS. THE PHYSIOLOGICAL ROLE MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN TRANSPORT IPTG, LACTOSE AND GLUCOSE. HAS BROAD SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0-2.4 min region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiol.
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proteome.
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1107
1150
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                                                                                                                                                                                        EG11754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Mizobuchi K., Nakata A.;
                                                                                                                                                                        IPR003662; sub_transporter
                                                                                                                                                 Sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                         274:22977-22984(1999).
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                                                                                                                                                transport;
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P21873;
01-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Cloning and sequence analysis of the genes encoding the alpha and beta subunits of the El component of the pyruvate dehydrogenase multienzyme complex of Bacillus stearothermophilus.";
Eur. J. Blochem. 191:337-346(1990).
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01-NOV-1995 (Rel. 32, Last annotation update)
Pyruvate dehydrogenase El component, alpha subunit (EC 1.2.4.1).
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MEDLINE=90345939; PubMed=2200674;
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Bacillus/Staphylococcus group; Geobacillus.
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                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                               Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53560; CAA37628.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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256 EGPTLIETLCFRYGPHTMSGDDPT
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                                                                                                                          Local
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                                               4 EGPTLRQWLAARAGPNGIEG--PT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: THIAMINE PYROPHOSPHATE.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Pyruvate + lipoamide = acetyldihydrolipoamide + CO(2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
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12; Conser
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-> A (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the human gene for lysosomal di-N-acetylchitobiase.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: INVOLVED IN THE DEGRADATION OF ASPARAGINE-LINKED
GLYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCOSAMINE
(1-4)N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END
OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.
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01-JUL-1993 (Rel. 26, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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MEDLINE=92406917; PubMed=1527079;
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PROSITE; PS01095; CHITINASE_18; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu B., Aronson N.N. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Lysosomal.
SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                             600873;
  PTLRQWLAARAGPNGIEGPTLRQWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF085706; AAC35852.1;
AF085700; AAC35852.1;
AF085701; AAC35852.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M95767; AAA35684.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF085703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF085702;
                                                     1 Similarity
11; Conserv
                                                                                                                                                                            Glycosidase; Signal; Lysosome; Glycoprotein.

1 38

BY SIMILARITY

39 385

DI-NACETYLCHITOBIASE.

143 143

PROTON DONOR (BY SIMILARITY).

143 143

PROTON DONOR (BY SIMILARITY).

193 193

N-LINKED (GLCNAC. ...) (POTENTIAL).

228 228

N-LINKED (GLCNAC. ...) (POTENTIAL).

262 262

N-LINKED (GLCNAC. ...) (POTENTIAL).

263 263

N-LINKED (GLCNAC. ...) (POTENTIAL).

264 265

N-LINKED (GLCNAC. ...) (POTENTIAL).
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193
228
262
299
385
                                                        Conservative
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AAC35852.1;
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AAC35852.1;
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                                                        Mismatches
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CNG1_CHIC
                   Query Match
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01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00888; CNMP_BINDING_1; PROSITE; PS00889; CNMP_BINDING_2; PROSITE; PS50042; CNMP_BINDING_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00520; ion_trans; 1.
SMART; SM00100; CNMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molday R.S.; Kaupp U.B.;

"Rod and cone photoreceptor cells express distinct genes cGMP-gated channels.";

Neuron 10.865-877(1993).

1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cyclic nucleotide gated channel, cone photoreceptor, alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X89598; CAA61757.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=93264082; PubMed=7684234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNG1_CHICK
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                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
  Local Similarity
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE PHOTORECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family
                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ion transport; cAMP-binding; Transmembrane; Vision;
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286
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344
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419
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                                                                       85031 MW;
  26.8%;
34.1%;
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TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
Score
Pred.
                                                                                          CAMP (POTENTIAL).
N-LINKED (GLCNAC.
                                                                                                                                          CAMP
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                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
CAMP (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
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DB 1;
76;
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RESULT 22
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DOMAIN
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CHAIN
                                                                                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 use
                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown K.E., Lawrence R., Sonenshein G.E.;
"Concerted modulation of alpha 1(XI) and alpha 2(V) collagen mRNAs bothne vascular smooth muscle cells.";
J. Biol. Chem. 266:23268-23273(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUL-1998 (Rel.
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                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                              EMBL; M82977; AAA30369.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
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207 IEGPPGPAGPAGLMGPPGLQGPT 229
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FUNCTION: MAY PLAY AN IMPORTANT ROLE IN FIBRILLOGENESIS BY FUNCTION: MAY PLAY AN IMPORTANT ROLE IN FIBRILLOGENESIS BY CONTROLLING LATERAL GROWTH OF COLLAGEN II FIBRILS.

SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(XI), ALPHA 2(XI), AND ALPHA 3(XI) ALPHA 3(XI) IS A POST-TRANSLATIONAL MODIFICATION OF ALPHA 1(II). ALPHA 1(V) CAN ALSO BE FOUND INSTEAD OF ALPHA 3(XI)-1(II) (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: BELONGS TO THE FIBRILLAR CLASS OF COLLAGENS. SIMILARITY: HIGH, TO ALPHA 1(V) AND ALPHA 3(V) CHAINS.
                         IEGPTLRQWLAARAGPNGIEGPT
                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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47.8%;
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                                                             Score 49; Ub
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                                                    Pred. No. 94;
2; Mismatches
                                                                                                                                              SHORT NONHELICAL SEGM TELOPEPTIDE.
TRIPLE-HELICAL REGION
                                                                                                                                                                                       NONHELICAL REGION. (INTERRUPTED)
                                                                                                                                   CROSSLINKING
                                                                                                                                                                                                                AMINO-TERMINAL PROPEPTIDE (POTENTIAL).
COLLAGEN ALPHA 1(XI) CHAIN.
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[8]
SEQUENCE OF 1-28 FROM N.A.
SEQUENCE OF 1-28 FROM N.A.
MEDLINE-89071759; PubMed=3200851;
Burbelo P.D., Martin G.R., Yamada Y.;
Burbelo P.D., Martin G.R., Vamada Y.;
"Alpha 1(IV) and alpha 2(IV) collagen genes are regulated bidirectional promoter and a shared enhancer.";
Natl. Acad. Sci. U.S.A. 85:9679-9682(1988).
                                                                                                                                                                                                                           SEQUENCE OF 1-28 FROM N.A.
MEDLIND=89066738; PubMed=3198626;
Kaytes P., Wood L., Theriault N., Kurkinen
"Head-to-head arrangement of murine type IV
J. Biol. Chem. 263:19274-19277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86196099; PubMed=3009468;
Sakurai Y., Sullivan M., Yamada Y.;
"Alpha 1 type IV collagen gene evolved differently from fibrillar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Extensive homology between the carboxyl-terminal peptides of mouse alpha 1(IV) and alpha 2(IV) collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kurkinen M., Condon M.R., Blumberg B., Barlow D., Quinones
Saus J., Pihlajaniemi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87250460; PubMed=3597383;
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complementary DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nath P., Laurent M., Horn E., Sobel M.E., Zon G., Vog "Isolation of an alpha 1 type-IV collagen cDNA clone synthetic oligodeoxynucleotide.";
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Wood L., Theriault N., Vogeli G.;
"CDNA clones completing the nucleotide and derived amino acid
sequence of the alpha 1 chain of basement membrane (type IV) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 147:217-224(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oberbaeumer I., Laurent M., Schwarz U., Sakurai Y., Yamada Y., Vogeli G., Voss T., Siebold B., Glanville R.W., Kuhn K.; "Amino acid sequence of the non-collagenous globular domain (NC1) of "Amino acid sequence of the non-collagenous globular domain (NC1) of the alpha 1(YV) chain of basement membrane collagen as derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85127033; PubMed=2578961;
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agen IV. Differential evolution of collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43:301-304(1986).
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Chem.
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EMBL: J03758; AAA37439.1; --
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EMBL: X06777; CAA29946.1; --
EMBL: M12679; CAAA5132.1; --
EMBL: M14042; AAA37342.1; --
EMBL: M12879; AAA37343.1; --
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EMBL: M13024; -; NOT_ANNOTATED,
EMBL: M13025; AAA37344.1; --
EMBL: M13027; AAA37344.1; --
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EMBL: J04448; AAA374477.1; --
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MEDLINE-88243724; PubMed-3379041;

Killen P.D., Burbelo P., Sakurai Y., Yamada Y.;

Killen P.D., Burbelo P., Sakurai Y., Yamada Y.;

"Structure of the amino-terminal portion of the murine alpha 1(IV collagen chain and the corresponding region of the gene.";

J. Biol., Chem. 263:8706-8709(1988),

-i- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

-i- DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILLITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.

-i- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-i- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                       DISULFID
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NONHELICAL REGION (NC1).

OR 1548 (BY SIMILARITY).

OR 1551 (BY SIMILARITY).

BY SIMILARITY.

OR 1662 (BY SIMILARITY).

OR 1665 (BY SIMILARITY).

OR 1665 (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (PO A -> P (IN REF. 2).

S -> L (IN REF. 2).
                                                                                                                                                                                  AMINO-TERMINAL PROPEPTIDE COLLAGEN ALPHA 1(IV) CHAIN TRIPLE-HELICAL REGION.
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the murine alpha 1(IV)
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01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93338437; PubMed=1307247; Chung-Honet L.C., Parente Christiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christiano A.M., Greenspan D.S., Lee S., Uitto J., "Cloning of human type VII collagen. Complete primary sequence of alpha l(VII) chain and identification of intragenic polymorphisms J. Biol. Chem. 269:20256-20262(1994).
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Mammalia; Eutheria;
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                                                                                                                                                          Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S., Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III; "Noncollagenous (NC1) domain of collagen VII resembles multidomain
                                                                                                                                                                                                                                                                                                                                              Parente M.G., Chung L.C., Bauer E.A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94327588;
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                                                                                                                     adhesion proteins involved in tissue-specific extracellular matrix.";
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  Tanaka
                    TISSUE=Keratinocytes; MEDLINE=92231902; Pub
                                                              SEQUENCE OF 340-675 FROM
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"The carboxyl-terminal half of type VII co collagenous NC-2 domain and intron/exon or corresponding region of the COLTA1 gene.";
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                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96081220; PubMed-8541842; Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Prettibial epidermolysis bullosa: genetic linkage to cidentification of a glycine-to-cysteine substitution in helical domain of type VII collagen."; Hum. Mol. Genet. 4:1579-1583(1995).
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Christiano A.M., Ryynaenen M., Uitto J.;
"Dominant dystrophic epidermolysis bullosa: identification of Gly-->Ser substitution in the triple-helical domain of type VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y., Lin A.N., Dietz H.C., Hovnanian A., Uitto J.; "A missense mutation in type VII collagen in two affected siblings with recessive dystrophic epidermolysis bullosa."; Nat. Genet. 4:62-66(1993).
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                                                                                                        MEDLINE=96220218; PubMed=8644729; Christiano A.M., McGrath J.A., Tan K.C., Uitto J.; Christiano A.M., McGrath J.A., Tan K.C., Uitto J.; Cylique substitutions in the triple-helical region of type VII collagen result in a spectrum of dystrophic epidermolysis bullophenotypes and patterns of inheritance.";
                                                                                                                                                                                                                                                                              Christiano A.M., Morricone A., Paradisi M., Angelo Cavalieri R., Uitto J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93291877; PubMed=8513326;
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"Molecular basis of dystrophic epidermolysis
the type VII collagen gene (CCL7A1).";
Hum. Mutat. 10:338-347(1997).
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Biochem. Biophys. Res. Commun. 183:958-963(1992).
genotype/phenotype
             Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., "Molecular basis of recessive dystrophic epidermolysis b
                                                                                                                                                                                                                                                                                                               MEDLINE=95164985;
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                                             VARIANT RDEB ARG-2575.
MEDLINE-96154068; PubMed-8592061;
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                                                                                                                                                                                                                                                 "A glycine-to-arginine substitution in the triple-helical type VII collagen in a family with dominant dystrophic epi
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21:169-179(1994).
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PubMed=8499916;
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                                                                                                  "Compound heterozygosity for a recessive glycine substitution and
                                                                                                                          Terracina M., Posteraro P., Schubert M., Sonego G., Atzori F., Zambruno G., Bruckner-Tuderman L., Castiglia D.;
                                                                                                                                                                                           MEDLINE=99019477; PubMed=9804332;
                                                                                                                                                                                                                         VARIANT RDEB ARG-1347
                                                                                                                                                                                                                                                                                                               bullosa
                                                                                                                                                                                                                                                                                                                              KOn A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Uitto J., "Novel COL7Al mutations in dystrophic forms of epidermolysis
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98410969; PubMed=9740253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Some, but not all, glycine substitution mutations in COLTA1 result in intracellular accumulation of collagen VII, loss of anchoring fibrils, and skin blistering,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luger T
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Naylor S.L., Kerbacher K., Zimmermann M., Krajci P.,
Gedde-Dahl T. Jr., Bruckner-Tuderman L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS DEB ARG-2009 AND ARG-2043.
MEDLINE=97358588; PubMed=9215684;
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"Influence of the second COL7Al mutation in determining the phenotypic severity of recessive dystrophic epidermolysis bullosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Modulation of disease severity of dystrophic epidermolysis
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Uitto J., Pope F.M., Eady R.A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of 18 new mutations in COLTA1 in
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MEDLINE-96183562; Publ
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                    Invest. Dermatol. 111:744-750(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Bruckner-Tuderman L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao L., Donaldson C.J., Smith G.W., vale W.W.; "The structures of the mouse and human urocortin genes."; Genomics 50:23-33(1998).
                                                                                                                          MOD_RES
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98292491; PubMed=9628819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                      InterPro; IPR000187; CRF.
InterPro; IPR003620; Urocortin_CRF
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                       PTLRQWLAARAGPNGIEGPTLRQW 29
PESSQWSPAAAAATGVQDPNLR-W 43
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RESULT 26
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RESULT 27
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Pfam; PF01391; Collagen; 2.

Pfam; PF01484; Col_cuticle_N; 1.

Pfam; PF01484; Col_cuticle_N; 1.

Cuticle; Connective tissue; Repeat; Multigene family; Collagen.

Cuticle; Connective tissue; Repeat; Multigene family; Collagen.

TRIPLE-HELICAL REGION.

DOMAIN 171 231 TRIPLE-HELICAL REGION.

DOMAIN 237 299 TRIPLE-HELICAL REGION.

DOMAIN 237 299 TRIPLE-HELICAL REGION.

CONFLICT 158 158 V -> A (IN REF. 2).

CONFLICT 328 238 G -> R (IN REF. 2).
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MEDLINE-89028667; PubMed=3180220;
Kramer J.M., Johnson J.J., Edgar R.S., Basch C., Roberts S.;
"The sqt-1 gene of C. elegans encodes a collagen critical for organismal morphogenesis.";
Cell 55:555-565(1988).
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cuticle collagen sqt-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

-i- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as its content use as long as its content use as long as its content use as long as long as its content use as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as lon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J03146; AAA65468.1;
EMBL; Z49907; CAA90084.1;
PIR; A31920; A31920.
WormPep; B0491.2; CE02104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
      Q9YFT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002486; Col_cuticle_N.
InterPro; IPR000087; Collagen.
                              SYK_AERPE
                                                                                                                                                                              270 GPEGPSGKQ---GRQGPDGTQGET 290
                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                    2 GIEGPTLRQWLAARAGPNGIEGPT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: THIS IS A COLLAGEN CRITICAL FOR ORGANISMAL MORPHOGENESIS MUTATIONS IN SQT-1 CAN LENGTHEN, SHORTEN, OR HELICALLY TWIST THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO OTHER COLLAGENS. COLLAGENS. ROL-6 AND SQT-1 BELOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND MAY ALSO PHYSICALLY INTERACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENTIRE ANIMAL.
                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                              Conservative
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                            26.5%;
45.8%;
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                                                                                                                                                                                                                                                                                                                         Score 48.5;
Pred. No. 3
                                    PRT;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRONG,
                                          562 AA
                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                    Length 324;
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tent is in
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _BP434
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-!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crenarchaeon, Aeropyrum pernix K1."; DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYSS OR APE0161.
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                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12,
01-AUG-1990 (Rel. 15,
01-OCT-1996 (Rel. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99310339; PubMed=10382966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeropyrum pernix
                                                                                                                                                                               Bacteriophage HK022.
Viruses; dsDNA virus
Lambda phage group.
                                                                                                                                                                                                                                                                                                                                              SIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P11683; P16408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prosite; ps00178; AA_TRNA_LIGASE_I; FALSE_NEG
Aminoacyl-tRNA synthetase; Protein biosynthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP000058; BAA79072.1; -
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MEDLINE=91346141; PubMed=1715186
                                       SPECIES=Phage
                                                                           SEQUENCE FROM N.A.
                                                                                                                                           Lambda phage group NCBI_TaxID=10712,
                                                                                                                                                                                                                                                                                                      Bacteriophage 434, and
                                                                                                                                                                                                                                                                                                                                                                                  Excisionase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VXIS_BP434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001412; tRNA-synt_I
InterPro; IPR002904; tRNA-synt_lys_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 GFEPPEGVWYEWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GIEGP--TLRQWLAARAG-----PNGIEGPTLRQWL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-lysyl-tRNA(Lys)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                              dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305
562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 "
309 "
; 65114 MW;
                                                                                                                                                       10742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.5%;
34.2%;
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Last annotation update)
(EC 6.1.1.6) (Lysine--tRNA ligase) (LYSRS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
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                                                                                                                                                                                                                              RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ت.
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"KMSKS" REGION.
; 753664E2937FBF27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48.5;
Pred. No. 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                         21-JUL-1986
21-JUL-1986
01-AUG-1992
                                                                                                  SEQUENCE FROM N.A.

MEDLINE-83189071; PubMed-6221115;
Sanger F., Coulson A.R., Hong G.F., Hill D.F., Pe
Sanger F., Coulson Dacteriophage lambda DNA.
    Nucleic Acids
               overlap of the int and
                  "DNA sequence of the int-xis-Pi region of
                                         Davies R.W.;
                                                    MEDLINE=81053845; PubMed=6253947;
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                          Lambda phage group. NCBI_TaxID=10710;
                                                                                                                                                                                                     Viruses;
                                                                                                                                                                                                                   Bacteriophage lambda
                                                                                                                                                                                                                                           Excisionase
                                                                                                                                                                                                                                                                                                 P03699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                              VXIS_LAMBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89342457; PubMed-2547971; Yagil E., Dolev S., Oberto J., Kislev N., Ramaiah N., Weisber "Determinants of site-specific recombination in the lambdoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are conserved in bacteriophages 434 and lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Limberger R.J., Campbell A.M.; "Functional elements of DNA upstream from the integrase operon that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=Phage 434;
MEDLINE=88167849; PubMed=2965063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker J., Limberger R., Schneider S.J., Campbell A.; "Recombination and modular exchange in the genesis of new lambdoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-64 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phages
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                                                                                                Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iphage HK022. An evolutionary change in specificity."
wol. Biol. 207:695-717(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: EXCISIONASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE ATT SITE.
                                                                                                                                                                                                                                                                                                                                                                             TLQEWNARQRRPRSLE--TVRRWV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S06533; S06533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M60848; AAA67901.1; -. X51962; CAA36222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61:135-144(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCTION: EXCISIONASE AND INTEGRASE ARE NECESSARY FOR THE PROPHAGE FROM THE HOST GENOME BY SITE-SPECIFIC RECOMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                    dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA;
                                                                                                                                                                                                                                                         (Rel.
                                                                                                                                                                                                                                                                   (Rel. 01, Created) (Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
    Res.
                                                                                            162:729-773(1982).
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                     01, Last sequence update)
23, Last annotation update)
and xis genes.";
8:1765-1782(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding.
R635 MW; 0E6A4843503344AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%;
                                                                                                                                                                                                    no
                                                                                                                                                                                                 RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                          72 AA.
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                      the bacteriophage lambda;
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                                                                                                                  Petersen
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                                                       use by non-profit institutions as long as its content is in no entities requires a license agreement (See http://www.inha...
                                                                                                                                                                                                                                                     MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
16-OCT-2001
16-OCT-2001
                 EMBL; AE004289; AAF95321.1; TIGR; VC2176; -.
Hypothetical protein; Complete proteome.
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                 Nature 406:477-483(2000).
                                                                                                                                                                                                                        cholerae.
                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                    Salzberg S.L
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=EL TOR N16961 / SEROTYPE 01;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein VC2176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA recombination; SEQUENCE 72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is prouved the Swiss Institute of Bioinformatics and the between the Swiss Institute of Bioinformatics are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoess R.H., Foeller C., Bidwell K., Landy A.; "Site-specific recombination functions of bacteriophage lambda: sequence of regulatory regions and overlapping structural genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A04321; RSBPXL
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MEDLINE=80234646; PubMed=6446713;
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FUNCTION: EXCISIONASE AND INTEGRASE ARE NECESSARY FOR THE EXCISION
OF PROPHAGE FROM THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION AT
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R605 MW; 0E6A4843502200AA CRC64;
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37.5%;
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                                                                    (See http://www.isb-sib.ch/announce/
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Result
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Maximum Match 100%
Listing first 45 summaries
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Sp_bacteria

Sp_fungl:*

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                                                                                                                                                                                                                                                                                                                                                                           Score
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Q918d4 polyangium
Q955e5 streptomyce
Q9v82 drosophila
Q20968 caenorhabdi
Q20968 caenorhabdi
Q20968 phasianus
Q91988 phasianus
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Q15177 homo sapien
Q26639 strongyloce
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Q96hc0 homo sapien	Q96HC0	4	591		51	45
Q18756 caenorhabdi	Q18756	S	589	27.9	51	44
Q9x757 klebsiella	Q9X757	N	381		51	43
Q943t6 oryza sativ	Q943T6	10	366		51	42
P95613 rhizobium g	P95613	N	326		51	41
Q9rk51 streptomyce	Q9RK51	2	322		51	40
005576 mycobacteri	005576	16	306		51	39
comamonas t	Q93PS5	Ν	289		51	38
0	OQUYEQ	17	281		51	37
Q93ji8 streptomyce	Q93JI8	N	264		51	36
caenorhabdi	Q20967	S	215	•	51	5
3 lagopus la	Q919U3	13	390		51.5	34
2	Q919U2	13	243		51.5	ω ω
Q91096 streptomyce	Q9L096	N	1349		52	32
Q9x7n5 streptomyce	Q9X7N5	N	396		52	31
061518 caenorhabdi	061518	Ŋ	230	-	52	30
Q20964 caenorhabdi	Q2096 <b>4</b>	ഗ	214		52	29
	Q96C78	4	814		52.5	28
ß	Q9RK76	N	539		52.5	27
	Q94LX0	10	333		52.5	26
	Q91907	13	1820		53	25
Q07563 mus musculu	Q07563	11	1433		53	24
Q9kzd5 streptomyce	Q9KZD5	N	967		<u>σ</u>	23
Q9rte6 deinococcus	Q9RTE6	16	326		53	22
	Q9S0M9	N	305	•	53	21
	091477	16	371		53.5	20
	091986	13	246		w ,	19
	Q919T0	13	246		53.5	18
Q9i872 phasianus c	Q91872	13	246		ω ·	17

## ALIGNMENTS

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Matches 13;	atc cal	SEQUENCE		Pfam; PF00		InterPro;	InterPro;	TIGR; TP0421;	EMBL; AEO(	Science 28	spirochete.";	"Complete	Venter J.C.;	Hatch B.,	McDonald I	Khalak H.,	Sodergren	Dodson R.,	Fraser C.N	MEDLINE=98	STRAIN-NICHOLS;	SEQUENCE FROM N.A	[1]	NCBI_TaxID=160;	Bacteria;	Treponema	TP0421.	CONSERVED	01-DEC-2001	01-NOV-1998	01-NOV-1998	083436;	36	CT 1
Conservative	milarity	683 AA;	proteome.	ς.	PF01436; NHL;	IPR001440;	InterPro; IPR001258;	121;	EMBL; AE001220; AAC65409.1;	Science 281:375-388(1998).		"Complete genome sequence	:.	Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,	McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,	Khalak H., Richardson D., Howell J.K., Chidambaram M.,	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,	Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,	Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G	MEDLINE=98332770; PubMed=9665876;	CHOLS;	FROM N.A.		)=160;	Spirochaetales;	pallidum.		Η,	_		)8 (TrEMBLrel.	FREDERIKANI	DEST TMIN	
	4 4	74518 MW;		1.		TPR.	NHL.		5409.1;	1998).		quence of		Roberts F	1 P., Bown	on D., Hov	um J.M., N	Hickey E	S.J., Wei	1bMed=9665								PROTE	19,	, 80	08,	PIKI,	DV.	
3; Mismacches	4 G								•			of Treponema pallidum,		(., Sandu	nan C., Co	ell J.K.	icLeod M.	E.K., Clay	nstock G	876;					Spirochaetaceae;					Last seque	Created)	77.1		
	16	F91407FA7094AAD1 CRC64;										ı pallidu		sky M., W	otton M.D	, Chidamb	e., Salzb?	ton R.,	.M., Whit										annotation update)	sequence update)		200	683 22	
12; Indets	Le	1 CRC64;										the		eidman J.,	., Fujii C	aram M., U	erg S., Pe	Ketchum K.	e O., Sutt					,	Treponema.				date)	te)				
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Q9S5E5;
Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2000
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01-OCT-2000
01-OCT-2000
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SC9H11.15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORF1,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                         STRAIN=A3(2);
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                                                                                                                                                                                                                                                          STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Umeyama T., Ping Chin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
NCBI_TaxID=1902;
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STRAIN=A3(2);
                          SEQUENCE FROM N.A.
                                                                              Submitted (MAY-2000)
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           "Multicopy suppressor gene Submitted (SEP-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20130945; PubMed=10662695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyangium cellulosum
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(TrembLrel. 13, Last sequence update)
(TrembLrel. 15, Last annotation update)
ORF3, ORF4, ORF5 GENES, COMPLETE CDS (PUTATIVE DNA-BINDING
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e of afsR mutant.";
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EMBL/GenBank/DDBJ databases.
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Devinglista C.C., Ferraz C., Ferrara S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai S.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue R C. Siden-Kiangs T. Simson M. Sknevi M. Schreit M.
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
CG7479 PROTEIN.
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509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VZ82;
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"A set of ordered cosmids and a detailed genetic and physical map
"A set of ordered cosmids and a detailed genetic and physical map
"A set of ordered cosmids and a detailed genetic and physical map
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13,
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Last annotation update)
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Pred. No.
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"The genome sequence of Drosophila melanogaster.";

Escience 287:2185-2195(2000).

R EMBL; AE003482; AAF47943.1; -.

R FlyBase; FBgn0035576; CG7479.

R InterPro; IPR002300; tRNA-synt_1a.

R InterPro; IPR002300; tRNA-synt_1.

R InterPro; IPR002302; tRNA-synt_1.

R InterPro; IPR002302; tRNA-synt_1.

R Pfam; PF00133; tRNA-synt_1; 1.

R Pfam; PF00133; tRNA-synt_1; 1.

R PFAM; PF00133; TRNA-SYNTHLEU.

R PGSITE; PS00178; AA_TRNA_LIGASE_I; 1.

SEQUENCE 869 AA; 99299 MW; E87ALECBEBB27B67 CRC64;
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Best Local
                                                                                                01-JAN-1998
01-JAN-1998
01-DEC-2001
Petunia hybrida (Petunia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

NCBI_TaxID=4102;

[1]
                                                                                                                                   024514
024514;
                                                                          AN11.
                                                                                                                                                                                                                                                                                                      Investigating biology.";
Science 282:2012-2018(1998).
EMBL; 273427; CAA97801.1; -.
SEQUENCE 214 AA; 23089 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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Gremblrel.
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(TrEMBLrel.
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Caenorhabditis.
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Last sequence update)
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                                                                                                                                                                                                                                                                               Score 58;
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                                                                                                                                                                                                                                                                                                       F41992EC471FF165 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ABC7 PRELIMINARY;
Q9ABC7;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97336075; PubMed-9192870; de Vetten N., Quattrocchio F., Mol J., Koes R.; "The anll locus controlling flower pigmentation in petunia encodes novel WD-repeat protein conserved in yeast, plants, and animals."; Genes Dev. 11:1422-1434(1997).

-i- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                           Complete proteome. SEQUENCE 361 AA;
                                                                                                                                                   InterPro; IPR002524; Cation_efflux.
InterPro; IPR002395; Kininogen.
Pfam; PF01545; Cation_efflux; 1.
                                                                                                                                                                                               TIGR; CC0303;
                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 19089 / CB15;
MEDLINE=21173698; PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                              Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
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                                                                                                                                         PRINTS; PR00334; KININOGEN.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 337 AA; 37857 MW; 7024CAED
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STRAIN=CV V26; TISSUE=COROLLA;
266
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                          12 LAARAGPNGIEGPTLRQWLAAR 33
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LALDATPRGIDTQKVRDWLAAR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGDDGQALIWELPTVAGPNGIDPMSMYSAGAEINQLQWSPAQRDWIA 325
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                                                        12;
                                                                     Similarity
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                                                      Conservative
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                                                                                                           38180 MW; 1A4F7F0A7C62EEB0 CRC64;
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Pred. No.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   Dimcheff D.E., Drovetski S.V., Krishnan M., Mindell D.P., "Cospeciation and horizontal transmission of avian sarcoma leukosis virus gag genes in galliform birds."; J. Virol. 74:3984-3995(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20219390; PubMed=10756010;
MEDLINE=20219390; Provetski S.V., Krishnan M., Mindell D.P.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                          Pfam; PF02813; Retro_M;
                                                                                                                                                                                                                                                                                                                   HSSP;
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     GGIEGPTLRQWLAARAG-PNGIE-
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InterPro; IPR002923; Chitin_synth.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onygenales; mitosporic Onygenales; paracoccidioides NCBI_TaxID=121759;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
              Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases EMBL; AB000519; BAA19135.1; -. IPR001575; Oxid_FAD_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=20210320; PubMed=10746225;
Nino-Vega G.A., Munro C.A., San-Blas G., Gooday G.W., Gow N.A.;
"Differential expression of chitin synthase genes during temperature-
induced dimorphic transitions in Paracoccidioides brasiliensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHITIN SYNTHASE
                                                                                                                                  SEQUENCE FROM N.A. STRAIN=H-7775;
                                                                                                                                                                                                                                                                                                            01-MAY-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                            P97011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brasiliensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                         Hiraga K., Eto T.,
                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                   Streptomyces sp
                                                                                                                                                                                                                                                                                            SORBITOL OXIDASE.
                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nino-Vega G.A.,
InterPro; IPRO
Pfam; PF01565;
                                                                                                                                                                                        NCBI_TaxID=1931;
                                                                                                                                                                                                             Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 GGPEGEGVATSLAGRDGPPRGVEQRAEPGCPDSAPGPALTDWVRIR 223
                                                                                             'Cloning of a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVNTWLTAASPGPNGEVGGTIDADLARRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycol. 38:31-39(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pF03142; Chitin_synth_2; 1.
pF00063; myosin_head; 1.
; SM00242; MYSC; 1.
TE; PS00079; MULTICOPPER_OXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                         Tes sp.

Firmicutes; Actinobacteria; Actinobacteria;

Streptomycetaceae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1744 AA;
                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
FAD_binding_4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San-Blas G.;
sis of the CHS4 gene of Paracoccidioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MULTICOPPER_OXIDASE1; UNKNOWN_1.
A; 193777 MW; DB7622D0A69F0705
                                                                                             encoding
                                                                                                                 Yoshioka
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Last annotation updat
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Pred. No. 1.5e+02
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                                                                                             sorbitol oxidase from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                 Oda K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB7622D0A69F0705 CRC64;
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RESULT 13
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Best Local Similarity
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01-JUN-2001 (Trembirel. 1

01-JUN-2001 (Trembirel. 1

P0416G11.19 PROTEIN.

P0416G11.19.
                    "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1. clone:P0416G11.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002968; BAB39267.1; -.
SEQUENCE 250 AA; 26094 MW; 617AB53A7738C4B7 CRC64;
                                                                                                    Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzae; Oryza. NCBI_TaxID=4530;
                                                                                                                            Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97442537; PubMed=9295275; Coyne K.J., Qin X.X., Waite J.H.; Coyne K.J., Qin X.X., Waite J.H.; "Extensible collagen in mussel byssus: A natural block copolymer."; Science 277:1830-1832(1997).
Science 277:1830-1832(1997).
EMBL; AF015539; AAB80719.1; -.
                                                                Sasaki T., Matsumoto T.,
                                                                        STRAIN-CV.
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                     Q9AS26
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Signal; Collagen.
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
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01-DEC-2001
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                                                                                                                                                                                                                                                525 GPKGPTGAQGPAGPAGPSGEQGP 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 GPVGOVWLKORVGDEGARSVMPAEWLGAR 243
                                                                                                                                                                                                                                                                  2 GIEGPTLRQWLAARAGPNGIEGP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                        21
902 AA;
                                                                          NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 AA;
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                      Conservative
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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902 C
78526 MW;
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52.2%;
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  29.5%; Score 54;
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17,
17,
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                                                                Yamamoto K.;
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Last annotation update)
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Pred. No. 89;
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                                                                                                                    Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                     Mismatches
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  10;
                                                      chromosome 1,
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Length 250;
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Q15177
В
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Q9I3U4
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Best Local :
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Best Local Similarity
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Q913U4;
01-MAR-2001 (TrEMBLrel. 16, Crei
01-MAR-2001 (TrEMBLrel. 16, Lasi
01-DEC-2001 (TrEMBLrel. 19, Lasi
PROBABLE PYRUVATE CARBOXYLASE.
                             Q15177 PRELIMINARY; PRT; 1366 AA. Q15177; O1 NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update) PREPRO-ALPHA2(1) COLLAGEN PRECURSOR.
  Homo sapiens (Human Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00364; biotin_lipoyl; 1.
Pfam; PF01039; CarboxyL_trans; 1.
Pfam; PF01289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00188; BIOTIN; 1.

PROSITE; PS00867; CPSASE 2; UNKNOWN_1.

PROSITE; PS00025; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

Biotin; Complete proteome; Pyruvate.

SEQUENCE 1095 AA; 116876 MW; 34370FB8BEC201AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K. S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000901; CPSase.
InterPro; IPR001064; Crystallin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AE004569; AAG04789.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 GARGPGPREWGPCGSLTVHGGPGAPGLTPAGAVGPTRQLHLRARA 87
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                                                                                                                                                                                                                                                                IEGGGLGRFAAEEVGPTGVQGP 807
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                         (Human)
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Chordata; Craniata;
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; Biotin_lipoyl.
; Carboxyl_trans.
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45.5%;
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                                                                                                                                                                                                                                                                                                                                                Score 54; DB 10, Pred. No. 1.5e+02;
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Vertebrata; Euteleostomi;
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                                                                 update)
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Makela J.K., Vuorio T., Vuorio E.;
"Growth-dependent modulation of type I collagen
levels in cultured human skin fibroblasts.";
Biochim. Biophys. Acta 1049:171-176(1990).
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Biochem. J. 252:633-640(1988).
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                    SEQUENCE FROM N.A.
MEDLINE=92348411; PubMed=1639795;
Exposito J.-Y., D'Alessio M., Solursh M., Ramirez F.;
"Sea urchin collagen_evolutionarily homologous to ver
                                                                                                                                                                                           Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
Echinoidea; Euechinoidea; Echinocea; Echinoida; S
                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
ALPHA-2 COLLAGEN.
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SIGNAL 1
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Pfam; PF01391; Collagen; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-97169389; PubMed=9016532;
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alpha-2(I) collagen.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Organization of the human pro-alpha2(I) collagen J. Biol. Chem. 262:16032-16036(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dalgleish R.;
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Q91872;
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proDom; pD002078; Fib_collagen_C;
smarr; sm00038; colf1; 1.
smarr; sm00214; vwc; 1.
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"Novel amino-terminal propeptide configuration in a fibrillar
procollagen undergoing alternative splicing.";
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[2]
SEQUENCE FROM N.A.
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InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWFC.
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J. Biol. Chem. 267:17404-17408(1992).
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01-DEC-2001
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178
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GGPEGEGVATSLAGRDGPPRGVEQRAEPGCPDSAPGPALTDWARIR 22:
                     GGIEGPTLRQWLAARAG-PNGIE------
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25008 MW;
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Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
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RESULT Q919T0

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Q919S6
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                                                                                                                             Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Dimcheff D.E., Drovetski S.V., Krishnan M., Mindell D.P., "Cospeciation and horizontal transmission of avian sarcoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                           NON_TER
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                                                                                                                                                                                                                                                     Polyprotein.
                                                                                                                                                                                                                                                                       Pfam; PF02813; Retro_M;
                                                                                                                                                                                                                                                                                                                                                   EMBL; AF225389; AAF64759.1;
                                                                                                                                                                                                                                                                                                                                                                     leukosis virus gag genes in galliform J. Virol. 74:3984-3995(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20219390; PubMed=10756010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phasianus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q919S6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q919T0;
Q919T0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF225383; AAF64753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02813; Retro_M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phasianus colchicus (Ring-necked pheasant).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GGPEGEGVATSLAGRDGPPRGVEQRAEPGCPDSAPGPALTDWARIR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9054;
1 GGIEGPTLRQWLAARAG-PNGIE-------GPTLRQWLAAR 33
                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGIEGPTLRQWLAARAG-PNGIE------GPTLRQWLAAR 33
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Pro; IPR004028; Retro_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                              IPR004028; Retro_M.
                                                                                                                                                                              246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
246 AA;
                                                                                                                                                                                                      246
                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                              1A6S.
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                                                                                                                                                                         25028 MW;
                                                                                                29.2%;
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                                                                      2; Mismatches 15; Indels
                                                                                                Score 53.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2,
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                                                                                                                                                                    25723F7101FE374A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                    birds.";
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                                                                                                34;
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                                                                                                                  DB 13; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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Q9S0M9
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Q91477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                   Kitayama S., Kikuchi M., Funayama T., Narumi I., Watanabe H.; "Cloning of structural gene of an alternative incision enzyme for DNA damage in Deinococcus radiodurans."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004556; AAG04656.1;
InterPro; IPR000205; NAD_binding.
Hypothetical protein; Complete proteome.
SEQUENCE 371 AA; 39174 MW; 016D60440BAD50D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-2043737; Pubbed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hanocck R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                 Endonuclease
                                                                                                                                                                                                                                                                          EMBL; AB033747; BAA85759.1;
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-KR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UV-ENDONUCLEASE
        228
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; eMOSeO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN PA1267
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01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9I477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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                                                                                                                                            Local
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                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGIEGPTLRQWLAARAGP-----NGIEGPTLR----QWLAARA 34
EDPSVREWVLRARATWOPPEWQVVHLSNGIEGPODRR 264
                                                   EGPTLRQW-LAARAG------PNGIEGPTLRQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermus/Deinococcus group; Deinococcales; Deinococcus
                                                                                                                                                                                                                    305 AA;
                                                                                                             Conservative
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                                                                                                                                                                                                                    33592 MW;
                                                                                                                                    29.0%;
40.5%;
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29.8%;
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16, Last sequence update)
19, Last annotation update)
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Last annotation update)
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                                                                                                                                      Pred. No.
                                                                                                                                                             Score 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53.5; DB 16; Length 371; Pred. No. 53;
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                                                                                                       Mismatches
                                                                                                                                                                                                                 B94D333243E2FEA4 CRC64;
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                                                                                                                                                             DB 2;
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                                                                                                                                                           Length 305;
                                                                                                       Indels
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                                                                                                    Gaps
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RESULT 23

Q9KZD5

ID Q9KZD

AC Q9KZD

DT 01-QC

DT 01-QC

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Q9RTE6
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE=2036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
UV DAMAGE ENDONUCLEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002022; AAF11370.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR1819
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Endonuclease; Complete proteome.
SEQUENCE 326 AA; 35693 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KZD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9KZD5;
                                                                                                                                                                                                              Submitted (APR-2000) to the
                                                                                                                                                                                                                                      Thomson N.R., Parkhill J., Barrell B.G.,
                                                                                                                                                                                                                                                           STRAIN=A3(2);
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2000)
                                                                                                                                                                                                                                                                                                                                                                    Saunders D.C.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
                     "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and
                                                     Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
                                                                                                           MEDLINE=97000351; PubMed=8843436;
                                                                                                                                        STRAIN=A3(2
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 EGPTLRQW-LAARAG------PNGIEGPTLRQ
     8 Mb Streptomyces coelicolor
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(TrEMBLrel. 13, Last
(TrEMBLrel. 16, Last
NDONUCLEASE, PUTATIVE.
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to the EMBL/GenBank/DDBJ databases
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Last annotation updat
I COMPLEX, SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                              Barrell B.G., Rajandream M.A.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
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             A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycetaceae;
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SUBUNIT.
             chromosome
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                                                                                        Eichner A.,
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                                                                                           Cullum J.,
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                                  physical map
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RESULT 24
Q07563
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-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AL353870; CABB9015.1; -
Interpro; IPR001750; Oxidored_q1.
Pfam; PF00361; Oxidored_q1; 1.
NAD; Oxidoreductase; Transmembrane.
Q9I907
Q9I907;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q07563 PRELIMINARY; PRT; 1433 AA.
Q07563;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROCOLLAGEN, TYPE XVII, ALPHA 1 (BULLOUS PEMPHIGOID
                                                                                                                                                                                                                                                                                                              MEDITINE-9332041; PubMed-8473327;
Li K., Tamai K., Tan E.M., Uitto J.;
Cloning of type XVII collagen. Complementary and genomic DNA
"Cloning of type XVII collagen. Complementary and genomic DNA
sequences of mouse 180-kilodalton bullous pemphigoid antigen (BPAG2)
predict an interrupted collagenous domain, a transmembrane segment,
and unusual features in the 5'-end of the gene and the 3'-untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COL17A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP180) (COLLAGEN XVII).
                                                                                                                                                                                                                                                                         EMBL; L08407; AAA37443.1; -. MGD; MGI:88450; Col17a1.
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                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                  InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 5.
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                                                                               25
                                                                                                                                                                                   Local
                                                                                                                                             2 GIEGPTLRQWLAARAGPNGIEGP 24
                                                                                                                                                                                                                                                                                                     BULLOUS PEMPHIGOID (BP).
                                                                                                                    GMEGPIGQRGLAGPMGPRGEPGP
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                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                       Cell adhesion
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                                                                                                                                                                                                                        1433 AA;
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    (Tremblrel. 15, Created)
(Tremblrel. 15, Last seq
(Tremblrel. 19, Last ann
                                                                                                                                                                        Conservative
                                                     PRELIMINARY;
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Rodentia;
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                                                                                                                                                                                                                           144087 MW;
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  Last sequence update)
Last annotation update)
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Pred. No. 1.7e+02;
                                                                                                                                                                                    Score 53; DB 11;
Pred. No. 2.6e+02;
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Sciurognathi; Muridae;
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                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                            B8F808832A19922C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae;
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(TrEMBLrel.

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Q9RK76
            RESULT 27
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01410; COLFI; 1.
Pfam; PF02210; TSPN; 1.
Pfam; PF0022078; Fib_collagen_C; 1
SMART; SM00038; COLFI; 1.
SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                     Perilla frutescens.

Perilla frutescens.

Perilla frutescens.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; perilla.

Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AB059642; BAB58883.1; -. SEQUENCE 333 AA; 36844 MW; A52E156D6843C8AA CRC64;
                                                                                                                                                                                                                "A WD-repeat-containing putative regulatory protein in anthocyanin biosynthesis in Perilla frutescens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1400 GKTGPVGPQGLAGKAGPEGLRG 1421
                                                                                                                                                                                                                                               Sompornpailin K., Makita Y., Yamazaki M.,
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE REGULATORY PROTEIN IN ANTHOCYANIN BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q94LX0
                                                  276 GDDGQSLLWELPTVAGPNGIDPMTMYSAGAEINQLQWSAAQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain of red seabream.";
Biochim. Biophys. Acta 1517:323-326(2001).
EMBL; AB045975; BAB03287.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21240220; PubMed=11342118;
Touhata K., Tanaka H., Yokoyama Y., Sakaguchi M., Toyohara H.;
"Structure of a full-length cDNA clone for the pro-1(V/XI) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Crañiata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000885;
InterPro; IPR001791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000087; Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sparidae; Pagrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO-ALPHA 1 TYPE V/XI COLLAGEN. COLV/XIA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=143350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pagrus major (Red sea bream) (Chrysophrys major)
                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                              2 GIEGPTLROWLAARAGPNGIEGPTL-----ROWLAAR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GIEGPTLRQWLAARAGPNGIEG 23
                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1820 AA; 181678 MW;
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                     36844 MW; A52E156D6843C8AA CRC64;
                                                                                                                              28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fib_collagen_C.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prenyltn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.0%;
                                                                                                                                          Score 52.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53;
Pred. No.
                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46E45E8AF7AD3DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AA
                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 1820;
                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                 Saito K.;
                                                                                                            12;
                                                                                                                                         Length 333;
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RESULT 28
Q96C78
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             Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96C78;
                                                                                                                                                                             Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TremBLrel. 19, Created)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 15 (METARGIDIN).
                                                                                                                 SEQUENCE
                                                                                                                                                               EMBL; BC014566; AAH14566.1;
                                                                                                                                                                                                                                        TISSUE-KIDNEY, AND RENAL CELL ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00728; Glyco_hydro_20; 1.
Pfam; PF02838; Glyco_hydro_20b; 1.
PRINTS; PR00738; GLHYDRLASE20.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 539 AA; 58624 MW; 0861929C641DAC56 (
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001540; Glyco_hydro_20.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; ALIJ2662; CAB59591.1; .
HSSP; P06865; 1QBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerdeno A.M., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 GGDEVPT-TEWELSPAARARAREGLAGPRALHPWFIAR 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE BETA-HEXOSAMINIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RK76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGIEGPTLRQW-----LAARAGPNGIEGP-TLRQWLAAR 33
                                     Similarity
                                                                                                                 814 AA;
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                         87717 MW;
                             28.7%;
44.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.7%;
                                   Score 52.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrell B.G.,
          6;
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                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
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                                                                                                            683A8368AD30996B CRC64;
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          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814 AA
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                             .6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1e+02;
                                                   DB 4; Length 814;
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  Indels
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728 LKGPTC-QYRAAQSGPSERPGPPQRALLA 755

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RESULT 30
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                        O61518 PRELIMINARY; PRT; 230 AA.
O61518: PRELIMINARY; PRT; 230 AA.
O61518: O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 25.8 KDA PROTEIN.
F17E9.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform investigating biology.", Science 282:2012-2018(1998).
EMBL; Z73427; CAA97797.1; -.
SEQUENCE 214 AA; 23608 MW; 63C30FDE325049F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q20964
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           none;
                                                "The sequence of C. elegans cosmid F17E9.";
Submitted (MAR-1998) to the EMBL/GenBank/DD
                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                        STRAIN-BRISTOL N2;
                                                                                                                               Science 282:2012-2018(1998).
                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
             STRAIN-BRISTOL N2;
                          SEQUENCE FROM. N.A.
                                                                            Woessner J.;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                     Vone;
                                                                                                                                                                                                                                                                                                                                                                                                                                    186 GGWSRPTIHQWEGTTTGPCGV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGIEGPTLROWLAARAGPNGI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.4%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                    EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
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Waterston R.;

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Search completed: Octol
Job time: 13.266 secs
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                                                                                                           Query Match
Best Local Similarity
"hes 9; Conserva"
                                                                                                                                                                                "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF047656; AACO5110.1; -.
Interpro; IPR003006; Ig_MHC.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 230 AA; 25772 MW; 48DB7079872B9432 CRC64;
                                                            202 GGWKKPTIHQWHGTTKGPCGV 222
                                                                                            1 GGIEGPTLROWLAARAGPNGI 21
                                                                                                                          Conservative
                 October
                                                                                                                                      28.4%;
                   9, 2002, 09:03:07
                                                                                                                           ω
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                                                                                                                                        Score 52; DB 5;
Pred. No. 49;
                                                                                                                             Mismatches
                                                                                                                             9;
                                                                                                                                                        Length 230;
                                                                                                                               Indels
                                                                                                                               0;
                                                                                                                             Gaps
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Max.

Listing II..

A_Geneseq_032802:*

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747574 segs, 111073796 residues
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194
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Copyright (c) 1993 - 2002 Compus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

Result No.	Score	Query	Query Match Length DB	DB	ID	Description
1	194	100.0	36	21	AAB16963	TPO-mimetic peptid
2	194	100.0	36	21	AAB17293	TPO-mimetic peptid
ω	194	100.0	36	21	AAY96525	Thrombopoietin mim
4	194	100.0	41	21	AAY96528	Thrombopoietin mim
ഗ	194	100.0	42	21	AAB17281	TPO-mimetic peptid
0	194	100.0	42	21	AAB17282	TPO-mimetic peptid
7	194	100.0	42	21	AAB17308	Synthetic TMP-TMP
8	194	100.0	42	21	AAY96530	Thrombopoietin mim
9	194	100.0	60	21	AAB17311	Synthetic TMP-TMP-
10	194	100.0	269	21	AAB16960	TMP-TMP-FC protein
11	194	100.0	269	21	AAY96531	Human IgG1 FC TMP

44 44 45	38 39 40	35 35 37	30 31 32	22 22 23 24 28	16 17 18 19	12 13 14
131.5 129.5 129.5 129.5 125.5	144 144 138.5 132	164.5 158 151.5 145	168 166 166	182 182 181 177.5 174 171	185 183.5 183.5 183.5 182.5	190 186 186
4667		44844	• 01 01 00 00 0	5.00-000	94 94 94 94	55.57
29 31 29	32 34 29 28	30123		& & & & & & & & & & & & & & & & & & &	3998766	268 36 36
21 21 21 21	21 21 21 21	21 21 21	21 21 21	<u> </u>		21 21 21
	652 652 728 728	AAB17290 AAB17289 AAB17288 AAB17287 AAB17297	AAB17299 AAY96521 AAB17300 AAY96522	AAB17306 AAY96526 AAB17296 AAB17292 AAB17302 AAB17291 AAB17291	AAB17307 AAB17307 AAB17394 AAB17295 AAB17304 AAB17304	AAB16959 AAB17301 AAY96523 AAB17303
	Thrombopoletin mim Thrombopoletin mim Thrombopoletin mim TPO-mimetic peptid TPO-mimetic peptid	TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid	3 P:	TPO-mimetic peptid Thrombopoletin mim TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid	TPO-mimetic peptid TPO-mimetic peptid Thrombopoietin mim TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid	

## ALIGNMENTS

DR	PI	PA	PR	PR	×	Эď	XX	PD	××	ΡN	×	SO	XX	KW	KW	ΚW	ΚW	ΚW	X	×	DE	XX	DΤ	X	AC	XX	ID	RESU AAB1
WPI; 2000-350702/30.	Feige U, Liu C, Cheetham J, Boone TC;	(AMGE-) AMGEN INC.		23-OCT-1998; 98US-0105371.		25-OCT-1999; 99WO-US25044.		04-MAY-2000.		WO200024782-A2.		Synthetic.	asthma; thrombosis; pharmaceutical.	matrix metalloprot	cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;	MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;	immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;	~	Modified peptide; therapeutic agent; fusion; Fc domain; cancer:		TPO-mimetic peptide TMP-TMP SEC ID NO: 14		31-OCT-2000 (first entry)		AAB16963;		AAB16963 standard; Protein; 36 AA.	RESULT 1 AAB16963

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RESULT 2
AAB17293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rc domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)a-FI-(X2)b, where: FI = an Fc domain; XI and X2 = are each

cindependently selected from -(LI)c-PI-(L2)d-P2.

(L1)c-PI-(L2)d-P2-(L3)e-P^3, or -(LI)c-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4

where FL, P2, P3, and P4 = are each independently sequences of

combined partially active peptides; L1, L2, L3, and L4 = are each

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes composition of matter (I) comprising an invention particle particles. And linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an pharmacologically active peptides, useful autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17293 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences used in the exemplification of the present invention.
                                                                             WPI; 2000-350702/30.
                                                                                                                                                      Feige U,
                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA
composition of matter comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                           Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                          98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                               Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
an
    FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fc domain and for treating cancer and
    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 3
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CC (X])a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2.

CC (L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of

CC where P1, P2, P3, and P4 = are each independently sequences of

CC independently linkers; and a, b, c, d, e, and f = are each independently

CC or 1, provided that at least 1 of a and b is 1. The composition can

CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

CC activities. DNAs, vectors and host cells from the present invention can

CC be used for producing pharmaceutical compositions. The compositions are

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC The use of an Fc domain (rather than a Fab domain) can provide a longer

CC hidi-1ife or incorporate functions such as Fc receptor binding, protein

CC A binding, complement fixation, and possibly placental transfer. AAA69443

CC to Ada69526 and AAB16955 to AAB18003 represent nuclectide and amino acid

CC sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatologica immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacologically active peptides, useful for treating cancer and autoimmune diseases \dot{\phantom{a}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 318; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin mimetic peptide compound 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96525 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
              (AMGE-) AMGEN INC
                                                  23-OCT-1998;
                                                                                                                    04-MAY-2000.
                                                                                                                                                      WO200024770-A2
                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                             Peptide
                                                                                 22-OCT-1999;
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                 98US-0105348
                                                                                     99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                              /label= TMP_1
15..18
                                                                                                                                                                                         /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                          /label= TMP_2
                                                                                                                                                                                                                                                            /label= linker
                                                                                                                                                                                                                                                                                                                                /note= "optionally linked to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194; DB 21; Pred. No. 1.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36
                                                                                                                                                                                                                                                                                                                                   FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                 molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a compound which binds to an mpl receptor comprising a thrombopoietin cc minetic peptide (TMMP) dimer joined by a linker [TMMP_1-(L.1)_nTMMP_2], cc is new. TMMP_1 and TMMP_2 are amino acid sequences varying from at least cc 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-X_1_4, X_1-X_1-0, X_1-X_1-1, X_1-X_1-3, and cc X_1-X_1_4, X_1-X_1-0, X_1-X_1-1, X_1-X_1-3, and cc X_1-X_1_4, X_1-X_1-0, X_1-X_1-1, X_1-X_1-3, and cc X_1-X_1-4, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-1, X_1-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 62; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2000
                                                                                                              04-MAY-2000
                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; anti-inflammatory; linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96528 standard; peptide;
                     23-OCT-1998;
                                                                22-OCT-1999;
                                                                                                                                                         WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                     98US-0105348
                                                                99WO-US24834.
                                                                                                                                                                                                  /label= linker
28..41
/label= TMP_2
                                                                                                                                                                                                                                                                      /label= TMP_1
20..27
                                                                                                                                                                                                                                                                                                                                       /note= "optionally linked to
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 194; DB 21;
Pred. No. 1.7e-16;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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AAB17281
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 65; 91pp; English.
                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Feige U,
                                    23-OCT-1998;
22-OCT-1999;
                                                                                 04-MAY-2000
                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                       AAB17281 standard; Peptide; 42
                  (AMGE-) AMGEN INC.
                                                               25-OCT-1999;
                                                                                                  WO200024782-A2
                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                   6 IEGPTLROWLAARAGGGGGGGGTEGPTLROWLAARA 41
                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Cheetham J;
Liu C,
                                                                                                                                                                                                                                                                                                                                                                                           41 AA;
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                    98US-0105371
99US-0428082
                                                               99WO-US25044.
 Cheetham
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 194; DB 21; 100.0%; Pred. No. 1.9e-16;
 J,
                                                                                                                                                                                                                                                                                                                                                        0;
 Boone TC
                                                                                                                                                                                                                                                                                                                                                         Mismatches
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AAB17282
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist MMP; inhibitor; crythropoietin; thrombopoietin; interleukin 1;
WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                 23-OCT-1998;
22-OCT-1999;
                                                                                           Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17282 standard; Peptide; 42
                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L12)d-F2-(L2)d-F2-(L3)e-P3-(L4)f-P4-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                           Liu C, Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                 98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
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Pred. No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist;
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AAB17308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            where P1, P2, P3, and P4 = are each independently sequences of independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMP; inhibitor; erythropoietin; thrombopoietin; interleukin i cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase; asthma: thrombogic characteristics.
                                                                                        Feige U, Liu C, Cheetham
                                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                     25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17308 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 - an Fc domain; X1 and X2 - are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)d-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                   98US-0105371
                                                                                                                                                                                                                                                                                                                  99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 194; DB 2
100.0%; Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
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                                                                                        Boone TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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AAY96530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: C(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

C(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2.

C(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently considered that at least 1 of a and b is 1. The composition can lave cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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Best Local
                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
   Example 2A; Page 48;
                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2000
                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96530 standard; Protein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases
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                                                                                                                                                                                                            2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                    Feige U,
                                                                                                                                                                                    AAA29225
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                                                                                                                                                                                                                                                                       Cheetham
91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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Pred. No. 2e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Example 2; Page 331; 608pp; English

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RESULT 9
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C AAY96529). A compound which binds to an mpl receptor comprising a TMP

C dimer joined by a linker [TMP_1 (L_1)_nTMP_2], is new. TMP_1 and TMP_2

CC are amino acid sequences varying from at least 10 to 14 residues in

CC Length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-X_1_3, X_2-X_1_4,

CC X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3, and X_1-X_1-4, X_1-X_1_0, X_2-X_1_1, X_1-X_1_3, and X_1-X_1-4, X_1-X_1_0, X_1-X_1-X_1-1, X_1-X_1-1, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                Novel composition of matter comprising pharmacologically active peptides, usef
                                                                         autoimmune diseases
                                                                                                                                                                                                                                                                                             Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17311 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Overlapping oligonucleotides were used to construct a synthetic gene encoding a thrombopoletin mimetic peptide (TMP), which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA
                                                                                                                                                                                                                    2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
                                                                                                                                                                                                                                                                                             Cheetham
                                                                                                    peptides, useful
                                                                                                                                                                                                                                                                                             J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 194; DB 2
Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                         Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                         TC;
                                                                                                                                          an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                                                                    cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC FC domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (XI)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each

CC (XI)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each

CC (LI)c-F1-(L2)d-F2-(L3)e-F3, or -(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4

CC (L1)c-F1-(L2)d-F2-(L3)e-F3, or -(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4

CC (where F1, F2, F3, and F4 = are each independently sequences of

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, L2, L3, and L4 = are each

CC (an FC domain) active peptides; L1, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cance autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; anta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB16960 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                      pharmacologically active autoimmune diseases -
                                                                                                                                                                       N-PSDB; AAA69446.
                                                                                                                                                                                                                                                     Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                              2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA
                                                                                                             composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombosis; pharmaceutical
                                                                                                                                                                                                                                                     Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                     Ç
                                                                                                                                                                                                                                                                                                                                                                98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044
                                                                                                                                                                                                                                                     Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 194;
Pred. No. :
                                                                                                                                                                                                                                                        Boone TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                      for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                      cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an
is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Example 2; Page 185-186; 608pp; English

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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (CC (X1)a-F1-(X2)b), where: F1 = an Fc domain; X1 and X2 = are each (CC (X1)a-F1-(X2)d-F2. (X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)
       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2, x_2-x_1_3, x_2-x_1_4, x_1-x_1_0, x_1-x_1_1, x_1-x_1_2, x_1-x_1_3, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin;
megakaryocyte; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                             Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-anaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IgG1 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96531 standard;
                                                                                                                                                                                                        diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                         Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                      AMGEN INC
                                                                                                                                                                                                                                                                                                              AAA29229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n; TgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; production; anti-human immunodeficiency virus; anti-HIV dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 194; DB 21; Pred. No. 1.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmunė disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist MMP; inhibitor; erythropoietin; thrombopietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X_1-X_14. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E; X_9 = W, Y or F; X_10 = L, I, V, A, F, M, or K; X_11 = A, I, V, L, F, S, T, K, H, or E; X_12 = A, I, V, L, F, G, S, or O; X_13 = R, K, T, V, N, Q or G; X_14 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
           Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating autoimmune diseases -
                                                           The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                   WPI; 2000-350702/30.
N-PSDB; AAA69445.
                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
22-OCT-1999;
                                                                                                                  Example
                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16959 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                            2; Page 182-183; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                              98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
P4 = are each independently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                               Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194; DB 21;
No. 1.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                              cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                               is:
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sequences

are each independently

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RESULT 13
AAB17301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
The present invention describes composition of matter (I) comprising a Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4, where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VE immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagon MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16925 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                   Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                   Novel composition of matter comprising pharmacologically active peptides, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                        autoimmune diseases
                                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                Feige U,
                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17301 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                   9905-0428082
                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044
                                                                                                                                                                                                                                                                                                                Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 190; DB 21;
Pred. No. 3.8e-15;
                                                                                                                                                                                                                                                                                                             Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                       sing an useful
                                                                                                                                                                                                                       for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 268;
                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF;
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                                                                                                           an
is:
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RESULT 14
AAY96523
Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                           Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96523 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                             22-OCT-1999;
                                                                                                                                                                                                                                                                                                                             04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                               Claim 16; Page 62; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive;
                                                                                                                                                                                                                              (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                              2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                              Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                              98US-0105348
                                                                                                                                                                                                                                                                                             99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "optionally modified by bromoacetyl 23..36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.9%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "optionally linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 186; DB 21;
Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ťο
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                              o
R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA69443
                                                                                                                   of.
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RESULT 15
AAB17303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1-X_1, X_1-X_1,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                       pharmacologically active peptides, useful for treating autoimmune diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis;
                                                                                                                                                             Example
                                                                                                                                                                                                                                                            Novel composition of matter comprising an
                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                   Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                1; Page 322;
                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                        Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.9%;
97.2%;
                                                                                                                                                                  608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 186; DB 21;
Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                             Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:359
                                                                                                                                                                                                                                                              Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
                                                                                                                                                                                                                                           cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0

Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)d-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of

The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)

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В
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Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L1)c-P3-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and inmunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                            The present invention describes composition of matter (I) comprising
                                                                                                                                                                      Example 1; Page 324; 608pp;
                                                                                                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                                                                                 WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                          98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
                                                                                                                                                                                                                                                                                                                   Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.4%;
97.2%;
                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 185; DB 2:
Pred. No. 2e-15;
                                                                                                                                                                                                                                                                                                                   Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
 independently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                            is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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CCCCCXXX
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AAY96524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                  Claim 16; Page 62; 91pp; English.
                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAAA6943 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                    WPI; 2000-365108/31.
                                                                                                                                                               Liu C,
                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                          04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatologica
                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                     WO200024770-A2
                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin mimetic peptide compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96524 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                              Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                   98US-0105348
                                                                                                                                                                                                                                                                                                                                          /label= linker
23..36
                                                                                                                                                                                                                                              99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                      /note= "optional" 15..22
                                                                                                                                                               Cheetham
                                                                                                                                                                                                                                                                                                                             /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                              /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.4%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 36;
                                                                                         for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP\_1-(L\_1)\_nTMP\_2], is new. TMP\_1 and TMP\_2 are amino acid sequences varying from at least

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_1-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_2, X_1-X_1_3, and X_1-X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E; X_9 = W, Y or F; X_10 = L, I, V, A, F, M, or K; X_11 = A, I, V, L, F, G, S, or Q; X_13 = R, K, T, V, N, Q or G; X_14 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoletin. The TMPs are useful for increasing the production of platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17294 standard; Peptide;
The present invention describes composition of matter (I) comprising (FC domain, pharmacologically active peptides, and linkers. Where (I) : (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-F1-(L2)d-F2, -(L1)C-F1-(L2)d-F2-(L3)e-F3, or -(L1)C-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4 where F1, F2, F3, and F4 = are each independently sequences of
                                                                                                                                                                                                                                                                             Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating of
                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                             2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                             Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
                                                                                                                                  Page 318; 608pp; English
                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                     99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                    98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.4%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 185; DB 2
Pred. No. 2e-15;
                                                                                                                                                                                                                                                                               Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                         cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosts, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69436 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; Interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; vascular endothelial growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17295 standard; Peptide; 38
                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                             Feige U,
                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
                                                                                                                                                                      autoimmune diseases
                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARA-GGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                      1; Page 319;
                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                         98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044
                                                                                                                                                                                                                                                             Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.6%;
97.3%;
                                                                                                                                       608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 183.5; DB 2
Pred. No. 3.1e-15;
                                                                                                                                                                                                                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۳.
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Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independent

are each independently

The present invention describes composition of matter (I) comprising

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
              The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L4)f-P4 -(L4)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently can be a composition can be considered that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1 cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
22-OCT-1999;
     have cytostatic,
                                                                                                                                                                                              Example 1; Page 323; 608pp; English
                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                                                                                                                   pharmacologically active
                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17304 standard; Peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-350702/30.
                                                                                                                                                                                                                                               composition of matter comprising an acologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĀĄ;
                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044
     antiasthmatic, thrombolytic
                                                                                                                                                                                                                                                                                                                                       Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                       Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183; DB 21;
No. 3.6e-15;
                                                                                                                                                                                                                                             Fc domain and for treating (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
and immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                 cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 21
AAB17305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
         The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P3-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, C, d, e, and f = are each independently linkers; and a, b, C, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
                                                                                                                                                                                                                                          Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17305 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; anta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGKPEGGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGG----GGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                          Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.1%;
92.3%;
pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 182.5; DB 1
Pred. No. 4.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                            Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
   compositions.
                                                                                                                                                                                                                                                                                                for treating
                                                                                                                                                                                                                                                                                                                   Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-P1-(X2)b, where: F1 = an FC domain: X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                         The present invention describes composition of matter (I)
                                                                                                                                                                                                                                        Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Feige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17306 standard;
                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371
99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                   Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.1%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 182.5; Db ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                   Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                           comprising . Where (I)
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin; mimetic; TMP; TPO; platelet; anti-human immunodeficiency virus; anti-HIV; immunosuppressive; anti-inflammatory; linker.
                                                                                                            Claim 16; Page 62; 91pp; English
                                                                                                                                      Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                    (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96526 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences used in the exemplification of the present invention
                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                        22-OCT-1999;
                                                                                                                                                                                                                                                                          WO200024770-A2
                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
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                                                                                                                                                                 2000-365108/31
                                                                                                                                                                                  Feige U,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                      98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                    mimetic peptide compound 7.
                                                                                                                              involve
                                                                                                                                                                                                                                         99WO-US24834
                                                                                                                                                                                                                                                                                                    /label= linker
19..32
                                                                                                                                                                                                                                                                                                                       /label= TMP_1
15..18
                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                   Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.8%;
                                                                                                                                                                                                                                                                                                                                              "optionally linked
                                                                                                                              thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 4.5e-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                an
                                                                                                                                                                                                                                                                                                                                                                                                            anti-anemic;
                                                                                                                                                                                                                                                                                                                                                                                                                     megakaryocyte; production,
                                                                                                                                                                                                                                                                                                                                                FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                                                                                                                                molecule"
                                                                                                                                                                                                                                                                                                                                                                                                            dermatological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1 -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each independently
independently linkers; and a, b, c, d, e, and f = are each independently
0 or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present inventions are
used for producing pharmaceutical compositions. The compositions are
used for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified peptide; therapeutic agent; fusion; Fc domain; cancer;
autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17296 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                       autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nutoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                              The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 AA;
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                                                                                                                                                                                                                                                invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
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Pred. No. 4.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
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                                                                                                                                                                                                                                                                                                                                        for treating cancer and
                                                                                                                                                                                                                                                                                                                                                           Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 36;
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           Fr. domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)d-P2-(L3)d-P2-(L3)e-P3.

(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently

or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosits, or autolumune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:348.
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                                                                                                                                                                                                                                                                                                                   Example 1; Page 317-318; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                            pharmacologically active peptides, useful for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an
                                                                                                                                                                                                                                                                                The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AA;
                                                                                                                                                                                                                                                                                                                                                             diseases
complement fixation, and possibly placental transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105371.
99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 181; "" - ... No. 6.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                  Fc domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                  is:
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CC FC domain, pharmacologically active peptides, and linkers. Where (1) is:

(C (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each

CC (L1)c-P1-(L2)d-P2. Where: F1 = an FC domain; X1 and X2 = are each

CC (L1)c-P1-(L2)d-P2. (L3)e-P^3, or -(L1)c-P1-(L2)d-P2. (L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of

CC pharmacologically active peptides; L1, L2, L3, and L4 = are each

CC independently linkers; and a, b, c, d, e, and f = are each independently

CC or 1, provided that at least 1 of a and b is 1. The composition can

CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

CC activities. DNAs, vectors and host cells from the present invention can

CC be used for producing pharmaceutical compositions. The compositions are

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CThe use of an FC domain (rather than a Fab domain) can provide a longer

CC half-life or incorporate functions such as FC receptor binding, protein

A binding, complement fixation, and possibly placental transfer. AAA69443

C conjenes used in the composition acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
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                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an pharmacologically active peptides, useful
   sequences used in
                                                                                                                                                                                                                                                                                                                              Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                  autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17302 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; wMMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                       present invention describes composition of matter (I) comprising domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                  diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105371
99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide; 40
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97.2%;
exemplification
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
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present
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Fr. domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(X2 independently selected from -(L1)c-P1, -(L1)d-P2-(L2)d-P2,

(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2,

(L3)e-P3-(L4)f-P4

(C2 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C3 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C4 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C5 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C6 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C7 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C8 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

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(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

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(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

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(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active peptides; L1, L2, L3, and L4 = are each

(C9 charmacologically active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sox
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 317; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEGPTLROWLAARAGGGKBRACGGGGIEGPTLROWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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99US-0428082
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87.5%;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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Sequence

34 AA;

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Length 34;

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RESULT 28
AAB17298
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNR; antagonist MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
Sequence
                                                                                                                                                                         The
                                                                                                                                                                                         Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                   Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                WPI; 2000-350702/30
                                                                                                                                                                                                                                                                  Feige U,
                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000
                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17298 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARA--GGGGGGIEGPTLRQWLAARA 34
                                                                                                                                                            present invention describes composition of matter (I) comprising domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                  Liu C,
                  used
36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
AA;
                  in
                                                                                                                                                                                                                                                                                                      98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                 99WO-US25044.
                                                                                                                                                                                                                                                                   Cheetham
               the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.1%;
                                                                                                                                                                                                                                                                   ٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                   Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171; DB 21;
No. 8.6e-14;
                                                                                                                                                                                                                                                                   TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion; Fc domain;
                                                                                                                                                                                                                  Fc domain and for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                             jan
is:
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Query Match

86 .6%;

Score 168;

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Best Local Query Match Matches

Similarity

94.4%;

Score 168; DB 21; Pred. No. 2.1e-13;

21;

Length 36;

0

Gaps

0

Conservative

0;

Mismatches

Sequence

36 AA;

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RESULT 29
ADB17299
ID ADB17299
ID AAB17299
ID AAB17299
AX AAB1
XX AAB1
XX Mod:
KW Mod:
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                                                   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)a-Fl-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each

condependently selected from -(L1)c-Pl, -(L1)d-P2-(L3)d-P2.

(L1)c-Pl-(L2)d-P2-(L3)e-P^3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

Where Pl, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; L1, L2, L3, and L4 = are each

independently linkers; and a, b, c, d, e, and f = are each independently

or 1, provided that at least 1 of a and b is 1. The composition can

thave cytostatic, antiasthmatic, thrombolytic and immunosuppressive

activities. DNAs, vectors and host cells from the present invention can

be used for producing pharmaceutical compositions. The compositions are

useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer

half-life or incorporate functions such as Fc receptor binding, protein

A binding, complement fixation, and possibly placental transfer. AAA69443

to AAA6926 and AAB16955 to AAB18003 represent nucleotide and amino acid

sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       auronmmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic m call immehance actions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc domain and for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
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Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
                    Thrombopoietic peptides which activate \mathfrak{mpl} receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                   Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                                                                                                                     WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclic or linear thrombopoietin mimetic peptide compound 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96521 standard; peptide;
                                                                                                                                                                                                                    WPI; 2000-365108/31.
                                                                                                                                                                                                                                   Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA
                associated ITP,
                                                                                                                                                                                                                                                                    98US-0105348
                                                                                                                                                                                                                                                                                     99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                            /note= "optional"
15..22
                                                                                                                                                                                                                                                                                                                                             /label= linker
23..36
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                    /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                    note= "optionally linked
                and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                                                                                                                                                                                                                                                                                                                                                                                      to an Fc molecule"
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Sequence

36 AA;

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                              Query Match
Best Local Similarity
Matches 34; Conserv
Conservative
                                       86.6%;
                                0;
                                Score 168; DB 21;
Pred. No. 2.1e-13;
0; Mismatches 2;
                                                Length 36;
                                 0;
                                 Gaps
                                 0
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Search completed: October Job time: 17.1874 secs 9, 2002, 08:58:56 В

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Result
No.
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum
          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                               76.5
76.5
76.5
          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*

1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptcdata/2/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptcdata/2/iaa/Dackfiles1.pep:*
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194
1 IEGPTLRQWLAARAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October 9, 2002, 08:55:27; Search time 5.98595 Seconds (without alignments) 146.898 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
        IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
        GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                        US-08-764-640-231
US-09-244-298A-231
US-09-256-704-231
US-08-764-640-13
US-08-73-225-13
US-08-973-225-13
US-08-973-225-13
US-09-244-298A-13
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US-09-516-704-185
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US-08-764-640-194
US-08-764-640-232
US-08-973-225-18
US-08-973-225-194
US-08-973-225-194
US-08-973-225-194
US-08-973-225-220
US-09-244-298A-194
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Sequence 231, App Sequence 231, App Sequence 231, App Sequence 13, App Sequence 13, App Sequence 13, App Sequence 13, App Sequence 193, App Sequence 193, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 17, App Sequence 185, App Sequence 185, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequ
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
69	69	69	69	69	69	69	69	69	69	69	69	69	69	73	73	73	73
				35.6						35.6							
15	15	15	15	15	15	14	14	14	14	14	14	14	14	16	16	16	16
w	w	N	N	N	N	4	4	ω	ω	w	ω	N	N	4	4	4	ω
US-08-973-225-200	US-08-973-225-196	US-08-764-640-215	US-08-764-640-209	US-08-764-640-200	US-08-764-640-196	US-09-516-704-199	US-09-516-704-195	US-09-244-298A-199	US-09-244-298A-195	US-08-973-225-199	US-08-973-225-195	US-08-764-640-199	US-08-764-640-195	US-09-516-704-232	US-09-516-704-194	US-09-516-704-18	US-09-244-298A-232
Sequence 200,	Sequence 196,	Sequence 215,	Sequence 209,	Sequence 200,	Sequence 196,	Sequence 199,	Sequence 195,	Sequence 199,	Sequence 195,	Sequence 199,	Sequence 195,	Sequence 199,	Sequence 195,	Sequence 232,	-	Sequence 18,	Sequence 232,
App	Ąpp	App	App	App	App	App	App	App	App	Appl	App						

## ALIGNMENTS

RESULT 1 US-08-764-640-231

PATENT NO. 5869451 5837683  GENERAL INFORMATION:  APPLICANT: Dower, William J.  APPLICANT: Dower, William J.  APPLICANT: Barrett, Ronald W.  APPLICANT: Gates, Christian  APPLICANT: Gates, Christian  APPLICANT: Gates, Christian  APPLICANT: Balasubramanian, Palaniappan  APPLICANT: Balasubramanian, Palaniappan  APPLICANT: Balasubramanian, Palaniappan  APPLICANT: Balasubramanian, Palaniappan  APPLICANT: Deprince, Randolph B.  APPLICANT: Deprince, Randolph B.  APPLICANT: Podduturi, Surekha  APPLICANT: Podduturi, Surekha  APPLICANT: Podduturi, Surekha  APPLICANT: Podduturi, Surekha  APPLICANT: Populences: 244  CORRESPONDENCE ADDRESS:  ADDRESSEE: Glaxo Wellcome  STREET: Five Moore Drive, P.O. Box 13398  CITY: Research Triangle Park  STATE: NC  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER READABLE FORM:  MEDIUM TYPE: Ploppy disk  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER READABLE FORM:  APPLICATION NUMBER: 9C-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 9K3281  TELEOMMUNICATION NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 9K3281  TELEOMMUNICATION NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 9K3281  TELEOMMUNICATION NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36.392  REFERENCE/DOCKET NUMBER: 36
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; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /product= "Ava"
US-08-764-640-231
Qy
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US-09-244-298A-231
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                                 Matches
                                                               Query Match
                                                   Best
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                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 11-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PEPTIDES TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                FEATURE:
                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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CITY: F
                                                                                                            LOCATION: 13
OTHER INFORMATION: /product= "Ava"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                TOPOLOGY: 1
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                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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nes 13; Conserv
                                                Local Similarity
                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                              LENGTH:
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 2 EGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLA 33
                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                               25 amino acids
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Wagstrom, Christopher R.
Hendren, Richard W.
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Cwirla, Steven E.
                                 Conservative
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                                                                                                                                              Modified-site
                                                                                                                                                                                                linear
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919-248-1000
-- TP NO: 231:
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                                             39.4%;
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                               Score 76.5; DB 3; Length 25; Pred. No. 0.0058; Rismatches 2; Indels
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Pred. No. 0.0058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 231: US-09-516-704-231
                                                                     RESULT 4
US-08-764-640-13
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US-09-516-704-231
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Sequence 13, Application US/08764640 Patent No. 5869451 Patent No. 5869451 5837683 GENERAL INFORMATION:
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                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                     Local Similarity 40.
les 13; Conservative
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                                                                                                                                                 2 DGPTLREWISFXA------DGPTLREWIS 24
                                                                                                                                                                               2 EGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/516,704
FILING DATE: 01-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, p.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 25 amino acids
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Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                                                                                                                                      Score 76.5;
Pred. No. 0.
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                      0.0058;
                                                                                                                                                                                                                                                       DB 4; Length 25;
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                                                                                                                                                                                                                             Sequence 193, Application US/08764640 Patent No. 5869451 Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/764
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUBLEC, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32
                                                                                                                               APPLICANT: APPLICANT:
                                                                APPLICANT:
                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
                                   APPLICANT:
                                                   APPLICANT:
                                                                                                  APPLICANT:
                                                                                                                  APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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ICANT: Yin, Qun
E OF INVENTION: 1
E OF INVENTION: 1
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                                                                                                                              Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 amino acids
                                            Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                              Balasubramanian, Palaniappan
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Hendren, Richard W.
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Cwirla, Steven E.
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 PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
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US-08-973-225-13
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CIASSIETZATION. 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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ZIP: 27709
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                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                      Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 232
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                                                                                                                                                                        CITY: Research Triangle Park STATE: NC
                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                            STREET: Five Moore Drive, P.O. Box 13398
APPLICATION NUMBER: US/08/973,225A
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R SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                Haselden, Sherril S. Mattheakis, Larry C. Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cwirla, Steven E. Duffin, David J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett,
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                                                                                                                                                                                                                                                                                          THROMBOPOIETIN RECEPTOR
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FILING DATE: 04-Dec-1997

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US-08-973-225-13
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US-08-973-225-193
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GENERAL INFORMATION:
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                                                                                                                                  TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 193:
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                                                                                                                                                                                     APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptid
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LENGTH: 14 amino acids
TYPE: amino acid
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                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                   MOLECULE TYPE: peptide
                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                              LENGTH: 14 amino acids
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100.0%;
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Pred. No.
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US-09-244-298A-13
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                                                                                                                       US-09-244-298A-13
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Best Local Similarity 100.0%;
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                                                             Matches
                                                                                         Query Match
                                                                            Best
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                        NAME: Hrublec, Robert T.
REGIRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
REFERENCE/DOCKET NUMBER: PK
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Relaction DATA:
CURRENT APPLICATION NUMBER: US,
APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 27709
                                                                         Local Similarity
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                               LENGTH:
                             1 IEGPTLRQWLAARA 14
IEGPTLRQWLAARA 14
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                                                                                                                                                                                  amino acid
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Cwirla, Steven E.
Gates, Christian
                                                             Conservative
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                                                                                                                                                      linear
                                                                                                                                                                                                                                            919-248-1000
                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                    11-DEC-1996
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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                                                                           37.6%; Score 73; DB 3; 100.0%; Pred. No. 0.008;
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Pred. No.
                                                             0;
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                                                              Mismatches
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US-09-244-298A-193; Sequence 193, Application US/09244298A

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RESULT 9

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                                                                                                                                                                                      Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                     Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PK TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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ZIP: 27709
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CITY: Research Triangle Park
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           TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                       APPLICANT: Dower, William J
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                       Cwirla, Steven E. Gates, Christian
                                                                                                                                      Barrett, Ronald W. Cwirla, Steven E.
                            Deprince, Randolph B.
Podduturi, Surekha
                                                                        Balasubramanian, Palaniappan
Wagstrom, Christopher R.
                                                                                                        Schatz, Peter J.
                                                             Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
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RECEPTOR
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US-09-516-704-193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 193, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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                                                                                                                             ZIP:
                                                                                                                               COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                         STREET: Five Moore Drive, P.O. CITY: Research Triangle Park
                                                                                                                                                                       STATE: NC
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Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Cwirla, Steven E.
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    Mismatches

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US-08-764-640-17

Sequence 17, Application US:

Patent No. 5869451

Patent No. 5869451 5837683
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Best Local Similarity
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                                     INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: PK.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                            STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                               CLASSIFICATION:
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NAME: Hrubiec, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-248-1000
NN FOR SEQ ID NO: 193:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08764640
15 amino acids
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                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balasubramanian, Palaniappan Wagstrom, Christopher R.
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Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yin, Qun
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Hendren, Richard W.
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                                                                                                                                                                                                                                                                                        Floppy disk
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                                       17:
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s; Pred. No. 0.008;
r: reatches 0;
                                                                                           PK3281
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-17
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US-08-764-640-185
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δÃ
                                                                                   ; MOLECULE TYPE: US-08-764-640-185
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Best Local Similarity
                                                     Query Match
                              Matches
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                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR
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                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                          NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                              TOPOLOGY:
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                                         Local Similarity
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1 IEGPTLRQWLAARA 14
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CANT: Dower, William J
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Cwirla, Steven E.
Gates, Christian
                            Conservative
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                                                                                                                Linear
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100.0%; Pr/
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100.0%;
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Pred. No.
                               0;
                                            Score 73; pred. No.
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                                            DB 2;
0.0086;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-973-225-17
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US-08-973-225-17
; Sequence 17, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
                                                                                                                                                                                    RESULT 15
US-08-973-225-185
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                                                                                                                         Sequence 185, Application US/08973225A Patent No. 6083913
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                Match 37.6%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARA 14
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
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Wrighton, Nicholas C.
TITLE OF INVENTION: PERTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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CITY: Research Triangle Park
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                                                                                                              Dower, William J.
                                                       Cwirla, Steven E. Duffin, David J.
Mattheakis, Larry C.
                                      Gates, Christian
                                                                                       Barrett,
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Mattheakis, Larry C.
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                                                                                             Ronald W.
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                                                                                                                                                                                                                                                                                                                                 0;
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; STRANDEDNESS: <Unknown>; FOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 185: US-08-973-225-185
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
PMFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                           TITLE OF INVENTION: PE
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                     STATE: NC
COUNTRY: US
ZIP: 27709
                                                                                       ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
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les 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Wrighton, Nicholas C.
TITLE OF INVENTION: PERTIDES AND COMPOUNDS THAT BIND TO
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ADDRESSEE: Glaxo Wellcome
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                                                                                                                                                                                                                                                                                                                                                                                                                                    7, Application US/09244298A 6121238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                       USA
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                                                                                                                                                                                                                                 Deprince, Randolph B. Podduturi, Surekha
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Wagstrom, Christopher R.
Hendren, Richard W.
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Cwirla, Steven E.
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                                                                                                                                                                                RECEPTOR
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                                                                                                           Box 13398
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0.0086;
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US-09-244-298A-185
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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                                REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO TITLE OF INVENTION: RECEPTOR
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                  STREET:
CITY: R
                                                                                                                  COUNTRY: US
ZIP: 27709
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REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                   NAME:
                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                  Research Triangle Park
                                                                                Hrubiec, Robert T
                                                                                                                                                                                                                                                                                                   NC
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Hendren, Richard W.
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Cwirla, Steven E.
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SYSTEM: PC-DOS/MS-DOS
                 919-248-1000
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100.0%; Pred. No. 0.0086;
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; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-516-704-17
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; MOLECULE TYPE: peptide
US-09-244-298A-185
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US-09-516-704-17
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GENERAL INFORMATION:
                                                   Matches
                                                                   Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                     Local Similarity
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1 IEGPTLRQWLAARA 14
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ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown> ATTORNEY/AGENT INFORMATION:
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                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/516,704 FILING DATE: 01-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Research Triangle Park
                                                                                                                                                                                                                           LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
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                                                   Conservative
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Hendren, Richard W.
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                                                                   100.0%;
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                                                                   37.6%; Score 73; 100.0%; Pred. No.
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0.0086;
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                                                                                     Length 15;
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RESULT 20
US-08-764-640-18
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                                                                                     Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
                                                                                                                                        Sequence 18,
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
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GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                           2 IEGPTLRQWLAARA 15
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709

COMPUTER READABLE FORM:

COMPUTER: Flappy disk

COMPUTER: IBM PC compatible

COMPUTER: Flappy PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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                                                                                                                                        Application US/08764640
                Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Hendren, Richard W.
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Balasubramanian, Palaniappan
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Cwirla, Steven E.
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                                                                                                                                                                                                                                                            Sequence 194, Application US/08764640 Patent No. 5869451 Patent No. 5869451 5837683
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Best Local Similarity
                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                APPLICANT: Yin, Qun
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                     APPLICANT:
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NUMBER OF SEQUENCES:
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STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product= "Beta-ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hrubiec, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 amino acids
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                                                                                Wagstrom, Christopher R. Hendren, Richard W. Deprince, Randolph B.
                                                                                                                                                                       Gates, Christian
                                                                                                                                                                                     Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                   Podduturi, Surekha
                                                                                                                                    Balasubramanian, Palaniappan
                                                                                                                                                        Schatz, Peter J.
                                                                                                                                                                                                          Barrett,
                                                                                                                                                                                                                            Dower, William J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                  RECEPTOR
                                  PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                           Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
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US-08-764-640-232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 232, Application | Patent No. 5869451 | Patent No. 5869451 | 5837683 | GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT:
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APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                   TITLE OF INVENTION: PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Research Triangle Park
                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                       COUNTRY:
                                                                                                                                                         ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
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Local Similarity 100.0%;
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FILING DATE: 11-DEC-1996
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                                                                                                                       USA
                                                                                                                                                                                                                                                                                               Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                          Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                            Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dower, William J.
                                                                                                                                                                                                                                                                    PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                  244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-232
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US-08-973-225-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                  TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 18:
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REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 514
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                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
THROMBOPOIETIN RECEPTOR
MOLECULE TYPE: peptide
                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Glaxo Wellcome
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                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
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                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                           REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                           LENGTH: 16 amino acids
                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NC
                  TOPOLOGY: linear
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Pred. No.
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SEQUENCE DESCRIPTION: SEQ ID NO: 194: US-08-973-225-194
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                                                                Matches
                                                                                Query Match
Best Local :
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                 Match 37.6%; Score /s, Local Similarity 100.0%; Pred. No. 0.0
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                              1 IEGPTLRQWLAARA 14
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                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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IEGPTLRQWLAARA 15
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                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                        NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                          LENGTH: 16 amino acids
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Mattheakis, Larry C.
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Cwirla, Steven E.
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                                                                            Score 73; DB 3; pred. No. 0.0092;
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                                                           0; Indels
                                                                                          Length 16;
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RESULT 26
US-09-244-298A-18
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US-08-973-225-220
                                                                                                                                                                        Patent No. 6121238
GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 18,
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                                                        APPLICANT:
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APPLICANT:
                                      APPLICANT:
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  APPLICANT:
                      APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
APPLICATION OF COMPANY
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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MEDIUM TYPE: Floppy disk
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                              Application US/09244298A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Glaxo Wellcome STREET: Five Moore Drive, P.O. Box 13398
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ZIP: 27709
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                                                                        Barrett, Ronald W. Cwirla, Steven E. Gates, Christian Schatz, Peter J.
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                  Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Deprince,
                                                                                                                                                       Dower, William J
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Mattheakis, Larry C.
Schatz, Peter J.
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Cwirla, Steven E.
Duffin, David J.
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Pred. No. 0.0092;
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US-09-244-298A-194
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel. CURRENT APPLICATION DATA:
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                                                                                                                                APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun
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APPLICANT: Yin, Qun
                                                                    CORRESPONDENCE ADDRESS:
                                                                                                      TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                  NUMBER OF SEQUENCES:
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OTHER INFORMATION: /pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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FILING DATE: 11-DEC-1996
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STATE:
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                   CITY:
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                   Research Triangle Park
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Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                      Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                    Five Moore Drive, P.O. Box 13398
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                                                                                                                                                                                          Wagstrom, Christopher R. Hendren, Richard W.
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                                                    Glaxo Wellcome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.6%; Score 73; DB 3; Length 16. 100.0%; Pred. No. 0.0092; tive 0; Mismatches 0; Indels
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                ATTORNEY/AGENT INFORMATION: NAME: Hrubiec, Robert T.
                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO TITLE OF INVENTION: RECEPTOR
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ZIP: 27709
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                                                CLASSIFICATION:
                                                             APPLICATION NUMBER: US/0 FILING DATE: 11-DEC-1996
                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            MEDIUM TYPE:
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ZIP: 27709
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REGISTRATION NUMBER:
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Hrubiec, Robert T.
--- winmher: 36,392
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US-09-516-704-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                          REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-248-100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                      FEATURE:
                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IEGPTLRQWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARE: Patentin Release #1.0, Version #1.30
               OTHER INFORMATION:
                                   LOCATION:
                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dower, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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-1. 232:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-516-704-194
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                                                                                     Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                        TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 194: SEQUENCE CHARACTERISTICS:
2 IEGPTLRQWLAARA 15
                                1 IEGPTLRQWLAARA 14
                                                                                                                                                 MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PK3281 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
operating SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dower, William J
                                                                    14;
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                                                                                                                                                                                                   LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                            NAME: Hrubiec,
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                                                                    Conservative
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Podduturi, Surekha
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Cwirla, Steven E
Gates, Christian
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                                                                               37.6%; Score 73; 100.0%; Pred. No.
                                                                                 100.0%;
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                                                                   0,
                                                                 Mismatches
                                                                                            DB 4; Length 16;
                                                                            0.0092;
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Search completed: October 9, 2002, 09:06:30

Job time : 5.98595 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:54:17; Search time 8.09368 Seconds

(without alignments) 427.397 Million cell updates/sec

US-09-422-838C-26 Title:

1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_71:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	`	hflX protein - Myo	, ×	2				E	11021	•	1 7	٠,					Subcritsin-like pr	-4	transcription fact	keratin 10 tune 1	3, 5, -0401 0-2000	myosin hosing chain	negozin neavy charm	near Octobritish - pre	process rise x	propable membrane	ming	LIN, SWA T	ndc protein - irui
	3 ID	2 T20961	2 G87033	2 \$72938	2 D70505		2 T26807	: T26808	KSNCLO	KSNCLT	JQ1094	T09084	B42687	B39490	JC2191	.TC557T.	A39490	JC5570	D96664	S29334	531224	KRHU0	S65543	MWAXIC	A42687	A48266	260310	200000	S COORD	S58064	*00000
	Length DB	200					331 2	333	619 1	619	201 2	490 2	209 2	487 2	652 1	962	969	975 2		443 1	445 1	593 1	777 2	1168 1	210 2	864	285	303	569	649	
Query	Match	35.6	35.3	35.3		33.0	33.0	33.0	32.7	32.7	32.5	32.5	32.2	31.7	31.7	31.7	31.7	31.7	31.4	31.4	31.4	31.4	31.4	31.4	31.2	31.2	30.9			30.9	
	Score	69	68.5	68.5	66.5	64	64		63.5	Э.	63	9			61.5	61.5	61.5	61.5	61	61	61	61	61	61	60.5	60.5	09	9	09	09	,
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hypothetical prote	tyrosine kinase -	recentor-like prot	hypothetical prote			homeotic protein H	hypothetical prote	prohable decynribo	hynothetical prote				Ü	helix-loon-heliv+	glycine-rich prote
T13690	158378	T04124	T13386	B84781	T06612	A53662	E96495	S57795	T10550	T48099	H85067	T35365	835500	JC6087	T49109
7	7	7	7	7	7	7	~	~	7	7	7	7	Н	7	7
806	888	962	1325	327	339	403	443	867	80	199	250	270	346	367	396
30.9	30.9	30.9	30.9	30.7	30.7	30.7	30.7	30.7	30.4	30.4	30.4	30.4	30.4	30.4	30.4
9	09	09	09	59.5	59.5	59.5	59.5	59.5	59	59	29	59	59	59	59
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT 1
```

hypothetical protein F15B9.5 - Caenorhabditis elegans

C; Species: Carnorhabditis elegans
C; Date: 15-0ct-1999 #sequence\_revision 15-0ct-1999 #text\_change 15-0ct-1999
C; Date: 15-0ct-1999 #sequence\_revision 15-0ct-1999 #text\_change 15-0ct-1999
C; Accession: T20961
R; Percy, C.
Submitted to the EMBL Data Library, August 1996
A; Reference number: Z19351
A; Reference number: Z19351
A; Reference number: Z19351
A; Reference number: Z19351
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A)Gene: CESP:F15B9.5 A;Map position: 5 A;Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1

Gaps ; 0 35.6%; Score 69; DB 2; Length 500; 56.5%; Pred. No. 3.3; Live 4; Mismatches 6; Indels Best Local Similarity 56.59 Matches 13; Conservative Query Match

ó

3 GPTLRQWLAARAGGGGGGGGIEG 25 δy

429 GSMLGRFLSNRGGGGGGGGGGGG 451 QQ

probable ATP/GTP-binding protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: 0.4pr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001
C;Accession: G8703
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Davies, R.M.; Davlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro an, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Authors: Rutter, S.; Seeger, R.; Parkhills: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002

A; Accession: G87033

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-488 <STO>

A; Cross\_references: GB:AL450380; NID:q13093026; PIDN:CAC31378.1; GSPDB:GN00147 C; Genetics:

A;Gene: ML0997 C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology

Query Match

35.3%; Score 68.5; DB 2; Length 488;

a

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pp

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C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C; Accession: T49792 P; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, May 2000 A; Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y41C4A.4a - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C.Accession: T26807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Y41C4A.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Experimental source: clone Y41C4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-331 <WIL>
A; Cross references: EMBL:AL032627; PIDN:CAB54381.1; CESP:Y41C4A.4a
A; Experimental source: clone Y41C4A
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
A;Experimental source: BAC clone B9J10; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.0%; Score 64; DB 2; Length 201; 57.1%; Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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Submitted to the EMBL Data Library, October 1998
A; Reference number: 220269
A; Accession: 726807
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:Y41c4A.4b
A;Introns: 24/3; 50/2; 81/3; 161/1; 230/1; 294/3
C;Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C; Superfamily: fos/jun DNA-binding domain homology
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submilted to the EMBL Data Library, October 1998
A;Reference number: 220269
A;Accession: T26808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 RAGGGGGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 RGGGGGGGVNG----RWSA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 57.19
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 GGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGGGGGGIEGPT 27
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                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: NCSP: B9J10.290
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R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Conon, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Ahathors: Sqrass, S. Muster, S.; Seeger, K.; Skelton, S.; Squares, S. Ahathors: Sqrass, S. Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Tile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MuID: 98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-495 <COL> A;Cross-references: GB:298209; GB:AL123456; NID:93261838; PIDN:CAB10901.1; PID:e332282; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Start codon: GTG
C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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hitx protein - Mycobacterium leprae
hitx protein - Mycobacterium leprae
c; Species: Mycobacterium leprae
c; Species: Mycobacterium leprae
c; Species: Mycobacterium leprae
c; Species: Mycobacterium leprae
c; Accession: $72938
A; Smith, D.R.; Robison, K.
Submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid B2235.
A; Reference number: $72587
A; Accession: $72938
A; Status: Preliminary
A; Residues: 1518
A; Mycolecule type: DNA
A; Residues: 1518
A; Mycolecule type: DNA
A; Residues: 1518
A; Mycolecule type: DNA
A; Residues: Mycobacterium leprae Cosmid B2235.
A; Mycolecule type: DNA
A; Residues: DNA
A; Residues: DNA
A; Residues: Mycobacterium leprae Cosmid B2235.
A; Mycolecule type: DNA
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A; Mycol
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:U00019; NID:g467079; PIDN:AAA17274.1; PID:g467091
C; Genetics:
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34.3%; Score 66.5; DB 2; Length 495;
Best Local Similarity 46.7%; Pred. No. 6;
Matches 14; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 35.3%; Score 68.5; DB 2; Length 518; Best Local Similarity 46.7%; Pred. No. 3.9; Matches 14; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein B9J10.290 [imported] - Neurospora crassa
                                                                                                7; Indels
                                                        46.7%; Pred. No. 3.7; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 PRLRGWGESMSROVGGRAGGSGGGVGLRGP 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PTLRQW-----LAARAGGGGGGGGIEGP 26
                                                                                                                                                                        4 PTLRQW-----LAARAGGGGGGGGIEGP 26
                                                                                                Conservative
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                                                                Best Local Similarity
Matches 14; Conserv
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 RAGGGGGGGIE----GPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 RAGGGGGGGKEVFKAGRTLLKVLKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A) Experimental source: strain cw-15 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.7%;
57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.7%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.59
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 48.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: genomic RNA A; Residues: 1-201 <ROT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-490 <MOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JQ1094
                                                  A; Introns: 86/3
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                  C; Genetics:
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A; Residues: 379-619 <GE2>
A; Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone: C; Genetics:
A; Cromment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone: C; Genetics:
A; Introns: 86/3
C; Superfamily: laccase
C; Keywords: copper: glycoprotein; oxidoreductase
C; Keywords: copper: glycoprotein; oxidoreductase
C; Keywords: copper: glycoprotein; oxidoreductase
F; 1-21/Domain: signal sequence #status predicted <PRO>
F; 2-4/Pomain: propeptide #status predicted <PRO>
F; 84-215/Domain: propeptide #status predicted <AMA>
F; 84-215/Domain: maino-terminal beta-barrel #status predicted <BBD>
F; 31-72/Domain: maino-terminal beta-barrel #status predicted <BBD>
F; 31-72/Domain: carboxyl-terminal beta-barrel #status predicted <BBD>
F; 319, 282, 295, 340, 422, 444, Banding site: carbohydrate (Asn) (covalent) #status predicted
F; 144, 480/Binding site: copper (His) (type 2) #status predicted
F; 477, 549, 554/Bainding site: Copper (His) (type 1) #status predicted
F; 477, 549, 554/Bainding site: Copper (His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                             C; Species: Neurospora crassa
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change ll-Jun-1999
C;Accession. A59523; A29565
R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and
A;Reference number: A28523; MuID:88087214
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: B28523
R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A;Reference number: A28523; MUID:88087214
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C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-619 <GER>
A; Cross-references: EMBL:M14554
A; Cross-neferences: EMBL:M14554
B; Germann, U.A.; Lerch, K.
Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
A; Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospora
A; Reference number: A29762; MUID:87067412
                                                                       ö
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 619;
33.0%; Score 64; DB 2; Length 333; 76.9%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                     laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)
N;Alternate names: urishiol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain TS)
                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 ROWLAARAGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 RODSQAERYGGGGGGCNSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: urishiol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.78;
57.78;
                     Local Similarity 76.9
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                        169 GGGGGGGGVPGPS 181
                                                                                                                15 GGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-619 <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A28523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A29762
Query Match
                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                RESULT 8
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C;Superfamily: laccase
C;Superfamily: laccase
C;Superfamily: laccase
C;Superfamily: laccase
C;Superfamily: signal sequence #status predicted <SIG>
F;12-14)Commain: signal sequence #status predicted <PRO>
F;22-49)Commain: signal sequence #status predicted <PRO>
F;24-49)Commain: amino-terminal beta-barrel #status predicted <BBI>
F;24-15)Commain: middle beta-barrel #status predicted <BBI>
F;245-372,Commain: middle beta-barrel #status predicted <BBI>
F;245-372,Commain: carboxyl-terminal beta-barrel #status predicted <BBI>
F;144,480,Mainq site: copper (His) (type 2) #status predicted
F;144,480,Mainq site: copper (His) (type 2) #status predicted
F;146,189,191,482,548,550/Binding site: copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 37, 53-66, 1998
A; Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylino
A; Reference number: 216411; MUID:98281574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:D12477; GB:D01129; NID:g222674; PIDN:BAA02044.1; PID:d1002526;
A:Experimental source: strain raspberry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pypothetical 20.2K protein - tomato ringspot virus (Species: tomato ringspot virus (Species: tomato ringspot virus (Species: 13-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999 (SAccession: JQ1094 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999 (S. Rott, M.E., Tremaine, J.H.; Rochon, D.M. A. Rott, M.E., Tremaine, J.H.; Rochon, D.M. A. Title: Nucleotide sequence of tomato ringspot virus RNA-2.

A. Reference number: JQ1093; MUID:91311402
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C:Species: L-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09084
R:Molendijk, A.J.; Irvine, R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 63; DB 2; Length 201; 61.5%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 490;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63.5;
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A)Cross-references: DDBJ:DB7994; NID:92330550; PIDN:BAA21792.1; PID:92330551 A)Cross-references: DDBJ:DB7:DB94; NID:92330551 A)Experimental source: brain cerebellum C; Comment: This enzyme is a processing protease and responsible for processing of var ch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Mori, K;; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; J. Biochem. 121, 941-948, 1997
A;Titler. A novel human PACE4 isoform, PACE4E is an active processing protease contain A;Reference number: JC5570; MUID:97335942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Residues: 1-652 7:50
A. Residues: 1-652 7:50
C. Comment: This protein consists of a signal peptide, a propeptide, a substilisin-lik
C. Comment: This protein cleaves precursor proteins at dibasic amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: JC2191
R;Tsuji, A.; Higashine, K.; Hine, C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y.
R;Tsuji, A.; Higashine, K.; Hine, C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y.
Biochem: Biochys. Res. Commun. 200, 943-950, 1994
A;Title: Identification of novel cDNAs encoding human kexin-like protease, PACE4 isof A;Reference number: JC2191; MUID:94235049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
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                                                                                               Gaps
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C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Superfamily: subtilisin-like proteinase
C; Keywords: glycoprotein; hydrolase; serine proteinase
F; 1-62/Domain: signal sequence #status predicted <SIG>
F; 63-149/Domain: propeptide #status predicted <PRO>
F; 196-434/Domain: subtilisin homology <SBT>
F; 196-434/Domain: subtilisin homology <SBT>
F; 205, 246, 347, 420/Active site: Asp, His, Asn, Ser #status predicted
F; 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C;Superfamily: subtilisin, hydrolase; serine proteinase C;Keywords: alternative splicing; hydrolase; serine proteinase F;196-434/Domain: subtilisin homology <SBT>
F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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    Length 487;
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Score 61.5; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 26;
1; Mismatches
                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: kexin-like protease isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.7%; Score 61.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:PACE4
A;Cross-references: GDB:131390; ONIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AARAGGGGGGGIEGPTLR-----QWL 32
                                                                                                                                                                                         11 AARAGGGGGGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AAGAGGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                                                                                                                                                                               24 AAGAGGAGGAGGAGGPGFRPLAPRPWRWL 52
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              31.7%;
                                                    48.3%;
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                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 15q26-15q26
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A; Residues: 1-962 <MOR>
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                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Dec-1993 #text_change 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-176, 'P', 178-209 <BER1>
A; Cross-references: GB:56923; NID:9240025; PIDN:AAB20548.1; PID:9240026
C; Comment: This protein is a targed-derived, diffusible neurotrophic factor.
C; Comment: The neurotrophins stimulate autophosphorylation and transduce signals through
C; Superfamily: nerve growth factor beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-487 <KIE>
A;Note: the lack of a domain necessary for correct folding and activity of other serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M86742; NID:g205775; PIDN:AAA41728.1; PID:g205776
R;Berkemeler, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenthal, Neuron 7, 857-866, 1991
A;Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.
A;Reference number: JH0503; MUID:92075279
A;Accession: JH0504
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A;Title: Identification of a second human subtilisin-like protease gene in the fes/fps A;Reference number: A39490; MUID:92075167
A;Reference number: B39490
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C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 31-Mar-2000
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C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C; Keywords: alternative splicing; hydrolase; serine proteinase
F; 196-434/Domain: subtilisin homology <SBT>
F; 205, 246, 420/Active site: Asp, His, Ser #status predicted
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F;1-20/Domain: signal sequence #status predicted <PRO>
F;21-79/Domain: propeptide #status predicted <PRO>
F;80-209/Product: neurotrophin-5 #status predicted <NEU>
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62.5; DB 2; Length 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7.3;
2; Mismatches
                                                                                                                      231 GP----LLAAGGGGGGGGGGSSPGDGSTARWDEWL 260
                                      3 GPTLRQWLAARAGGGGGGGI---EGPTLR--QWL 32
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Best Local Similarity 42.5%;
Matches 17; Conservative
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A;Residues: 1-209 <BER>
A;Accession: JH0505
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A; Residues: 1-209 <IPA>
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transcription factor Brn-2 [validated] - human N;Alternate names: class III POU domain protein brain-2; transcription factor Oct-3 N;Contains: transcription factor Brn-2; transcription factor Arabachistic factor Brn-2; transcription factor Oct-5a; transcription factor Arabachistic factor Brn-2; transcription factor Oct-5a; transcription factor Arabachistic factor Arabachistic factor Arabachistic factor Brn-2; transcription factor Oct-5a; transcription factor factor Oct-5a; transcription factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor factor 
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R; Schreiber, E.; Tobler, A.; Malipiero, U.; Fontana, A.
submitted to the EMBL Data Library, April 1992
A; Bescription: The human N-Oct 3 cDNA encodes three neuroectodermal cell lineage rest
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R; He, X.; Treacy, M.N.; Simmons, D.M.; Ingraham, H.A.; Swanson, L.W.; Rosenfeld, M.G.
Nature 340, 35-42, 1989
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A;Reference number: S05042; MUID:89295573
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Dec-2000
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R;Schreiber, E.; Tobler, A.; Malipiero, U.; Schaffner, W.; Fontana, A.
F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 280-350;351-404 <HEX>
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A; Residues: 1-415 <STO>
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les 12; Conserv
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                                                                                    Query Match
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                                                                                                                                                                    Matches
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A; Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing A; Reference number: JC5570; MUID:97335942
A; Accession: JC5570
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C:Comment: This enzyme is a processing protease and responsible for processing of variou
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riviefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A:Title: Identification of a second human subtilisin-like protease gene in the fes/fps
A; Reference number: A39490; MUID:92075167
A; Accession: A39490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
                                                                                                                       Gaps
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C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: alternative splicing; hydrolase; serine proteinase
F;150-969/Product: serine proteinase PACE4 #status predicted <SIG>
                                   Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 969;
                                                                                                                       Indels
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F;205,246,420/Active site: Asp, His, Ser #status predicted
                                   DB 2;
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Pred. No. 37;
1; Mismatches
                          Score 61.5; 1
Pred. No. 37;
                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:131390; OMIM:167405
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                                                                                                                                                                                          11 AARAGGGGGGGGIEGPTLR-----QWL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.78;
                          31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: kexin homolog
                                                              Local Similarity 48.3
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 15q26-15q26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-969 <KIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-975 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A39490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
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Dynochetical protein T12P18.5 [imported] - Arabidopsis thaliana Chypothetical protein T12P18.5 [imported] - Arabidopsis thaliana (mouse-ear cress)

C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Dar-2001
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: C.Species: Arabidopsis thaliana (C.Species)
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                                                                                                                           Gaps
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     Length 975;
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                                                                                                               7; Indels
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           DB 2;
                                                                38;
                                                                                                               1; Mismatches
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     Score 61.5;
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                                                          Pred. No.
                                                                                                                                                                                                                                                                                         24 AAGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                                                                                                                         11 AARAGGGGGGGGIEGPTLR-----OWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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31.78;
                                                    48.3%;
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                            A. Experimental source: tissue-type brain
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
DB:POU3F2; OFF
A;Gene:
C;Genetics:
C;Cuperfamily: transcription factor Brn-1; homeobox homology;
C;Superfamily: transcription factor Brn-2 #status experimental homology
C;Superfamily: transcription factor Brn-2 #status experimental <MATI>
F;125-143/Region: glutamine-rich
F;125-144/Region: glutamine-rich
F;131-145/Region: plutamine-rich
F;131-145/Region: histidine/proline-rich
F;131-155/Region: histidine/proline-rich
F;200-443/Product: transcription factor Oct-5a #status experimental <MAT2>
F;211-259/Region: histidine/proline-rich
F;211-259/Region: histidine/proline-rich
F;211-259/Region: histidine/proline-rich
F;211-259/Region: histidine/proline-rich
F;211-259/Region: histidine/proline-rich
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F;211-259/Region: histidine/proline-rich
F;211-259/Region: histidine/proline-rich
F;211-259/Region: histidine/proline-rich
              A;Title: cDNA cloning of human N-Oct 3, a nervous-system specific POU domain transcripti
A;Reference number: $30296; MUID:93181199
A;Accession: $30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M. Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A; Title: Structure and evolution of four POU domain genes expressed in mouse brain. A; Reference number: S31223; MUID:95228768
A; Accession: S31224
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C; Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
E; 88-90,Region: glycine-rich
F; 125-151/Region: glutamine-rich
F; 123-165/Region: histidine/proline-rich
F; 213-261/Region: histidine/proline-rich
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N.Alternate names: class III POU domain protein brain-2
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Spate: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
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2; Mismatches
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                                                                                                                                         A; Status: nucleic acid sequence not shown
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Nucleic Acids Res. 21, 253-258, 1993
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N;Alternate names: cytokeratin 10
C;Species: Homo sapiens (man)
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66.7%;
                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-25, 'G', 27-443 <SCW>
A; Cross-references: EMBL:211933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.4%;
66.7%;
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Matches 10; Conservative
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Best Local Similarity
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A; Residues: 1-445 <HAR>
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: 452-463, 'P', 465-507, 'Y', 523-593 < KOR2>
A; Cross-references: PIDN: AAB21314.1; PID: 9244508
A; Molecule type: Sequence extracted from NCBI backbone (NCBIP: 79431)
B; Tkachenko, A.V.; Buchman, V.L.; Bliskovsky, V.V.; Shvets, Y.P.; Kisselev, L.L.
Gene 116, 245-251, 1992
A; Title: Exons I and VII of the gene (Ker10) encoding human keratin 10 undergo struct
A; Reference number: PC1102; MUID: 92339897
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A; Introns: 209/3; 237/2; 289/3; 343/3; 385/3; 458/2; 592/3
A; Note: this gene encodes variants with considerable length polymorphism
A; Note: mutations in this gene can cause epidermolytic hyperkeratosis and keratosis p
C; Complex: heterotetramer of two type I and two type II proteins, usually keratin 1 (
C; Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone lambda-KH10-5
B; Korge, B.P.; Gan, S.O.; McBride, O.W.; Mischke, D.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 910-914, 1992
A;Title: Extensive size polymorphism of the human keratin 10 chain resides in the C-t A; Reference number: A38182; MUID:92141228
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A; Residues: 130-278, YV', 281-311, 'I', 313-339, 'V', 341-373, 'R', 375-407, 'Q', 409-459, 'RS', 56-579, 'P', 581-593 *CDARL**) ** COSS-references: EMBL: M19156; NID: 9186769
A; Cross-references: EMBL: M19156; NID: 9186769
A; Note: the sequence from Fig. 3 is inconsistent with the nucleotide sequence from Fi
R; Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
B; Marmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
A; Reference number: S14667
A; Accession: S14669
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A;Note: the translated sequence in GenBank entry HUMKRT10A, release 111.0, differs fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 struct
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A;Residues: 130-278,'YV',281-311,'I',313-339,'V',341-373,'R',375-407,'Q',409-459,'RS'
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 10-Dec-1999 C;Accession: S02158; C38182; B38182; PC1102; S14666; S14669 B;Rieger, M.; Franke, W.W. J. Mol. Biol. 204, 841-856, 1988 A;Title: Identification of an orthologous mammalian cytokeratin gene. High degree of A;Reference number: S02158; MUID:89125611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 'G',198-407,'Q',409-450,'G',452-486,491-524,534-593 <TKA>
A; Residues: 'G',198-407,'Q',409-450,'G',452-486,491-524,534-593 <TKA>
A; Cross-references: GB:M77653, NID:9186629; PIDN:AAA59199.1; PID:9186629
A; Experimental source: embryonic skin, clone HK51
R; Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M.
Mol. Biol. Rep. 12, 277-283, 1987
A; Title: Sequence of a cDNA encoding human keratin No 10 selected according to shacesion: S14666; MUID:88122104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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A;Cross-references: EMBL:X14487; NID:928316; PIDN:CAA32649.1; PID:928317
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A;Molecule type: DNA
A;Residues: 452-593 <KORL>
A;Cross-references: PIDN:AAB21315.1; PID:9244509
A;Note: sequence extracted from NCBI backbone (NCBIP:79427)
A;Accession: B38182
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F;146-456/Domain: helical rod #status predicted <ROD>
F;457-593/Domain: tail <TAI>
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A;Cross-references: GDB:118828; OMIM:148080
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Best Local Similarity 52.6%;
Matches 10; Conservative
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A;Note: this gene and protein are called MIB in this paper R;Brzeska, H.; Lynch, T.J.; Martin, B.; Korn, E.D. J. Biol. Chem. 264, 19340-19348, 1989 A;Title: The localization and sequence of the phosphorylation sites of Acanthamoeba A;Reference number: A34448; MUID:90037074
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35.0%;
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60.0%;
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(Species: Acarthamoeba castellani)
(C. Species: Acarthamoeba castellani)
(C. Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 19-Jan-2001
(C. Accession: A33891; C34448; A24146
(R. Jung, G.; Korn, E.D.; Hammer III, J.A.
(R. Jung, G.; Korn, E.D.; Hammer III, J.A.
(A. 67205)
(A. Title: The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like and non-my A; Reference number: A33891; MUID:88016163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Chen, C.N.; Denome, S.; Davis, R.L. Proc. Natl. Agad. Sci. US.A. 88, 9313-9317, 1986
A;Title: Molecular analysis of cDNA clones and the corresponding genomic coding sequence A;Reference number: A26651; MUID:87092243
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A; Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 262/3; 294/1; 407/3; 496/2; 534/2; 588/3; 7
A; Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 262/3; 294/1; 407/3; 496/2; 534/2; 588/3; 7
C; Superfamaily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'
C; Keywords: alternative splicing; phosphodiesterale hydrolase
F; 137-777/Product: cAMP-dependent 3', 5'-cyclic-nucleotide phosphodiesterase, splice form
F; 439-667/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                  splice form II
                                                                                                                                                                                                                       3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific, splice form III N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase, cAMP-specific, splice form III C;Species: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                   C; Date: 28-Oct-1995 #sequence_revision 19-Jul-1996 #text_change 17-Nov-2000 C; Casession: 85544; 819662; 865544; A26611 R; Odiu, Y.; Chen, C.N.; Malone, T.; Richter, L.; Beckendorf, S.K.; Davis, R.L. J. Mol. Biol. 222, 553-56, 1991 A; Title: Characterization of the memory gene dunce of Drosophila melanogaster. A; Reference number: 819662; MUID: 92085274
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A;Residues: 1-1168 <JUN>
A;Cross-references: GB:J02974; NID:g155624; PIDN:AAA27707.1; PID:g155625
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A;Residues: 'MVCSFCCCCYNFRN',4,'P',6,'S',94-777 <Q14>
A;Cross-references: EMBL:X55174
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7 RQWLAARAGGGGGGGGIEG 25
                                     A;Cross-references: EMBL:X55174
A;Accession: S19662
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A;Residues: 137-777 <Q12>
A;Cross-references: EMBL:X55174
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A; Residues: 416-777 <CHE>
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A; Residues: 1-777 <QIU>
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Aintrons: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 321/3; 4
C; Superfamily: protozoan myosin heavy chain IB: myosin motor domain homology; SH3 hom
C; Steyords: actin binding; ATP: hydrolase; nucleotide binding; P-loop; phosphoprotein
F;10-653/Domain: myosin motor domain homology cMMOT>
F;101-108/Region: nucleotide-binding motif A (P-loop)
F;513-564/Region: actin binding #status predicted
F;671-1168/Domain: carboxyl-terminal <CTD>
F;511-1168/Domain: basic
F;523-378/Region: almine/glycine/proline-rich
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A;Note: sequence extracted from NCBI backbone (NCBIN:93810, NCBIP:93811)
R;Berkemeler, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenth Neuron 7, 857-866, 1991
A;Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.
A;Reference number: JH0503; MUID:92075279
A;Molecule type: protein
A;Residues: 308-314, X',316-329 <BRZ>
C;Comment: In this protein, the coiled-coil rod-like region found in many myosin heav
he protein is globular and does not self-associate into filaments.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; wate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999 C; Accession: A42687; JH0503 R; Ip, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992 A; Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distriant A; Reference number: A42687; MUID:92212967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-210 <BER>
C;Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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F:1034-1168/Region: alamine/glycine/proline-rich
F:107/Binding site: ATP (Lys) #status predicted
F:311/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-24/Domain: signal sequence #status predicted <SIG>F;25-80/Domain: propeptide #status predicted <PRO>F;81-210/Product: neurotrophin-4 #status predicted <NEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60.5; 1
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 19pter-19qter
C;Superfamily: nerve growth factor beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:134723; OMIM:162662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown
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Gaps

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Indels

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Keratin, 59K type I cytoskeletal - mouse
N;Alternate names: 59-kDa type I keratin
C;Species: Mus musculus (house mouse)
C;Date: 15-Nov-1984 #sequence_revision 04-Dec-1986 #text_change 10-Dec-1999
C;Accession: A02940
R;Krieg, T.M.; Schafer, M.P.; Cheng, C.K.; Filpula, D.; Flaherty, P.; Steinert, P.M.;
J. Biol. Chem. 260, 5867-5870, 1985
A;Title: Organization of a type I keratin gene. Evidence for evolution of intermediat
A;Reference number: A02940; MUID:85207552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: initiator Met not shown
A; Note: the authors translated the codon GAG for residue 41 as Gly
C; Comment: Fourier analysis has identified a 7-residue repeating pattern (heptad) bet forms a stable alpha-helical coiled coil but is interrupted by three short regions wi C; Comment: Most of the introns of the gene encoding this protein are located within the sequence at or near the beginning of heptad repeats. Several of these sites are co C; Comment: The amino and carboxyl ends are rich in glycine, serine, and aromatic resi
                                                          A; Cross-references: EMBL: U19028; NID: 9609380; PID: 92340034; GSPDB: GN00012; MIPS: YLR33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L00193; GB:K00391; NID:9198625; PIDN:AAA39391.1; PID:9387397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X60063; NID:g62927; PIDN:CAA42665.1; PID:g62928 C;Superfamily: jun transforming protein; fos/jun DNA-binding domain homology C;Keywords: DNA binding; nucleus; transcription regulation F;237-277/Domain: fos/jun DNA-binding domain homology <FUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                       DB 2; Length 285;
18;
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                                                                                                                                                                     A;Map position: 12R
C;Keywords: transmembrane protein
F;142-158/Domain: transmembrane #status predicted <TM1>
F;201-217/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                           Score 60; DB 2; Pred. No. 18; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cycoession: $20099
R:Hartl, M.: Hutchins, J.T.: Vogt, P.K.
Oncogene 6, 1623-1631, 1991
A;Rille: The chicken junb gene and its product.
A;Reference number: $20099; WUID:92019832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transforming protein junD - chicken
                                                                                                                                                                                                                                                                                                                                           30.9%;
ilarity 57.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AAAAGGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AARAGGGGGGGGIEGPTL 28
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
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A; Residues: 1-569 <KRI>
                             1-285 <DUZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
                                                                                                                                    A; Gene: MIPS:YLR338w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A02940
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                             A; Residues:
                                                                                                   C; Genetics
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                                                                                                                                                                                                                                                                                                                                    N.Alternate names: protein tyrosine kinase tykl
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 16: Feb-1994 #sequence_revision 12-Apr-1996 #text_change 04-Feb-2000
C;Accession A48565 #37452; A60189
R;Toyoshima, H.; Kozutsumi, H.; Maru, Y.; Hagiwara, K.; Furuya, A.; Mioh, H.; Hanai, N.;
Proc. Natl. Acad Sci. U.S.A. 90, 5404-5408, 1993
A;Title: Differently spliced cDNAs of human leukocyte tyrosine kinase receptor tyrosine
A;Reference number: A48266; MUID:93296146
A;Accession: A48266
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(S.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: alternative splicing; ATP; phosphorransferase; tyrosine-specific protein kin
F:508-784/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Reference type: mRNA
A; Residues: 1-664 < TOY>
A; Residues: 1-664 < TOY>
A; Residues: 1-664 < TOY>
A; Crossreferences: GB: D106105; NID: 9440854; PIDN: BAA03679.1; PID: d1004194; PID: 9440855
A; Crossreferences: GB: D166105; NID: 9440854; PIDN: BAA03679.1; PID: d1004194; PID: 9440855
A; Rote: sequence modified after extraction from NCBI backbone
A; Note: the authors translated the codon CAG for residue 42 as Arg
A; Note: sequence extracted from NCBI backbone (NCBIN: 133811)
B; Krolewski, J.J.; Dalla-Pavera, R
ENBO J. 10, 2911-2919, 1991
A; Reference number: S1452; MUID: 92007735
A; Accession: S17452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-41, 'R',43-219,'L',221-273,335-864 <KRO>
A; Cross-references: EMBL:X60702; NID:g34419; PIDN:CAA43113.1; PID:g34420
B; Krolewski, J.J.; Lee, R.; Eddy, R.; Shows, T.B.; Dalla-Favera, R.
Oncogene 5, 277-282, 1990
A; Title: Identification and chromosomal mapping of new human tyrosine kinase genes.
A; Reference number: A60189; MUID:90191712
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N;Alternate names: hypothetical protein L8300.13-a
C;Species: Saccharomyces cerevisiae
C;Species: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 05-Nov-1999
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A60189
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
14; Indels
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                                                                                                                                        129 GSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                                  3 GPTLRQWL------AARAGGGGGGGGGTEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;516-524/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                     protein-tyrosine kinase (EC 2.7.1.112) ltk - human
3; Mismatches
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1; Mismatches
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63.6%;
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Matches 14; Conservative
   14; Conservative
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A: Residues: 608-716 <KR2>
C:Genetics:
A:Gene: GDB:LTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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   Matches
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5; Indels

DB 2; Length 323;

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12; Conservative
    Matches
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Submitted to the EMBL Data Library, July 1995
A;Description: hdc, an imaginal specific gene required for adult morphogenesis in Drosop
A;Reference number: S58064
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A; Residues: 1-806 <MUR>
A; Cross-references: EMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA21318.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Bescription: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217699
A;Accession: T13690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hdc protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan.1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1998
C;Accession: S58064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Drosophila melanogaster
C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C.Accession: T13690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein EG0003.2 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                         30.9%; Score 60; DB 1; Length 569; 43.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60; DB 2; Length 806;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%; Score 60; DB 2; 76.9%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                F;179-192/Region: linker II
F;193-293/Region: coil 1B
F;294-309/Region: linker 12
F;310-328/Region: linker 12
F;329-336/Region: linker 2
F;329-37/Region: coil 2B
F;355/Region: stutter
F;458-569/Domain: tail <END>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: FlyBase:FBgn0025833
A;Introns: 37/3; 448/3; 611/2; 690/3
A;Note: EG:EG0003.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:hdc
A;Cross-references: FlyBase:FBgn0010113
                                                                                                                                                                                                                                                                                                                                                                                                                      : |: ::|:|||||||| : : |
9 KQFSSSRSGGGGGGGCSVRVSSTR 31
                    F;1-143/Region: El and V1 subdomains
                                                                                                                                                                                                                                                                                                                                                                                                7 ROWLAARAGGGGGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%;
54.5%;
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 43.59
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9°
Matches 10, Conservative
                                         F;144-457/Domain: rod <ROD>
F;144-178/Region: coil 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 GGGGGGGVNGNT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GGGGGGGIEGPT 27
F;1-143/Domain: head <HED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S58064
                                                                                                                                                                                                                                                                                                           Query Match
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T13690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 29
S58064
                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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2.5 .e. .• 

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:51:41; Search time 4.29977 Seconds (without alignments) 324.181 Million cell updates/sec Run on:

US-09-422-838C-26 194 1 IEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 36 Title: Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P06811 neurospora	74	'n	_	043819 homo sapien	уошоц	qallu		mus m	P12252 drosophila	P13645 homo sapien	acant	sorgh		homod	qallu		076324 drosophila			P08923 mus musculu	P22293 drosophila	P53783 mus musculu	009029 mesocricetu	рошо	homod	homo	lucil			mus m	inl homo	homo
SUMMARIES		ΩI																JUND_CHICK	SXL_CERCA	DCO_DROME	FXD2_HUMAN	K1CJ_MOUSE	KLTK_MOUSE	SUS_DROME	SOX1_MOUSE	BET3_MESAU	HB9_HUMAN	ONC2_HUMAN	ZIN_HUMAN	ECR_LUCCU	DYHA_CHLRE	HXD9_HUMAN	HXD9_MOUSE	HH3R_HUMAN	EVX2_HUMAN
		Match Length DB	619 1	619 1														323 1	348 1	440 1	497 1	569 1	888		391 I										
æ	Query	Match	32.7	32.7	32.5	32.2	32.2	31.7	31.4	31.4	31.4	31.4			31.4	31.2	31.2	0.0 0.0	30.9	9.00	3.00 9.00	30.9	30.9	30.9	30.7	30.4	30.4	30.4	30.4	30.4	30.4	30.2	29.9	29.9	29.9
		Score	63.5	ω,	0	62.5		61.5	19	61	61	19	70	٠ ١	To 0,	50.5	60.5	0 0	90	30	0 0	0 0	90		U. V	700	90,0	υ. 6	υ. υ.	59		58.5	28	28	28
	Result	No.	н.	03 (	<b>-</b> 77 -	41	η,	، م	~ 0	<b>30</b> (	2,0	7.0	7.	77	T .	<b>†</b> 1	CT .	9 T	17	8 6	H (	20	77	770	223	4 2 0	7 7	26	17	87.0	67	30	31	32	e e

P31361 mus musculu	P20264 homo sapien	O83933 treponema p O54839 mus musculu	O55165 rattus norv	P25764 oryza sativ	P01317 bos taurus	P01318 ovis aries	P97273 cavia porce	P04574 sus scrofa	P04632 homo sapien
BRN1_MOUSE BRN1_RAT	BRN1_HUMAN	EOMD_MOUSE	KF3C_RAT	PHYB_ORYSA	INS_BOVIN	INS_SHEEP	TTF1_CAVPO	CANS_PIG	CANS_HUMAN
7 7	П,		П	-	П	-	Н	+	1
495	500	7TC 688	196	1171	105	105	112	266	268
99	0 0	ת ת	6	σ	9	و	4	4	4
29.9	29	2 6	29	29	29.	29.	29.	29.	29.
58 58	28	28	28	28	57.5	57.5	57	57	57
34 35	36	38	39	40	41	42	43	44	45

## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-501-1989 (Rel. 11, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-COT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS).
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- COFÁCTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-:- SUBCELLULAR LOCATION. Secreted (Potential).
-:- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 619;
                                                                                                                COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
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COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                            FDED6D78B65048E3 CRC64;
                                                                                PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 63.5; Dillarity 57.7%; Pred. No. 9.9; Conservative 0; Mismatches
                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                          7 RQWLAARAGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                        39 RQDSQAERYGGGGGGCNSPTNRQCW 64
                                                                                                                                                                                                                                                                                                                                      X.
                                                                                                                                                                                                                                                                                                                                      68198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAC2_NEUCR
P10574;
                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                            CARBOHYD
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                                                           CHAIN
PROPEP
DOMAIN
DOMAIN
                                      SIGNAL
                                                  PROPEP
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                                                                                                                                                       METAL
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                                                                                                                                   METAL
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There are no restrictions on
ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. . .) (POTENTIAL).
C. . .) (POTENTIAL).
C. . .) (POTENTIAL).
C. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%; Score 63.5; DB 1; Length 619; 57.7%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
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COPPER (TYPE 1) (PROBABLE).
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COPPER (TYPE 1) (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rott M.E., Tremaine J.H., Rochon D.M.; "Nucleotide sequence of tomato ringspot virus RNA-2."; J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBB6CCDE18841145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 20.2 kDa protein in RNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
   the European Bioinformatics Institute.
                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                         EMBL, M18334, AAA33592.1; -.
PIR, B28523, KSNCTT
Interpro; IPR001117; Cu-oxidase.
Interpro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                                                                                           LACCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ROWLAARAGGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 RQDSQAERYGGGGGGCNSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91311402; Pubmed=1856689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68120 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                             Glycoprotein; Repeat SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YR21_TRSVR
P25245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nepovirus.
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                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  METAL
    Db
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ć

Gaps

6

12; Indels

Length 209;

Score 62.5; DB 1;

Pred. No. 4.8; 2; Mismatches

17; Conservative

Matches

Local Similarity

. .) (POTENTIAL).

-> P (IN REF. 2). DF5112C05C5D5B85 CRC64;

22332 MW; 32.28; 42.5%;

209 AA;

CONFLICT

N-LINKED (GLCNAC.

200 75 177 169

NEUROTROPHIN-5

POTENTIAL.

PROSITE; PS00248; NGF\_1; 1. PROSITE; PS50270; NGF\_2; 1. Growth factor; Signal.

HSSP; P34130; 1B8M.
InterPro; IPR002072; NGF.
Pfam; PP00243; NGF; 1.
PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM0140; NGF; 1.

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

22 80 96 140 157 75

DISULFID DISULFID DISULFID CARBOHYD SEQUENCE Query Match

PROPEP SIGNAL

CHAIN

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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                  4;
                                                                                                                                                                                      32.5%; Score 63; DB 1; Length 201;
                                                                                                                                                                                                                5; Indels
                                                                                                                                                            9038506E18D7B450 CRC64;
                                                                                                                                                                                                               1; Mismatches
                                                                                                                      POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                        RAGGGGGGGIE----GPTLRQWLAA 34
                                                                                                                                                                                                                                                       13 RAGGGGGGGKEVFKAGRTLLKVLKA 38
                                                                                                                                                            20194 MW;
                                                               EMBL; D12477; BAA02044.1; -. PIR; JQ1094; JQ1094.
                                                                                                                                                                                                61.5%;
                                                                                                                                                                                                                Conservative
                                                                                                                     22
66
148
                                                                                         HSSP; P04002; IWFA.
Hypothetical protein.
DOMAIN 15 2
                                                                                                                                                            201 AA;
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tes 16; Conserv
                                                                                                                                                          SEQUENCE
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                                                                                                                                  DOMAIN
                                                                                                                                               DOMAIN
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SEQUENCE FROM N.A.
MEDLINE=92212967; PubMed=1313578;
IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.,
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-92075279; Pubmed-1742028;
Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                             01-FEB-1994 (Rel. 28, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
(NT-4) (Neutrophic factor 4).
                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: COULD SERVE AS A TARGET-DERLYED TROPHIC FACTOR FOR SENSORY AND SYMPATHETIC NEURONS.
-!- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN, HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRYO AND ADULT
                                                                                                                                                                                                                                                                                                              Mammalian neurotrophin-4: structure, chromosomal localization
                                                                                                                                                                                                                                                                                                                             tissue distribution, and receptor specificity"; Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992)
                                  209 AA
                                  PRT;
                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuron 7:857-866(1991).
                                                                                                                                           NTF5 OR NTF4 OR NT4.
                                                                                                                                                                                                     NCBI_TaxID=10116;
                              NT5_RAT
P34131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        trkB."
RESULT 4
```

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EMBL; M86742; AAA41728.1; -. EMBL; S69323; AAB20548.1; -.

PIR; JH0504; JH0504. PIR; B42687; B42687.

-!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

TISSUES.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- FUNCTION: THOUGHT TO PLAY A ROLE IN EITHER MITOCHONDRIAL COPPER TRANSPORT OR INSERTION OF COPPER INTO THE ACTIVE SITE OF COX.
-:- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-:- TISSUE SPECIFICITY: UBUIQUITOUS.
-:- DISEASE: DEFECTS IN SCO2 ARE THE CAUSE OF FATAL INFANTILE CARDIOENCEPHALOMYOPATHY WITH COX DEFICIENCY. THIS DISEASE IS CHARACTERIZED BY HYPERTROPHIC CARDIOMYOPATHY, LACTIC ACIDOSIS, AND GLIOSIS. HEART AND SKELETAL MUSCLE SHOW REDUCTIONS IN COX ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX DEFICIENCIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20014747; Pubmed-1054592.

MEDLINE-20014747; Pubmed-1054592.

Papadopoulou L.C., Sue C.M., Davidson M.M., Tanji K., Nishino I., Sadlock J.E., Krishna S., Walker W., Selby J., Glarum D.M., Van Coster R., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S. De Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A., Fartal infantile cardioencephalomyopathy with COX deficiency and mutations in SCO2, a COX assembly gene.";
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS FIC LYS-140 AND PHE-225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smink L.J., Burton J.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                      128 GSPLROYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
3 GPTLRQWL-----AARAGGGG---GGGGIEGPTLRQWLA 33
                                                                                                                                                                  043819, 0901887;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                               SCO2 protein homolog, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SCO1/2 FAMILY.
                                                                                                                                                       266 AA.
                                                                                                                                       PRT;
                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Monocytes;
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                       SCO2_HUMAN
                                                                                                          RESULT 5
SCO2_HUMAN
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4

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5
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAC4_HUMAN STANDARD; PRT; 969 AA.
P32122; 015099; 015100; 09UEJ1; 09UEJ2; 09UEJ7; 09UEJ8; 09UEJ9; 09UEC7; 09Y4G9; 0015100; 09Y4H1; 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1901 (Rel. 40, Last annotation update)
Paired basic anno acid cleaving enzyme 4 precursor (EC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barr P.J.; "Identification of a second human subtilisin-like protease gene in the fes/fps region of chromosome 15."; DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of novel cDNAs encoding human kexin-like protease, PACE4 isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95071480; PubMed-7980617;
Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                 MIM; 5049.),
MIM; 20110;
MIM; 2020110;
Interpro; IPR003782; SCO1_SenC.
Pfam; PF02630; SCO1-SenC; 1.
Mitochondrion; Transit peptide; Disease mutation; Polymorphism.
TRANSIT 12 266 SCO2 PROTEIN HOMOLOG.
VARIANT 20 20 R-> P (IN DBSNP:140523).

VARIANT 140 140 E-> K (IN FIC).

/FTIG=VAR_008874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                              Score 62.5; DB 1; Length 266; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.9;
2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LRQWLAARAGGG--GGGGGIEGPTLR---------------------36
                                                                                                                                                                                                                                                                                               /FIId=VAR_008875.
BC2F40E057329BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 204:1381-1382(1994). [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31ochem. Blophys. Res. Commun. 200:943-950(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Hepatoma, and Kidney;
MEDLINE-92075167; PubMed-1741956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94235049; PubMed-8179631;
                                              EMBL; AF177385; AAF05313.1; -. EMBL; AL021683; CAA16671.1; -.
                                                                                                                                                                                                                                                                                                                 266 AA; 29810 MW;
                                                                                                                                                                                                                                                                                                                                              Query Match 32.2%;
Best Local Similarity 37.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               convertase 4) (SPC4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PACE4 isoforms.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'ISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuda Y.;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAC4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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MEDICINE—97335942; PubMed=9192737;
MORI K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
"A novel human PACE4 isoform, PACE4E is an active processing protease
containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                                                                                                                                                                      MEDLINE-98021085; PubMed-9378725; A-II; CS; D; E-I; E-II). MEDLINE-98021085; PubMed-9378725; Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; Mori Corganization and alternative splicing of human PACE4 (SPC4), kexin-like processing endoprotease."; J. Blochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                 "Endopergreease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Blochem. J. 339:639-647(1999).
           TISSUE=Placenta; Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A., Matsuda Y.;
                                                                                                                                                                                                                                                                                Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Functional analysis of human PACE4-A and PACE4-C isoforms: identification of a new PACE4-CS isoform.";
                                                                                                                                                                                                                                                                                                                                                          Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W., Moehring T.J.;
                                                   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                          SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II)
                                         "Identification of a novel PACE4 isoform, PACE4E.";
                                                                                                                                                                                                                                                              ALTERNATIVE SPLICING (ISOFORM PACE4CS).
SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99233559; PubMed=10215603;
                                                                                                                                                                                                                                                                          MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98408849; PubMed=9738469;
                                                                                                                                                                                                                                                                                                                   FEBS Lett. 396:31-36(1996).
                                                                                        TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                             PROCESSING
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EXPRESSED IN PLACENTA. PACE4E-1 IS EXPRESSED IN CEREBELLUM, PLACENTA AND PITUITARY. PACE4E-1I IS AT LEAST PRESENT IN
                                                                                  CEREBELLUM.
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- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
  - ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACEAD LACKS THE PROPEPTIDE DOMAIN.
    SIMILARIY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.

SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

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Gaps

7;

1; Mismatches

31.7%; Score 61.5; Pred. No.

48.38;

Similarity

Query Match Best Local

14; Conservative

Matches

BAA21625.1;

AB001908;

JOINED. JOINED. JOINED.

BAA21625.1; BAA21625.1;

BAA21625.1; BAA21625.1;

AB001905;

EMBL; EMBL; EMBL;

EMBL;

EMBL;

BAA21625.1;

AB001906; AB001907;

JOINED.

BAA21625.1; BAA21625.1; BAA21625.1;

AB001901; AB001902; AB001903; AB001904;

AB001900;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

JOINED JOINED

BAA21624.1; J BAA21625.1; BAA21625.1; J

AB001913; AB001914; AB001898;

BAA21624.1;

AB001912;

DB 1; Length 969; Indels

JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. JOINED.
JOINED. JOINED. JOINED. JOINED. JOINED.
JOINED.
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JOINED.
JOINED. JOINED. JOINED. JOINED. JOINED. JOINED. AB001914; BAA21620.1; -. AB001898; BAA21620.1; JOINED AB001900; BAA21620.1; JOINED JOINED. BAA21624.1; JOINED. BAA21624.1; JOINED. BAA21624.1; JOINED. JOINED JOINED JOINED JOINED JOINED JOINED JOINED EMBL; M80482; AAA59998.1; -. AB001901; BAA21620.1; AB001902; BAA21620.1; AB001903; BAA21620.1; AB001904; BAA21620.1; AB001905; BAA21620.1; BAA21623.1; BAA21624.1; BAA21623.1; BAA21624.1; BAA21622.1 BAA21623.1 BAA21623.1 BAA21623.1 BAA21623.1 BAA21623.1 BAA21623.1 BAA21623.1 BAA21624.1 BAA21624.1 BAA21624.1 BAA21624.1 BAA21621. BAA21621. BAA21622. BAA21622. BAA21622 BAA21621 BAA21621 BAA21621 BAA21621 BAA21621 BAA21621 BAA21621 BAA21621 BAA21622 BAA21623 BAA21623 BAA21624 BAA21621 AB001904; AB001905; AB001910; AB001911; AB001914; AB001900; AB001902; AB001914; AB001898; AB001904; AB001909; AB001901; AB001908; AB001914; AB001902; AB001901; AB001905; AB001906; AB001907; AB001908; AB001902; AB001903; AB001906; AB001898; AB001906; AB001907; AB001900; AB001902; AB001900; AB001901; AB001903; AB001904; AB001905; AB001908; AB001909; AB001901; AB001903; AB001907 EMBL; 

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                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAR-2000 (Rel. 39, Last annotation update)
FORKhead box protein D3 (HNF3/FH transcription factor genesis) (Winged helix protein CWH-3).
                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                          Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K., Abberrant cell growth induced by avian winged helix proteins."; Cancer Res. 57:123-12911997.
i. FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding, Nuclear protein; Transcription regulation.
DOMAIN 67 70 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ALA.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORK-HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY - ALA
11 AARAGGGGGGGGIEGPTLR-----QWL 32
                  24 AAGAGGAGGAGGAGGFRPLAPRPWRWL 52
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
MEDLINE=97141794; PubMed=8988052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00339; FH; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS00039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFĀC; T02495; .
InterPro; IRRO1766; Fork_head.
Pfan; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U37274; AAC60066.1; -. HSSP; Q63245; 2HFH.
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 1
117 2
394 AA;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                              FXD3_CHICK
P79772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                             FXD3_CHICK
                                                                                                                                                                                                                               FOXD3
                                q
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324A4B36B9E31899 CRC64;

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                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of a large family of POU-domain regulatory genes in mammalian brain development.";
Nature 340:35-42(1989).

"I- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO THE RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALE-SITES, ('GCAT') AND (TAAT'), SEPARATED BY A NONCONERVED SPACER REGION OF 0, 2, OR 3 NUCLEOTIOES. POSITIVELY REGULATES THE GENES UNDER THE CONTROL OF CORTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II PROWOTERS (BY SIMILARITY).

-: SUBCELLULAR LOCATION: NUCLear.

-: ALTERNATIVE PRODUCTS: 3 ISOFORMS; N-OCT 3 (SHOWN HERE), N-OCT 5A AND N-OCT 5B, ARE PRODUCED BY ALTERNATIVE INTIATION.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The brn-2 gene regulates the melanocytic phenotype and tumorigenic potential of human melanoma cells."; Oncogene 11:691-700(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schreiber E., Tobler A., Malipiero U., Schaffner W., Fontana A.; "cDMs cloning of human N-Oct3, a nervous-system specific POU domain transcription factor binding to the octamer DNA motif."; Nucleic Acids Res. 21:253-258
                                                                                                                                                                                                                                   P2025; Q14960;

01-FEB-1991 (Rel. 17, Created)

01-VUL-1993 (Rel. 26, Last sequence update)

16-CCT-2001 (Rel. 40, Last annotation update)

Nervous-system specific octamer-binding transcription factor N-OCT

Randn-specific homeobox/POU domain protein 2) (BRN-2 protein)

FOOUTPE OR BRN2 OR OTF7 OR OCT7.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He X., Treacy M.N., Simmons D.M., Ingraham H.A., Swanson L.W., Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angus J., Thomson F., Murphy K., Baker E., Sutherland G.R., Parsons P.G., Sturm R.A.;
    Score 61; DB 1; Length 394;
Pred. No. 12;
                                          2; Indels
                                                                                                                                                                                                                      443 AA.
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
MEDLINE-89295573; PubMed-2739723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93181199; PubMed-8441633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95380176; PubMed-7651733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 280-404 FROM N.A.
31.4%;
84.6%;
                      Best_Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                      STANDARD;
                                                                               13 RAGGGGGGGGIEG 25
                                                                                                                   82 RGGGGGGGGEEG 94
                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL LINEAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissue-Liver;
                                                                                                                                                                                                                      OC3N_HUMAN
      Query Match
                                                                                                                                                                              RESULT 8
OC3N_HUMAN
                                                                                                                                                                                                                                       ò
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PROMOTERS (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE NEUROECTODERMAL
CELL LINEAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Nervous-system specific octamer-binding transcription factor N-OCT 3
(Brain-specific homeobox/POU domain protein 2) (BRN-2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 89:3280-3284(1992).
-!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO THE RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALF-SITES, ('GCAT') AND ('TAAT'), SEPRRATED BY A NONCONSERVED SPACER REGION OF 0, 2, OR 3 NUCLEOTIDES. POSITIVELY REGULARES THE GENES UNDER THE CONTROL OF CORTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hara Y., Rovescalli C., Kim Y., Nirenberg M.; Structure and evolution of four POU domain genes expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                             PROSITE; PS00465; POU_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61; DB 1; Length 443; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> G (IN REF. 2).
2CAC852328334A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 13;
2; Mismatches
                                                                                                                                                                                                                                                                                      Activator; Alternative initiation.
CHAIN 181 443 N-OCT 3.
CHAIN 200 443 N-OCT 5A.
CHAIN 181 181 FOR N-OCT 5B.
INIT_MET 200 200 FOR N-OCT 5B.
                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92228768; PubMed=1565620;
                                                                                                                                                                                      SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Pour
                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     46921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.4%;
66.7%;
                                                                                                                               Pfam; PF00046; homeobox; 1.
                                                                                                                                                        PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
EMBL; Z11933; CAA77990.1;
                L37868; AAB59611.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 QWLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 OWITALSHGGGGGG 74
                                                                                                                                             Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                               S05043; S05043.
                                             S29334; S29334.
                                                                        FRANSFAC; T00630; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     26
443 AA;
                                                         P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                    PROSITE; PS00035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissue=Brain;
                                                                                     MIM; 600494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OC3N_MOUSE
ID OC3N_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P31360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain."
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
               EMBL;
                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---
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                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
cAMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Learning/memory)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00035; P00_1; 1.
PROSITE; PS00465; P00_2; 1.
DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 223-584 FROM N.A.
MEDLINE-87092243; Pubmed-3025834;
Chen C.-N., Denome S., Davis R.L.;
"Molecular analysis of cDNA clones and the corresponding genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.4%; Score 61; DB 1; Length 445; 66.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of the memory gene dunce of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 90 POLY-GLY.
125 149 POLY-GLN.
268 338 POU.
356 415 HOMEOBOX.
445 AA; 47149 MW; 1A47F10950EECE8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92085274; Pubmed=1660926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanogaster.";
J. Mol. Biol. 222:553-565(1991).
                                                                                                                                                                                                                                                      PIR; S31224; S31224.
HSSP; P14859; 10CT.
MGD; MGI:101895; Pou3f2.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                    EMBL; M88300; AAA39961.1; -.
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00046; homeobox; 1. Pfam; PF00157; pou; 1. PRINTS; PR00028; POUDOMAIN. Probom; PD000583; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 QWITALSHGGGGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QWLAARAGGGGGGG 22
                           TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNA1_DROME
P12252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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  δ
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                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PART OF CAMP BINDING SITE (BY SIMILARITY TO MAMMALIAN REGULATORY SUBUNIT OF TYPE 2 CAMP DEPENDENT PROTEIN KINASE).
             for cAMP phosphodiesterase.";
Proc. Natl. Acad. Sci. U.S.A. 83:9313-9317(1986).
-! CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O = ADENOSINE 5'-PHOSPHATE = LATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
-!- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
-!- SUBUNIT: MONOMER:
-!- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE GENERATED BY THE USE OF
                                                                                                                                                                                               DIFFERENT TRANSCRIPTION START SITES AND SPLICE PATTERNS.
DISEASE: MUTATION OF DUNCE PRODUCES FEMALE FLIES THAT ARE STERILE.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
coding sequences of the Drosophila dunce+ gene, the structural gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%; Score 61; DB 1; Length 584; 75.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLY-RICH.
99239BE33C620501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PSO0126; PDEASE_I; 1. Hydrolase; cAMP; Alternative splicing. DOMAIN 305 310 PART OF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X55171; CAA38960.1; JOINED
EMBL; X55172; CAA38960.1; JOINED
EMBL; X55173; CAA38960.1; JOINED
EMBL; X55174; CAA38960.1; JOINED
EMBL; X55175; CAA38960.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAA38960.1; JOINED. CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M14978; AAC34201.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X55167; CAA38960.1; -.
EMBL; X55168; CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00387; PDIESTERASE1.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 AA; 64875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003607; HDc.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M14979; AAC34201.1;
EMBL; M14980; AAC34201.1;
EMBL; M14981; AAC34201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0000479; dnc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M14982; AAC34201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555 ALRAGGGGGGGGGMAP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551
567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00233; PDEase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A26651; A26651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X55170;
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                                                                                                                                                                                                                                                                               FAMILY.
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P13645;
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MEDLINE-92141228; PubMed-1371013;
Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.;
Extensive size polymorphism of the human keratin 10 chain resides in
"Extensive size polymorphism of the human keratin 10 chain resides in
the C-terminal V2 subdomain due to variable numbers and sizes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94216497; PubMed-7512983; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; "Genetic mutations in the K1 and K10 genes of patients with epidermolytic hyperkeratosis. Correlation between location and disease severity.";
J. Clin. Invest. 93:1533-1542(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
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                                                                                                                                                                                                                                                                                                                                                                                           "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
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                        MEDLINE-89125611; PubMed-2464696; Rieger M., Franke W.W.; "Identification of an orthologous mammalian cytokeratin gene. High degree of intron sequence conservation during evolution of human
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                                                                                                                                                                                                                                                                                                                                    TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
Mssmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
                                                                                                                                                                                                                                                    Tkachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
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MEDLINE-92376531; PubMed=1380725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92386600; PubMed-1381287;
                                                                                                                                    MEDLINE-88122104; Pubmed-2448602;
                                                                                                                                                                                                                           SEQUENCE OF 197-593 FROM N.A. MEDLINE=92339897; Pubmed=1378806;
                                                                                                                                                                                                  Mol. Biol. Rep. 12:277-283(1987).
                                                                                                                                                                                                                                                                                                                                  SECUENCE OF 180-184 AND 577-589.
                                                                                             Mol. Biol. 204:841-856(1988).
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                                                                                                                        SEQUENCE OF 130-593 FROM N.A
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                    SEQUENCE FROM N.A.
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                                                                                  cytokeratin 10.
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1 POLYMORPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN THE GLYRICH REGION (POSITIONS 490-560).

2 1-1 DISEASE: DREFECTS IN KRT10 ARE THE CAUSE OF EDIDERMOLYTIC HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL HYPERREATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL ETCHNOLYTIC CHARACTERIZED BY BLISTERING AND A MARKED THICKENING OF THE STRATUM CORNEDM. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH CORNEDM. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS.

REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS.

MITHIN A FEW WEBERS, THE ENTYHRODERMA AND BLISTER FORMATION DIMINISH AND HYPERKERATOSSS DEVELOP. TRANSMISSION IS AUTOSOMAL DISEASE: DEFECTS IN KRT10 ARE SPORADIC.

1 DISEASE: DEFECTS IN KRT10 ARE PROTYPIC VARLANT OF EPIDERMOLYTIC HYPERKERATOSIS. IT RESEMBLES CLINICAL AND HISTOLOGIC FEATURES OF HYPERKERATOSIS. IT RESEMBLES CLINICAL AND HISTOLOGIC FEATURES OF BOTH EPIDERMOLYTIC HYPERKERATOSIS AND ICHTHYOSIS BULLOSA OF
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Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
Fuchs E.;
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-:- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
-:- CAUTION: REF 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN
                                                                                                                                                                                                                                                                                                                     MEDLINE-94117870; Pubmed-7507152;
McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
VARIANT EHK ASN-160.
BEDLINE-94117868; Pubmed-7507150;
Rothnagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.;
"Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and clinical mosaicism in a type of epidermal nevus."; New Engl. J. Med. 331:1408-1415(1994).
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MEDIINE-88016163; PubMed=3477803;
Jung G., Korn E.D., Hammer J.A. III;
"The heavy chain of Acanthameaba myosin IB is a fusion of myosin-like and non-myosin-like sequences.";
Proc. Natl. Acad. Sci. U.S.A. 84:6720-6724(1987).
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PRINTS; PR01248; TYPEIKERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
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R -> C (IN EHK).
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M -> T (IN EHK).
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N -> H (IN EHK).
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R -> P (IN EHK).
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01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID=5755;
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InterPro; IPR002957; Keratin_I.
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Aarhus/Ghent-2DPAGE; 7405; IEF
M19156; AAA59468.1; -. M77663; AAA59199.1; -. L20218; AAB59438.1; -. L20219; AAB59439.1; -.
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MIM; 113800;
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MEDLINE=90037074; PubMed=2530230;

REDLINE=90037074; PubMed=2530230;

REDLINE=90037074; PubMed=2530230;

RESEAR H., Lynch T.J., Martin B., Korn E.D.;

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Myosin; ATP-binding; Phosphorylation; Multigene family; SH3 domain.
                                                                                                                             a true myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN HEAD-LIKE.
TAIL HOMOLOGY REGION 1 (TH.1)
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                                        MEDLINE-86259656; PubMed-3014500;
Hammer J.A. III, Jung G., Korn E.D.;
"Genetic evidence that Acanthamoeba myosin I is a
Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
PHOSPHORYLATION
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InterPro; IPR001609; myosin_head.
Jean; PF000063; myosin_head; 1.
Pfam; PF00018; SH3; 1.
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PRINTS; PR00452; SH3DOMAIN.
PRODOM; PR000355; myosin_head; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
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PARTIAL SEQUENCE FROM N.A.
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HSSP; P08799; 1LVK.
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Matches 12;
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                  Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-i- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-i- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. 58M;
MEDILINE=91198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                      Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.; "The phytochrome gene family in tomato and the rapid differential evolution of this family in angiosperms."; Mol. Biol. Evol. 17:362-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HÖMODIMER (BY SIMILARITY).
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Phytochrome B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS5012; PAS; 2.
PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003018; GAF.
InterPro; IPR003594; HATBASS_C.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR0003661; His_KinA.
InterPro; IPR001369; PAS.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPASS_C; 1.
                                                                                                                                                                                                                                                                                             STRAIN=CV. 58M;
MEDLINE-20188796; Pubmed=10723737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF182394; AAB41398.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 208-1178 FROM N.A.
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SMART; SW00387; HATPASS_C; 1.
SWART; SW00388; HISKA; 1.
SWART; SW00091; PAS; 2.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
NTF5 OR NTF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92212967; PubMed=1313578; IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R., IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R., Yancopoulos G.D.; Persson H., Yancopoulos G.D.; Mammalian neurotrophin-4: structure, chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92075279; PubMed=1742028;
Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
MEDLINE=20095835; PubMed=10631974;
Robinson R.C., Radzlejewski C., Spraggon G., Greenwald J.,
Kostura M.R., Burtnick L.D., Stuart D.I., Choe S., Jones E.Y.;
"The structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: HIGHEST LEVELS IN PROSTATE, LOWER LEVELS IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC AND ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein Sci. 8:2589-2597(1999).
-i- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY SYMPATHETIC NEURONS.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                          Score 61; DB 1; Length 1178;
                                                                                                                                                                                                        CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                      1178 AA; 129136 MW; C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue distribution, and receptor specificity.", Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                                                                                   HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 210 AA.
                                                                                                                                                                                                                                                                                                                        Pred. No. 31;
1; Mismatches
                                                                                                                                                 POLY-HIS.
                                                                                                                                                                             POLY-GLY
                                                            PAS 1.
PAS 2.
                                                                                                                                                                                                                                                                                             31.4%;
75.0%;
                           Repeat; Multigene family DOMAIN 668 739
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                12 ARAGGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuron 7:857-866(1991).
                                                               739
873
1170
31
54
372
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenthal A.;
                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NT5 HUMAN
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                           BINDING
                                                                                        DOMAIN
DOMAIN
                                                                                                                                                 DOMAIN
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
NT5_HUMAN
                                                                                                                                                                                                                                                                                                                                                          Matches
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CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

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QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krolewski J.J., Dalla-Favera R.,
"The ltk gene encodes a novel receptor-type protein tyrosine kinase.";
EMBO J. 10:2911-2919(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toyoshima H., Kozutsumi H., Maru Y., Hagiwara K., Furaya A., Mioh H., Hanai N., Takaku F., Yazaki Y., Hirai H.; "Differently spliced cDNAs of human leukocyte tyrosine kinase receptor tyrosine kinase predict receptor proteins with and without a tyrosine kinase domain and a soluble receptor protein."; Proc. Natl. Acad. Sci. U.S.A. 90:5404-5408(1993).
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene Res. 5:199-204(1990).
-!- FUNCTION: THE EXACT FUNCTION OF THIS PROTEIN IS NOT KNOWN. IT IS
PROBABLY A RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Leukocyte tyrosine kinase receptor precursor (EC 2.7.1.112) (Protein tyrosine kinase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                        76 N-LINKED (GLCNAC. . .) (POTENTIAL). 22426 MW; DBC6A30195E139AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human ltk: gene structure and preferential expression in human leukemic cells.";
                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                      Length 210;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                     Score 60.5; DB 1;
Pred. No. 7.6;
                                                                                                                                                                                                                                                                                              3 GPTLRQWL------AARAGGGGGGGGGIEGPTLRQWLA 33
                                                                                                                                                                                 NEUROTROPHIN-5.
                                                                                                                                                                                                                                                                                                                                                                   864 AA
                                                                                                                                                                                                                                                                Pred. No. 7.6;
3; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                             POTENTIAL.
                                                                                                                    SWART; SM00140; NGF; 1.
PROSITE; PS00248; NGF_1; 1.
PROSITE; PS50270; NGF_2; 1.
Growth factor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=93296146; PubMed=7685902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92007735; PubMed=1655406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 416-864 FROM N.A.
MEDLINE-90206632; PubMed-2320375;
Maru Y., Hirai H., Takaku F.;
                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                      31.2%;
35.0%;
                   EMBL; M86528; AAA60154.1; -.
                                                                            InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1. PRINTS; PR00268; NGF. ProDom; PD002052; NGF; 1.
                                                                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                             24
80
210
170
199
                                               PDB; 1B8M; 09-FEB-99.
PDB; 1B98; 26-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                            JH0503; JH0503,
A42687; A42687.
                                                                                                                                                                                                                                 210 AA;
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                   MIM; 162662;
                                                                                                                                                                                                                                                                                                                                                                                                                                     LTK OR TYK1
                                                                                                                                                                                                                                                                                                                                                                 KLTK_HUMAN
P29376;
                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                       PROPEP
                                                                                                                                                             SIGNAL
                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                        KLTK_HUMAN
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                             RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G -> VAAASGDGAAPAPGARAAWGPGERAFLGAGSPAQRG
EAPGPRRFPPPLPAG (IN ISOFORM LAMBDA P1).
tyrosine phosphate.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; LAMBDA P1, LAMBDA P2 (SHOWN HERE) AND LAMBDA P3; ARE PRODUCED BY ALTERNATIVE SPLICING.
--- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

VLINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> GTKRLAGTVDSRLLLSSELGWVSAAGSRRO (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART: SM00219; TYTKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00239; RECEPTOT_TYR_KIN_II; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> GTKŘLAGTVDSRLÍLSM (IN REF. 3).
SCA -> MR (IN REF. 3).
97143DD57684A657 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEUKOCYTE TYROSINE KINASE RECEPTOR
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ς.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Receptor; Glycoprotein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM LAMBDA P3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN ISOFORM LAMBDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q -> R (IN REF. 2).
V -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOFORM LAMBDA P3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60.5; DE
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor_tyr_kin_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000019; Buk_pkinase.
InterPro; IPR002011; Receptor_tyr.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                               EMBL, D16105, BAA03679.1; -.
EMBL, X60702; CAA43113.1; -.
EMBL, X52213; CAA36460.1; -.
PIR, S17452; S17452.
HSSP, P00523; 2PTK.
MIM, 151520; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91653 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EG-PTLRQWLAARAGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 EGVPGSRRW----AGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
449
654
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                                                                                                       PROTEIN KINASES.
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449
652
654
864 AA;
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Matches 14; Conserv
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TRANSMEM
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MOD_RES
CARBOHYD
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CONFLICT
CONFLICT
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DOMAIN
NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
DOMAIN 59 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 1; Length 323;
Pred. No. 12;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A7F6D21A97DBB676 CRC64;
                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-AAY-2000 (Rel. 39, Last annotation update)
Transcription factor jun-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC MOTIF.
LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartl M., Hutchins J.T., Vogt P.K.; "The chicken jund gene and its product."; Oncogene 6:1623-1631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sex-lethal protein homolog (CCSXL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60063; CAA42665.1; -. PIR; S20099; S20099.
HSSP; P05412; IFOS.
TRANSFAC; T02196; -. InterPro; IPR00112; Leuzip_Jun.
InterPro; IPR00112; Leuzip_Jun.
Ffam; PF00170; bZIP; I.
PRINTS; PR00043; LEUZIPPRJUN.
SMART; SM00348; BRLZ; I.
PROSITE; PS00036; BZIP_BASIC; I.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-92019832; PubMed-1923529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98171464; PubMed-9502730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 AA; 33205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.9%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AAAAGGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266
298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155
242
270
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BENAKIO
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DOMAIN
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061374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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   SOURCE STATE TO SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVIC
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                                                                                                                                                                                             -: SUBCELLULAR LOCATION: Nuclear.
-: ATTERNATUE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS
-: ATTERNATUE PRODUCTS: DIFFERENT ISOFORMS E1, E2 AND E3 (SHOWN
HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-: DEVELOPMENTAL STAGE: EXPRESED IN BMBRYOS OF BOTH SEXES. ALSO
EXPRESSED IN THE PROGRAPTOR CELLS OF THE GENALINE.
-: SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
Saccone G., Peluso I., Artiaco D., Giordano E., Bopp D., Polito L.C., "The Ceratitis capitata homologue of the Drosophila sex-determining gene Sex-lethal is structurally conserved, but not sex-specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDILINE-98337188; Pubmed-9674431;
Kloss B., Price J.L., Saez L., Blau J., Rothenfluh A., Wesley C.S.,
Young M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Discs overgrown protein kinase (EC 2.7.1.-) (Double-time protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Drosophila clock gene double-time encodes a protein closely related to human casein kinase I epsilon.";
Cell 94:97-107(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL,
HSSP, P193.5-,
InterPro; IPR000504,
R Pfam; PF00076; rrm; 2.
DR PRIMT; PR00961; HUDSXLRNA.
DR PROSTIE; PS000360; RRM; 2.
DR PROSTIE; PS00030; RRM; 2.
DR PROSTIE; PS00030; RRM; 1.
DR PROSTIE; PS00030; RRM; 1.
T 188 RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                        DECELOPMENT 125:1495-1500(1998).
-!- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
POLY-PRO.
MISSING (IN ISOFORM A1).
CABA3DA5C2C8874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF026145; AAC38968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%;
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312
37
348 AA;
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es 10; Conserv
                                                                                                                                                                      DETERMINATION.
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                                                                                       requlated."
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076324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
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0
                                                                            Price J.L., Blau J., Rothenfluh A., Abodeely M., Kloss B., Young M.W.,
"Double-time is a novel Drosophila clock gene that regulates PERIOD
                                                                                                                                                                                                                   OSCILLATIONS OF THE CLOCK GENES PERIOD (PER) AND TIMELESS (TIM).
DBT REDUCES THE STABILITY AND THUS THE ACCUMULATION OF MONOMERIC PER PROTEINS, PROBABLY THROUGH PHOSPHORYLATION. NO EVIDENT CIRCADIAN OSCILLATION IS DETECTED IN HEAD.
-!- SUBJUNT: FORMS A COMPLEX WITH PER.
-!- TISSUE SPECIFICITY: EXPRESSED IN PHOTORECEPTOR CELLS OF THE EYES AS WELL AS IN THE REGION SITUATED BETWEEN THE OPTIC LOBE AND THE
                                                                                                                                                                                                  -!- FUNCTION: INVOLVED IN CIRCADIAN RHYTHMS, VIABILITY AND MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (Rel. 39, Last annotation update)
renkhead box protein D2 (Forkhead-related protein FKHL17) (Forkhead-related transcription factor 9) (FREAC-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CASEIN KINASE I SUBFAMILY. COULD BE THE ORTHOLOG OF CKI-EPSILON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M->I: IN DBTL; LENGTHENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P->S: IN DBTS; SHORTENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Biological rhythms; Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                        CENTRAL BRAIN. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60; DB 1; Length 440; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B875891D5747391D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILA POLY-ALA. POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P40233; ICSN.
FlyBase; FBqn0002413; dco.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERIOD
[2]
MUTAGENESIS, AND FUNCTION.
MEDLINE=98337187; PubMed=9674430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF055583; AAC39134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48073 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 PERRPSIRMRQGGGGGGG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.9%;
55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.0 Matches 11; Conservative
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PROSITE; PS00107; PROTEI
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                                                                                                                                          protein accumulation.";
Cell 94:83-95(1998).
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RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARA RARARARA RARARA A RARARA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KICJ_MOUSE STANDARD; PRT; 569 AA.
P02535; P08731;
21-JUL-1986 (Rel. 01, Created)
10-AUG-1988 (Rel. 08, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (56 kDa cytokeratin)
KRRIO OR KRTI-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                       SEQUENCE FROM N.A.

MEDLINE=98066765; PubMed=9403061;

Enstsson S., Betz R., Lagercrantz S., Larsson C., Ericksson S.,

Cederberg A., Carlsson P., Enchaeck S.;

"Cloning and characterization of freac-9 (FKHLI7), a novel kidney-
expressed human forkhead gene that maps to chromosome 1p32-p34.";
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                  Enerbaeck S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAAF498D216BE019 CRC64;
                                                                                                                                                                                                                              -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
-1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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FORK-HEAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF042832; AAC15421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 PTALLRQGLKTDAGGGAGGG 405
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                                                                                                                                                     Genomics 46:78-85(1997).
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250
306
409
426
445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q63245; 2HFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 14; Conserv
                             NCBI_TaxID=9606;
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                                                                                                                                                                                    REVISIONS.
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DNA_BIND
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Q -> R (IN REF. 2).

WYEKHONSQ -> VVREAROLKP (IN REF. 2).

KSDLEM -> QSVLEL (IN REF. 2).

H -> L (IN REF. 2).

E -> A (IN REF. 2).

EGRYCV -> VESLLER (IN REF. 2).

GGSHGGS -> CGGRGGG (IN REF. 2).
                                                                                                                                                                                                                 -i- SUBDNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
-i- KERATIN 10 IS GENERALLY ASSOCIATED WITH KERATIN 1.
-i- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
MICROFIBELLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)
(40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
                                                                                                                            SEQUENCE FROM N.A. MEDLINE-83192464; PubMed-6188955; Stainert P.M., Rice R.H., Roop D.R., Trus B.L., Steven A.C.; Stainert P.M., Rice R.H., Roop of a mouse epidermal keratin subunit and implications for the structure of intermediate filaments."; Nature 302:794-800(1983).
                                                              "Organization of a type I keratin gene. Evidence for evolution of intermediate filaments from a common ancestral gene."; J. Biol. Chem. 260:5867-5870(1985).
                    MEDLINE-85207552; PubMed-2581944;
Krieg T.M., Schafer M.P., Cheng C.K., Filpula D., Flaherty P.,
Steinert P.M., Roop D.R.;
                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S -> C (IN REF. 2).
S -> F (IN REF. 2).
S -> F (IN REF. 2).
Y -> L (IN REF. 2).
E -> G (IN REF. 2).
AG -> G (IN REF. 2).
MISSING (IN REF. 2).
SY -> GC (IN REF. 2).
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-> R (IN REF. 2)
-> G (IN REF. 2)
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PR0SITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin.
INIT_MET 0 0
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EMBL; M10081; AAA39391.1; JOINED.
EMBL; V00830; CAA24214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P10968; 1WGC.
MGD; MGI:96685; Krtl-10.
InterPro; 1PR001664; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
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PIR; S07330; S07330.
          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-22115335; PubMed-1662793; Haase V.H., Snijders A.J., Cooke S.M., Teng M.N., Kaul D., le Beau M.M., Bruns G.A., Bernards A.; "Alternatively spliced ltk mRNA in neurons predicts a receptor with a larger putative extracellular domain."; Oncogene 6:2319-2325(1991).
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Leukocytes express a novel gene encoding a putative transmembrane protein-kinase devoid of an extracellular domain.";
Nature 333:672-676(1988).
-!- FUNCTION: THE EXACT FUNCTION OF THIS PROTEIN IS NOT KNOW, IT IS PROBABLY A RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
-!- CATALXTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernards A., de la Monte S.; "The ltk receptor tyrosine kinase is expressed in pre-B lymphocytes and cerebral neurons and uses a non-AUG translational initiator.";
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                            ő
                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Leukocyte tyrosine kinase receptor precursor (EC 2.7.1.112).
                                                                             DB 1; Length 569;
                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snijders A.J., Haase V.H., Bernards A.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
S -> G (IN REF. 2).

GQ -> RR (IN REF. 2).

KS -> SGT (IN REF. 2).

; EEC59D4D8FFE484D CRC64;
                                                                                                                                                                                                                                                           888 AA.
                                                                                          21;
                                                                                                              7; Mismatches
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                                                                                Score 60;
Pred. No.
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88232962; PubMed-2836739;
Ben-Neriah Y., Bauskin A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90291994; PubMed=2357970;
                                                                                                                                              7 ROWLAARAGGGGGGGGGIEGPTLR 29
                                                                                                                                                               9 KOFSSSRSGGGGGGSVRVSSTR 31
                                                57711 MW;
                                                                                30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 9:2279-2287(1990).
                                                                                                                10; Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASES.
   543
547
555
569 AA;
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C
                                                                                                                                                                                                                            RESULT 21
KLTK_MOUSE
ID KLTK_MOUSE
AC P08923;
                                 CONFLICT
   CONFLICT
                                                                                  Query Match
                                                                                                  Local
                                                                                                                Matches
                                                                                                                                                                                                                                                                           q
      FF
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
SOX1_MOUSE
                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                      qq
  ï
                                                                                                                                                                                    Phosphorylation; Receptor; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Plerygota, Neoptera: Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91169252; PubMed-1963868; Voelker R.A., Graves J.P., Gibson W., Elsenberg M.T.; Mobile element insertions causing mutations in the Drosophila suppressor of sable locus occur in DNase I hypersensitive subregions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-911726, PubMed-1703632, Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T., "The Drosophila suppressor of sable gene encodes a polypeptide with regions similar to those of RNA-binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              PROSITE; PSO107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSO109; PROTEIN_KINASE_TYR; 1.
PROSITE; PSO1039; RECEPFOR_TYR_KIN_II; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                        LEUKOCYTE TYROSINE KINASE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        30.9%; Score 60; DB 1; Length 888; 63.2%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                     3FFCA80AB4863C55 CRC64;
                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                 M -> V (IN REF. 4).
Q -> H (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AGG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1322 AA.
       EMBL; X52621; CAA36848.1; ALT_SEQ.
EMBL; X07984; CAA30793.1; ALT_INIT.
PIR; S00904, S00904.
PIR; S12792; S12792.
HSSP; P11362; IFGK.
MGD; MGI:9840; LLK.
INTERPRO; IPR000719; Euk_pkinase.
InterPro; IPR000719; Tyr_pkinase.
                                                                                                                                                                                                                                                  PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                      94436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suppressor of sable protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    196 PGWRRW----AGGGGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                   63.2%;
                                                                                                            PRINTS; PR00109; TYRKINASE. SMART; SM00219; TYFKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLROWLAARAGGGGGGG 22
SMBL; M90470; AAA39451.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-9 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 63.2 tes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                   Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                    271
789
875
888 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUS_DROME
                                                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SU(S)
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUS_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                    a
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                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 5'-transcribed nontranslated sequences.";
Genetics 126:1071-1082(1990).
-!- FUNCTION: AFFECTS THE TRANSCRIPT LEVELS OF THOSE ALLELES THAT IT
                                                                                                                                                                                       -!- DEVELOPMENTAL STAGE: AT ALL STAGES.
-!- SIMILARITY: HAS REGIONS SIMILAR TO THOSE OF RNA-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A comparison of the properties of Sox-3 with Sry and two related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes, SOX-1 and SOX-2.";

penes, SOX-1 and SOX-2.";

Development 122:509-520(1996).

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-! TISSUE SPECIFICITY: MAINLY IN THE DEVELOPING CENTRAL NERVOUS SYSTEM. EXPRESSED IN DEVELOPING UROCENITAL RIDGE.

-!- SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M., Norris D., Rastan S., Stevanovic M., Goodfellow P.N., Lovell-Badge R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 1; Length 1322;

        DOMAIN
        446
        474
        GLN-RICH (OPA-REPEAT).

        DOMAIN
        1087
        1162
        RNA-BINDING (BY SIMILARITY).

        SEQUENCE
        1322 AA;
        143555 MW;
        D5F534EB5702EA08 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIGHLY CHARGED DOMAIN.
                                                                                                                SUPPRESSES. MAY BE INVOLVED IN RNA METABOLISM-:- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 43;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96189340; PubMed=8625802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39612; A39612.
FlyBase; FBgn0003575; su(s).
InterPro; IPR000571; Zf-CCCH.
Pfam; PF00642; Zf-CCCH; Z.
RNA-binding; Nuclear protein.
DOMAIN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M57889; AAA28920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA42010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 GGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X59364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOX-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOX1 OR SOX-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOX1_MOUSE
P53783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E47) NEURODI HETEROIMERS AND ACTS AS A STRONG REPRESSOR OF NEURODI AND MYOD-RESPONSIVE GENES, PROBABLY BY HETERODIMERIZATION WITH CLASS A BASIC HELIX-LOOP-HELLY FACTORS. DESPITE THE PRESENCE OF AN INTACT BASIC DOWALN, DOES NOT BIND TO DNA.

-! SUBUNIT: HETERODIMER WITH OTHER BHLH PROTEINS, LIKE TCF3 (E47).

-! SUBCELLULAR LOCATION: NUCLEAR (POCENIAL).

-! SIMILARITY: BELONGS TO THE BASIC HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA.
9F81ED667F947C05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pram: PF00010; HLH; 1.
SMART: SW00353; HLH; 1.
PROSTITE; PS00038; HELIX_LOOP_HELIX; 1.
Noclear protein; Transcription regulation; Repressor.
DOMAIN 11 14 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                  POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                       POLY-GLY
                                                                                                                                                                                                                                                                POLY-GLY
                                                                                                                                                                                                                                                                                           POLY-ALA
                                                                                                                                                                                                                                  HMG BOX
                       HSSP; 005066; 1HRY.
MGD; MGI:98377; SOXI.
InterPro; IPR000910; HMG_12_box.
Efam; PF00505; HMG_box; I.
SMART; SM00398; HMG; I.
DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96140430; PubMed-8552091;
                                                                                                                                                                                                                                                    150 PC
204 PC
288 PC
306 PC
364 PC
39237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LSGPA----GARGGGGGGGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.7%;
illarity 54.5%;
Conservative 1
EMBL; X94126; CAA63846.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S80870; AAB50691.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BET3_MESAU
009029;
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                  DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BET3_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FERNAL DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
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                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLUTAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND PANCREATIC TISSUES.
-i- SIMILARITY: TO DROSOPHILA HOMEOBOX PROTEIN PROBOSCIPEDIA.
                                                                  POLY-GLY.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrison K.A., Druey K.M., Deguchi Y., Tuscano J.M., Kehrl J.H.; "A novel human homeobox gene distantly related to proboscipedia is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; Transcription regulation.
                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                           DB 1; Length 367;
18;
                                                                                                                                                                                                                                                                                   6; Indels
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                                                                                                                                                                           6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in lymphoid and pancreatic fissues."; J. Biol. Chem. 269:19968-19975(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 AA.
                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                Score 59;
Pred. No.
                       POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
MEDLINE=94327547; PubMed=7914194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U07663; AAB60647.1; JOINED. P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1. Homeobox; DNA-binding; Nuclear pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                           35905 MW;
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61.1%;
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                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                           367 AA;
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P50219;
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DOMAIN
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DB 1; Length 401;

Score 59;

30.48:

Query Match

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      ZIN_HUMAN
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                                                                                                16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
One cut domain family member 2 (ONECUT-2 transcription factor) (OC-2).
                                                                                                                                                                                                   Gaps
        Gaps
                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franscription regulation; Homeobox; DNA-binding; Nuclear protein;
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AF21E052EFBE5DA1 CRC64;
        5;
                                                                                  485 AA.
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0; Mismatches
        1; Mismatches
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                                                  PRT;
                                                                                                                                                                                              MEDLINE-99115605; PubMed-9915796;
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003350; CUT.
InterPro; IPR001356; Homeobox.
Pfam; PF02376; CUT; 1.
Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52482 MW;
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                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y18198; CAB38253.1; -.
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64.78;
                                         37 ASGTGGGGGGGGASGGT 53
                         11 AARAGGGGGGGGIEGPT 27
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        11; Conservative
                                                                                   STANDARD;
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37
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                                                                                                                                             Homo sapiens (Human)
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Best Local Similarity
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75
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485 AA;
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les 13; Conserv
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=9606;
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MIM; 604894; -
                                                                                  ONC2_HUMAN
095948;
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DNA_BIND
DNA_BIND
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EMBL; BC004910; AAF2>.

EMBL; BC004910; AAH04910.-

DR InterPro; IPRO1680; W040.

DR PRINTS; PR00320; GPROTEINBRPT.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

DR PROSITE; PS00678; WD_REPEATS_1; 1.

TOMAIN 169 136 CALMODULIN-BINDING (POTENTIAL).

FT DOMAIN 165 182 CALMODULIN-BINDING (POTENTIAL).

TFPAT 489 528 WD 2.

TFPAT 489 528 WD 2.

TFPAT 489 528 WD 5.

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-!- SIMILARITY: BELONGS TO THE STRIATIN FAMILY OF WD-REPEAT PROTEINS.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
-!- CAUTION: The name "Zinedin" probably originates from the name of the famous soccer player from Marseille (Zinedine Zidane)!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: BINDS CALMODULIN IN A CALCIUM DEPENDENT MANNER. MAY FUNCTION AS SCAFFOLDING OR SIGNALING PROTEIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-BOUND (BY
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Zinedin, SGZNA, and striatin are calmodulin-binding, WD repeat proteins principally expressed in the brain."; J. Biol. Chem. 275:19970-19977(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20347911; PubMed=10748158;
Castets F., Rakitina T., Gaillard S., Mogrich A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                    01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
753 AA
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PRT;
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Best Local Similarity 78.6
Matches 11; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monneron A.;
ZIN_HUMAN
                                                                                                                                                                                                                                        Zinedin.
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0
                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR InterPro; IPR000556; Hormone_rec_lig.
DR InterPro; IPR000558; Strdhormone_receptor.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-cd, 1.
DR Ffam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-cd, 1.
DR PRINTS; PR00047; STROIDEINGER.
DR SMART; SM00409; STROIDEINGER.
DR SMART; SM00439; ZTROIDEINGER.
DR SMART; SM00439; ZTROIDEINGER.
DR SMART; SM00439; ZTROIDEINGER.
DR SMART; SM00439; ZTROIDEINGER.
DR SMART; SM00430; ZTROIDEINGER.
DR SMART; SM00430; NUCLEAR_RECEPTOR; 1.
DR RECEPTOR; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                    MEDLINE-97449774; PubMed-9304790;
Hannan G.N., Hill R.J.;
Hannan G.N., Hill R.J.;
"Cloning and characterization of LCECR: a functional ecdysone receptor from the sheep blowfly Lucilia cuprina.";
Insect Blochem. Mol. Biol. 27:479-488(1997).
-!-FUNCTION: RECEPTOR FOR ECOYSONE. BINDS TO ECDYSONE RESPONSE ELEMENTS (ECRES) (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: Nuclear.
-!-SUBLIBRITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
                                                                                                                                                       Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Score 59; DB 1; Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4-TYPE. HORMONE-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C1511452ED37D359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODULATING (POTENTIAL).
NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 4499 AA.
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1; Mismatches
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                                                                                                                             receptor) (20E receptor).
ECR OR NR1H1.
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                                                           STANDARD;
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366
321
361
674
44 AGKGGGGGGSPGPT 57
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337
337
454
6
757 AA;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                   NCBI_TaxID-7375;
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DYHA_CHLRE
ID DYHA_CHLRE
AC Q39610;
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                                                         ECR_LUCCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                          MEDLINE-97329535; PubMed=9186009;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas reinhardtii flagellar alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYNEIN HAS ATPASE ACTIVITY.
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                       Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00429; IPT; I.
PROSITE; PS50194; FILAMIN_REPEAT; I.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 1; Length 4499;
Pred. No. 1.6e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
W; 319AC7FD30F1591A CRC64;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dynein alpha chain, flagellar outer arm (DHC alpha).
0DA11 OR ODA-11.
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COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                               Cell Motil. Cytoskeleton 37:120-126(1997).
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94274778; PubMed=8006077;
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InterPro; IPR001798; Kelch.
InterPro; IPR001736; PLD.
Pfam; PF00630; Filamin; 1.
Pfam; PF01344; Kelch; 3.
SWART; SM00382; AAA; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1142-4499 FROM N.A.
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InterPro; IPR001298; Filamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L26049; AAA57316.2; -.
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Best Local Similarity 60.05
Matches 12; Conservative
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                                                                                                                                                                                                   NCBI_TaxID=3055;
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1716
2019
2369
2717
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SEQUENCE
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-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio E., Morelli F., Stornaluolo A., Nigro V., Simeone A., Boncinelli E.; "The human HOX gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Nuclear.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LIMB BUDS.
-i- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peschle C., Duboule D.;
MoX4 genese encode transcription factors with potential auto- and
cross-regulatory capacities.";
EMBO J. 10:4177-4187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complementary homeo protein gradients in developing limb buds.";
Genes Dev. 3:641-650(1989).
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zappavigna V., Renucci A., Izpisua-Belmonte J.-C., Urier G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 264-342 FROM N.A.
BEDLINE-89306602; PubMed-2268311;
Oliver G., Sidell N., Fiske N., Heinzmann C., Mohandas T., Sparkes R.S., de Robertis E.M.;
                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
HOXD9 OR HOX4C.
                                                                                                                                                            342 AA.
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SER/THR-RICH.
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                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Spinal cord;
MEDLINE=92097538; PubMed=1756725;
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PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001356; Homeobox.
4194 GETLFKTVVEVAGGGGGGG 4213
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SMART; SM00389; HOX; 1.
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                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S18649; S18649.
PIR; S05958; S05958.
PIR; A32830; A32830.
HSSP; P02834; 1B81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 142982;
                                                                                                                                                         HXD9_HUMAN
P28356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC;
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Gaps
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                                                    Score 58.5; DB 1; Length 342; Pred. No. 19;
                                                                                      Indels
           266 E -> A (IN REF. 2).
35580 MW; 731981FE25C5ACD7 CRC64;
                                                                                      2; Mismatches
                                                                                                                                                                                               9, 2002, 09:00:13
                                                                                                                                                  103 GRYVRSWMEPLPGFPGGAGGGGGGGGP 131
                                                                                                                    3 GPTLRQWLAARAG-----GGGGGGGIEGP 26
                                                          30.2%;
                                                                         44.88;
                                                                                       13; Conservative
                                                                                                                                                                                             Search completed: October
Job time: 5.3831 secs
                            342 AA;
                                                          Query Match
Best Local Similarity
DNA_BIND
CONFLICT
                              SEQUENCE
                                                                                          Matches
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:52:16; Search time 12.8993 Seconds (without alignments) 482.803 Million cell updates/sec Run on:

US-09-422-838C-26 194 Title: Perfect score:

1 IEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 36 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL\_19:\* Database :

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_nammal:\*
sp\_mammal:\* sp\_unclassified:\* sp\_vertebrate:\* sp\_organelle:\*
sp\_phage:\*
sp\_plant:\* sp\_bacteriap:\* sp\_rvirus:\* sp\_rodent:\* sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

Result Ouery No. Score Match Length DB ID No. Score Match Length DB ID 174 38.1 360 10 094629 37.9 431 13 094069 35.6 50 5 019476 6 68.5 35.3 488 10 09508 6 68.5 35.3 518 2 094076 6 68.5 35.3 518 2 094076 6 6 83.1 125 10 094078 11 66.5 34.3 202 10 09FTZ5 14 66.5 34.3 495 16 033230 15 66.5 34.0 55.9 10 094855	SUMMARIES	Description ,	09140	VG9 Q9pvq9 coturnix co	Q943K0	09sdk6	0				٥	0			ď			
Score Match Length DE Autor Length DE Autor Length DE Autor Match Length DE Autor Match Length DE Autor Match Length DE Autor Match Autor	Š	1D	635160	Q9PVG9	Q943K(	09SI	0194	090	0498	1760	O9HE	09W0	09F	033	Q9AD	09Y	09A	0000
SCORE 73.5 73.5 73.5 73.5 73.5 73.5 73.5 68.5 68.5 68.5 68.5 68.5 68.5 66.5 66		DB	101	13	10	10	S	16	7	10	m	S	10	16	7	13	10	-
SCORE 73.5 73.5 73.5 73.5 73.5 73.5 73.5 68.5 68.5 68.5 68.5 68.5 68.5 66.5 66		Length	360	431	253	439	500	488	518	125	176	170	202	495	496	377	529	613
<b>ω</b> 1		% Query Match	38.1	37.9	36.6	36.1	35.6	35.3	35.3	35.1	35.1	34.5	34.3	34.3	34.3	34.0	34.0	0 70
Result No. No. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Score	74	73.5	7.1	70	69	68.5	68.5	99	68	67	66.5	66.5	66.5	99	99	99
		Result No.		7	٣	4	5	9	7	8	0	10	11	12	13	14	15	3.5

Q9ar44 oryza sativ	Q9nyw9 homo sapien	Q9y566 homo sapien	073628 anolis caro	Q9vjk4 drosophila		Q9u2il caenorhabdi	Q9u2i0 caenorhabdi	096755 branchiosto	Q941w9 oryza sativ	٥	10		Q9m699 catharanthu	Q942r8 oryza sativ	Q96sq2 homo sapien	004270 chlamydomon	Q9byd8 homo sapien	Q96jg7 homo sapien	Q96134 homo sapien	Q9sxi9 oryza sativ	Q9c0il homo sapien		Q9pux6 gadus morhu	Q9jkb4 mus musculu	Q91d54 oryza sativ	Q93h33 streptomyce	Q9pud8 lampetra fl	Q9nec7 leishmania
Q9AR44	6MXN60	Q9Y566	073628	Q9VJK4	Q9VV01	090211	090210	096755	094 IW9	Q9LI16	Q91BC5	Q9M6A1	669M60	Q942R8	096502	004270	Q9BYD8	096JG7	Q96L34	61XS6O	Q9C011	Q9AFI5	O9PUX6	Q9JKB4	Q9LD54	093Н33	Q9PUD8	Q9NEC7
10	4	4	13		2				10	10	12			10	4	10	4	4	4	10	4	7		11		7	13	2
243	1548	2161	447	452	309	331	333	422	207	584	99	137	160	186	474	490	688	689	752	841	775	165	286	334	381	540	642	664
33.8	33.8		33.5		33.0	33.0	33.0	33.0	32.7	32.7	32.5	32.5	32.5			2							32.0	7		32.0	32.0	32.0
65.5	65.5	L)	65	65	64	64	64	64	63.5	63.5	63		63			63	63	63	63	63	62.5	62	62	62	62	62	62	62
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Gaps
                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE:
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Submitteed (JUN-2000) to the EMBL/GenBank/DDBJ databases.
Submitteed (JUN-2000) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR00571; Zf-CCCH.
InterPro; IPR00542; Zf-CCCH; 4.
SRART; SM00356; Zf-CCCH; 4.
SEQUENCE 360 AA; 37368 MW; 5105598D7EIC77B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              38.1%; Score 74; DB 10; Length 360; 56.0%; Pred. No. 1.4; tive 2; Mismatches 9; Indels
                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                            360 AA.
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUTATIVE ZINC FINGER PROTEIN. P0462H08.19.
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 56.0
Matches 14; Conservative
                            PRELIMINARY;
                                                                                                                                     Oryza sativa (Rice).
                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                              69LGC9
RESULT 1
               629760
                                 Οy
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RESULT 2 Q9PVG9 ID

PRT; PRELIMINARY; Q9PVG9

431 AA.

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80 GPTVGVRVAYRAGAGGGGGGGFRGFALK 106

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RESULT 4
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                                                               Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9%; Score 73.5; DB 13; Length 431; 42.9%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.6%; Score 71; DB 10; Length 253; 55.6%; Pred. No. 2.1; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                           SEQUENCE FROM N.A.
Liu Y., Xue J.X., Zhang W., Fu D.C., He R.Q., Xue Z.G.;
"grain-2, a Pour-box gene expressed in quali embryos.";
Submitted (EP-1998) to the EMBL/GenBank/DDBJ databases-
:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-: SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003235; BAB64100.1; --
SEQUENCE 253 AA; 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0027; HOMEOBOX_1; 1.
PROSITE; PSO0017; HOMEOBOX_2; 1.
PROSITE; PSO0018; POU_1; 1.
PROSITE; PSO00465; POU_2; 1.
DNA-binding; HOMEOBOX; Nuclear protein.
SEQUENCE 431 AA; 43722 MW; 1DC47E53F9ACC7D5 CRC64;
         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P0039A07.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 QWLAARA-------GGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 QWIAALSHGGPGGGGGGGGGGGGGGGGGGGTA---WAAAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                            EMBL: AF091043; AAF00040.1; -. HSSP; P14859; 1OCT.
INCEPPO: IPR001356; HOMGODOX.
INTERPO: IPR000327; POU.
                                                                                                                                                                                                                                                                            Pfam; PF00046; homeobox; 1. Pfam; PF00157; pou; 1. PRINTS: PR000028; POUDOMAIN. ProDom; PD000583; POU; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 55.6
Matches 15; Conservative
                                                    POU-BOX PROTEIN BRAIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone: P0039A07."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q943K0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                             Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0705D01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 10; Length 439;
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGGGGG-----IEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 5; Length 500; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000492; BAA84610.1; -.
Hypothetical protein.
SEQUENCE 439 AA: 47297 MW: 533EEC240CEA1BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percy C.M.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53946 MW; 1416327086FE7CF6 CRC64;
                                                              01-MAY-2000 (TTEMBLrel. 13, Last sequence update) 01-DEC-2001 (TTEMBLrel. 19, Last annotation update) HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6;
    439 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 69; DB 56.5%; Pred. No. 6.7; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                          01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:21012-2018(1998).
EMBL: Z78013: CAB01420.1: -.
InterPro; IPR001254; Trypsin.
PROSITE; PS50240: TRYPSIN.DOM; 1.
Hydrolase; Scrine protease.
SEQUENCE 500 AA, 53946 MW; 1416:
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GPTLRQWLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.1%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, F15B9.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.09
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                    NCBI_TaxID=4530;
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                        09SDK6;
Q9SDK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 019476
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019476
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Rown D., Chillingworth T., Connor R., Davies R.M., Davlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherford S., Stevens K., Simon S., Simmonds M., Skelton J., Squares R., Salares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                    Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.3%; Score 68.5; DB 2; Length 518; 46.7%; Pred. No. 7.8; tive 2; Mismatches 7; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00019; AAA17274.1; -.
SEQUENCE 518 AA; 56001 MW; 6641916CC84F374B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 AA; 52800 MW; 188918856F9774AA CRC64;
                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
POSSIBLE ATP/GTP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583920; CAC31378.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68.5; Di
Pred. No. 7.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                             STRAIN=TN;
MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000765; GTP1_OBG.
PRINTS; PR00326; GTP1OBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.38;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 488 AA;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leproma; ML0997;
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                            030060
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RESULT 6
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              022260
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Gaps
                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Schlte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRATHECY. NIPPONBARE;
SASSAI T., MATSHOOTO T., Yamamoto K.;
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.1%; Score 68; DB 10; Length 125; 42.9%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%; Score 68; DB 3; Length 776; 57.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR002094; BAA96216.1; -.
Hypothetical protein
SEQUENCE 125 AA: 13396 MW; C609DBDD097BC505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL451109; CAC18624.2; -.
Hypothetical protein.
SEQUENCE 776 Aa; 82771 MW; C9BEA870D94A37DE CRC64;
                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 EGAAAR-WRAARSPARGGORGGHRRRGGGGGGGGRERPRRR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EGPTLRQWLAARA------GGGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                219 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
4 PTLRQW-----LAARAGGGGGGGGIEGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678 GGGGGGGVVDDDGEPDFAGWLAAQA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGGGGGGI---EG-PTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 16, (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.9
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
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                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                             clone:P0483F08."
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01-DEC-2001 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                        Q9LWC8;
                                                                                                        Q9LWC8
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                                                                          RESULT 8
                                                                                           O9LWC8
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Gaps

7;

14; Conservative

Matches

Best Local Similarity

202 AA.

PRT;

PRELIMINARY;

Q9FTZ5

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Gotage R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
Burton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Worthan J.R., Hale G., Change M., Miklos G.L.G.,
RA Beeson K.Y. Basu A., Baxedhale J., Baytaktaroglu L., Beasley E.M.,
Beeson K.Y. Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Bratel R.C., Davengolu L., Beasley E.M.,
Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Decthan M.R., Bouck J., Busketein P., Brottler P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goog F. Gorrell J.H., Galz, Galbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Harvey D., Heiman T.J., Hernandez J.R., Harvey D., Heiman T.J., Hernandez J.R., Harvey D., Heiman T.J., Hernandez J.R., Moshrefi A.,
RA Hostin D., Houston K.A., Hewland T.J., Wei M.-H., Ibeywan C.,
Jalall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Herkulvo G., Milshina N.V., Li J., Li Z., Liang Y., Lin X.,
Mullshina N.W., Noberry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Musish D.M., Nelson D.L.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., San K.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. Shier S., Shon H., Wang S., Shon W., Subbs R.A., Shon G., Shon C., Shon C., Shon S., Shon S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Meptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.5%; Score 67; DB 5; Length 170; llarity 50.0%; Pred. No. 3.7; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19099 MW; 477D79D55ADF4CE5 CRC64;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
CG13807 PROTEIN.
                                         170 AA.
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003474; AAF47627.1; -. FlyBase; FBqn0035323; CG13807. InterPro; IPR002952; Eggshell. PRINTS; PR01228; EGGSHELL.
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                    Q9W033
Q9W033;
RESULT 10
                    Q9W033
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RESULT 11

O9FTZ5

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ij
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglaneier K., Gas S., Barry C.E. III, Tekaia F., Davies K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:337-544(1998).
EMBL; 298209; CAR10901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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                                                                                                                                                                                                                                                                                                                                    Score 66.5; DB 10; Length 202; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.3%; Score 66.5; DB 16; Length 495;
                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0486E04.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003818; BAB16519.1; -.
SEQUENCE 202 AA; 19763 MW; BFC2520037F8E274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Last annotation update)
                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches 13;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Cres 01-JAN-1998 (TrEMBLrel. 05, Lasi 01-DEC-2001 (TrEMBLrel. 19, Lasi HYPOTHETICAL 53,3 KDA PROTEIN. HFLX OR RV2725C OR MYCY154,05C. Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l protein; Complete
495 AA; 53327 MW;
                                                                                                                                                                                                                                                                                                                                         34.3%;
39.0%;
                          (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 16,
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                STRAIN-CV. NIPPONBARE;
                                                                                                      Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserva
                                                                      P0436E04.1 PROTEIN.
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=4530;
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           09FTZ5;
01-MAR-2001
01-MAR-2001
                                                          01-MAR-2001
                                                                                         P0436E04.1
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Q9ASE5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_PaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
MEDILINE=97000351; Pubmed=8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger K.J., Harris D.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                         Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL; AL512667; CAC21636.2; -.

InterPro. IPRO03838; DUF214.

Fram; PF05887; DUF214; 1.

SEQUENCE 496 AA; 49548 MW; 54E110C4F86231A4 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66.5; DE
Pred. No. 12;
2; Mismatches
                                                         496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GGGGIEGP 26
                                                                                                                Created)
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                                                         PRT;
                                                                                                                                                                                                  PUTATIVE INTEGRAL MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.3%;
46.9%;
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                                                                                                                                         (TrEMBLrel. 17, (TrEMBLrel. 18,
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SMART; SM00389; HOX; 1.
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                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1902;
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                                                                                                             01-JUN-2001
                                                                                                                                         01-JUN-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                     Q9AD76;
                                                      09AD76
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RESULT 13
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                              09AD76
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MEDLINE=20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
Nagase T. Kikuno P., Ishikawa K., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human
genes. XVII. The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro.";
DNA Res. 7:43-150(2000).
EMBL; AB040891; BAA95982.1; -.

NON_TER I I SEQUENCE 612 AA; 65593 MW; 9AA4061D21E1E9FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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STRAIN=CV. NIPPONBARE;
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                  DB 13; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 10; Length 529;
Pred. No. 15;
2; Mismatches 4; Indels
                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0456F08.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AP002901; BAB39414.1;
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00205; NAD_binding.
InterPro; IPR00205; NAD_binding.
Pfam; PF0159; Amino_oxidase; 1.
SEQUENCE 529 AA; 55981 MM; 0A5DAS5CDD076D24 CRC64;
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 377 AA; 37998 MW; C2DBC19402D3A172 CRC64;
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01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-0c7-2000 (TrEMBLrel. 15, Last annotation update)
KIRAL458 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                            2; Mismatches
                                                                          Score 66;
Pred. No.
                                                                                                                                                                                                                              265 QGYTAASYYGVECGGGGGGGGGGGPYL 291
                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                            34.0%;
48.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2001 (TrEMBLrel. 18,
P0456F08.14 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.0%;
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                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
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Oryza sativa (Rice)
                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Wamamoto K.;
Sasaki T., Matsumoto T.;
Sasaki T., Wamamoto K.;
Cloyas astiva nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:POSB1F09.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. NIPPONBARE;
SasAtl T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0498A12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. NIPPONBARE;
Saski T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:OSJNBAG004B13.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOSTATIN RECEPTOR-INTERACTING PROTEIN SPLICE VARIANT B.
34.0%; Score 66; DB 4; Length 612; 63.6%; Pred. No. 17; tive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P0498A12.7 PROTEIN (OSJNBA0004B13.18 PROTEIN) (P0581F09.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AP003012; BAB3999.1; -. EMBL, AP003018; BAB3964.1; -. EMBL, AP0030318; BAB64224.1; -. SEQUENCE 243 AA; 26243 MW; 029E9344C20E0EC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                PRT;
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                                                                                       4 PTLRQWLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                      P0498A12.7 OR P0581F09.21.
                       Best Local Similarity 63.6
Matches 14; Conservative
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nes 12; Conservé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
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    Query Match
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                                                                                                                                              of
SEQUENCE FROM N.A.

MEDLINE-20020275; PubMed=10551867;
Zitzer H., Honck H.H., Bachner D., Richter D., Kreienkamp H.J.;
Zitzer H., Honck H.H., Bachner D., Richter D., Kreienkamp H.J.;
Somatostatin receptor interacting protein defines a novel family multidomain proteins present in human and rodent brain.";

M. Biol. Chem. 274:32997-33001(1999).

SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Zitzer H., Hoenck H.-H., Richter D., Kreienkamp H.-J.;
Zitzer G., Hoenck H.-H., Richter D., Kreienkamp H.-J.;
"The somatostatin receptor interacting protein (SSTRIP) defines a novel family of multidomain postsynaptic density proteins.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF163302; AAD45121.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                              Zitzer H., Hoenck H., Baechner D., Richter D., Kreienkamp H.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF26728; AAF35887.1; -. InterPro; IPR001478; PDZ. InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.8%; Score 65.5; DB 4; Length 1548; 38.1%; Pred. No. 49;
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U-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOSTATIN RECEPTOR INTERACTING PROTEIN SPLICE VARIANT A.
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SEQUENCE 2161 AA; 225019 MW; 5FEFC969CBE98701 CRC64;
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PROSITE; PS50297; ANK REP_REGION; 1.
PROSITE; PS50106; PDZ; 1.
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InterPro; IPR002110; ANK.
InterPro; IPR00110; ANK.
InterPro; IPR001605; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM; InterPro; IPR0018; SAM; InterPro; IPR0018; SAM; InterPro; SMART; SM00248; PDZ; InterPro; SMART; SM00444; SAM; InterPro; SMART; SM00444; SAM; InterPro; SMART; SM00326; SH3; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPr
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Best Local Similarity 38.15
Matches 16; Conservative
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Matches 16; Conserv
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PROSITE; PS50002;
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Eukaryota;
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Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                                                                                                                    Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
NCBI_TaxID=28377;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 13; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                            Anolis carolinensis (Green anole) (American chameleon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homeobox; Nuclear protein. 47160 MW; AFA362894FCBC419 CRC64;
  (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 14, Last annotation update)
                                                                                                 Last sequence update)
Last annotation update)
                                                                  A
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2; Mismatches
                                                                  447
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2000 (TrEMBLrel. 14, Last anno
                                                                                       Created)
                                                                PRT;
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MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                            MEDLINE-97475689; PubMed-9335144;
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%;
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1. Pfam; PF00157; pou; 1. PRINTS; PR00028; POUDOMAIN. Probom; PD000583; POU; 1.
                                                                                      01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00035; POU_1; 1. PROSITE; PS00465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11:11 : 1111111
56 QWIAALSHGGGGGGG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 QWLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG5953 PROTEIN.
                                                                                                                        BRAIN-2 GENE
                                                                                                                                    BRAIN-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09VJK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VJK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG5923
                                                                  073628
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                                             RESULT 20
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                                                         073628
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RA SULTON G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA MAN K.H., Oboyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayal A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.H., Agbayal A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beneson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Gherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Horsin N.L., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Harris N.L., Evangelista C.C., Ferraz C., Rerindson J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush R., Mixon K., Nusskern D., Lai Z.,
Andrei B., McIntosh T.C., McLeod M.P., Nosherfi A.,
Ra Mourt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Sunders R., Pollard J., Puri V., Reese M.G.,
Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
Ra Streas R.M., Roodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ra Sheng X.H., Zhong W., Zhong W., Zhong X., Zhu X., Smith H.O.,
Rang Z.-Y., Wassarman D.A., Weibstebbell M. Weissenbech J.,
Rang Genome sequence of Drosophila melanogaster.",
B. Remis R. Reginoloza893. Carlor M. Weissenbech S.,
Rangel R. P. Reginoloza893. Carlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Man R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65; DB 5; Length 452;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.5%;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AAGGGGGGGGGVVGP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., basam D.A., Dang Z., Bayraktaroglu L., Botchier P.,
RA Burtis K.C., basam D.A., Dang E., Davenport L.B., Davies P.,
RA Ghablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wein M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
RA Jalali M., Murbhy B., McIncosh T.C., McIron J.A., Liu X.,
Rasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McIeod M.P., McOherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Rank Rang D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Spler E., Spradling A.C., Stapleron M., Strong R., Sun H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skrupski M., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstook G., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhang X.,
RA Zhang X.H., Zhong W., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Whors E.W., Valley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng K.A., Myers E.W., Woldey R., Sulle M., Scheler T.,
Rh Shor S. A., Myers E.W., Rubin G.M., Venter J.C.,
Rh Pannerson R.A., Weinstock G.M., Weinschaber H.,
Rh Rheng Z.-Y., Wassarman D.A., Weinscholley K.C., Wu D., Yang S., Yao Q., Zheng R.,
Rh Panner S., Polley K.C., Wu D., Yang S., Yao Q., Zheng R.,
Rh Panner S., Manner S., Polley K.C., Stapler T.,
Rh Panner S., Wang S., Polley K., Smith H.O.,
Rh Panner Sequence of Drosophila melanogaster T.,
Rh Reiner K., Salander S., Polley R., Scheler T.,
Rh Reiner R., Wang S., Polley R., Scheler T.,
Rh Reiner R., Wang S., Polley R., Scheler T.,
Rh Rei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.0%; Score 64; DB 5; Length 309; 57.9%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steward C.A.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 AA; 33224 MW; 9DAEB67784852A93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0036583; CG13055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2185-2195(2000).
EMBL; AE003528; AAF49521.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 SRSGGGGGGGGVAGVILQE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003102; pKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                            Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERMEDIATE FILAMBURT PROTEIN El
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                            ;
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                                                                                                             5; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Length 333;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Pfam; PF00170; bZIP; 1.
Pfam; PF02173; pKID; 1.
SMART; SM00338; BRLZ; 1.
PROSITE: PS00036; BZIP_BASIC; 1.
DNA-binding; Nuclear protein.
SEQUENCE 331 AA; 34985 MW; A414C19D4ADCC91E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGURET: SECOND SERVER TO THE PROSITE; PSO0036; BZIP_BASIC; 1.

DNA-binding; Nuclear protein.

SROUENCE 333 AA; 35261 MW; BF02CE6398F6D058 CRC64;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
science 282.2012-2018(1998).
-1- SUBCELDULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
InterPro: IPRO01871; bXIP.
InterPro: IPR001871; bXIP.
                                                                                                          33.0%; Score 64; DB 76.9%; Pred. No. 15; Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.0%;
76.9%;
                                                                                                                      Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.0
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                      167 GGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00170; bZIP; 1
Pfam; PF02173; pKID; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 GGGGGGGVPGPS 181
                                                                                                                                                                     15 GGGGGGGGIEGPT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steward C.A.;
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                                                                                                           Query Match
                                                                                                                                                                                                                                                                                       Q9U2IO;
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ESPUENCE FROM N.A.
MEDLINE=99019308; PubMed=9804163;
Karabinos A., Riemer D., Erber A., Weber K.;
"Homologues of vertebrate type I, II and III intermediate filament (IF) proteins in an invertebrate: the IF multigene family of the cephalochordate Branchiostoma.";
FEBS Lett. 437:15-18(1998).
EMBL: AJ010294, CAA09908 I; -
LITERION OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD OF THE CARD 
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBL_TaxID=4530.
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STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                  33.0%; Score 64; DB 5; Length 422; 61.9%; Pred. No. 19; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003233; BAB55526.1; --SEQUENCE 207 AA; 21266 MW; F514ABC36A6DC403 CRC64;
                                                                                                                                                                                                                                                                                                                                          422 AA; 44892 MW; 85FE742F07751B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AARAGGGG-----GGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                InterPro; IPR001664; IF:
InterPro; IPR002957; Keratin_I.
InterPro; IPR003489; Ribosomal_S30.
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PRINTS; PR01228; EGGSHELL.
PRINTS; PR01248; TYPEIKERATIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GGGGGGGIEG-----PTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 61.9
es 13; Conservative
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Y., Yu J., Wang L., Hu X., Bao W., Li G., Chen C., Han H., Hu S.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                 STRAIN-CV. NTPPONDARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0708602.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001539; BAA92923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.5%; Score 63; DB 12; Length 66; 68.8%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                           Indels
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF325155; AAL01786.1; -.
Hypothetical protein.
SEQUENCE 66 AA: 6998 MW; C5626A8FFA9C9E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence Analysis of the Spodoptera litura Multicapsid Nucleopolyhedrovirus Genome.";
Virology 287:391-404(2001).
                                                                                                                                                                                                            al protein.
584 AA; 63515 MW; 351C684C8BBBD9CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spodoptera litura nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                           8:
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                                                                                                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       113 RWWTATRSSDPGIGSGGGGGGGGAPTRRR 141
                                                                                                                                                                                                                                                                                                                                                          7 ROWLAARA-----GGGGGGGGGIEGPTLRQ 30
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                                                                                                                                                                    InterPro; IPR001345; PG_mutase. Pfam; PF00300; PGAM; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                            32.78;
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Matches 14; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                            SEQUENCE FROM N.A.
Veau B., Oudin A., Clastre M., Chenieux J.C., Rideau M., Hamdi S.;
Veau B., Oudin A., Clastre M., Chenieux J.C., Rideau M., Handi S.;
Veau B., Oudin A., Clastre M., Chenieux J.C., Rideau M., Handing uncife."
Dinding motifs."
Dinding motifs."
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, APZ00311; AAF31402.1; -
HSSP; P09651: 1HA1.
FRSP; P09651: 1HA1.
FRSP; P00651: Trm: 1.
SMART; SM00360; RRW: 1.
FRGSTTE; PSS0102: RRW: 1.
FRGSTTE; PSS0102: RRW: 1.
FRGSTTE; PSS0102: RRW: 1.
SEQUENCE 137 AA: 14162 MW; 4FABADB9C7A988FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioldeae;
Vinceae; Catharanthus.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
Vinceae; Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.5%; Score 63; DB 10; Length 137; 50.0%; Pred. No. 8.1; ative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE GLYCINE-RICH RNA-BINDING PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 9, 2002, 09:03:08 Job time : 13.9826 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TLRQWLAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 TVNEAQSRGSGGGGGGGFRGP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TLRQWLAARAGGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.5%
Query Match
Best Local Similarity 50.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match · 32.5%
Best Local Similarity 50.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                          NCBI_TaxID=4058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669M60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2002, 08:50:51; Search time 16.1874 Seconds (without alignments) 247.023 Million cell updates/sec October Run on:

US-09-422-838C-27 190 1 IEGPTLRQCLAARAGGGGGGGGIEGPTLRQCLAARA 36 Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

747574 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_032802:\* Database :

/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:\*
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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\*
SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\*
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SIDSI/gogdata/hold-geneseq/geneseqp embl/AA1991.bAT: \*
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SIDSI/gogdata/hold-geneseqg/geneseqp-embl/AA1993.bAT: \*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1995.bAT: \*
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SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.bAT: \*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.bAT: \*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1999.bAT: \*
SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA2000.bAT: \* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	TPO-mimetic peptid	TPO-mimetic peptid	Cyclic or linear t	TPO-mimetic peptid	Linear thrombopoie	TPO-mimetic peptid	TPO-mimetic peptid	Thrombopoietin mim	Thrombopoietin mim	TPO-mimetic peptid	TPO-mimetic peptid
	ID	AAB17298	AAB17299	AAY96521	AAB17300	AAY96522	AAB16963	AAB17293	AAY96525	AAY96528	AAB17281	AAB17282
	DB	21	21	21	21	21	21	21	21	21	21	21
	Query Match Length DB	36	36	36	36	36	36	36	36	41	42	42
dР	Query Match	100.0	100.0	100.0	90.5	90.5	88.4	88.4	88.4	88.4	88.4	88.4
	Score	190	190	190	172	172	168	168	168	168	168	168
	Result No.	-	7	m	4	S	9	7	ω	σ	10	11

THE THE THE THE THE THE THE THE THE THE	Thrombopoletin mim TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid
	AAY96527 AAB16975 AAB16976 AAB17286 AAB17285 AAB16970
355555555555555555555555555555555555555	21 21 21 21 21 21
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88888888888888888888888888888888888888	2.1.0
168 168 168 168 160 150 150 150 150 150 151 151 151 151 15	116.5 116.5 112.5 112.5 106
11111111111111111111111111111111111111	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

RESULT 1 **AAB17**298

AA. AAB17298 standard; Peptide; 36

AAB17298;

(first entry) 31-OCT-2000 TPO-mimetic peptide sequence SEQ ID NO:354.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoinmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

Synthetic

WO200024782-A2.

04 - MAY - 2000

99WO-US25044 25-OCT-1999; 

98US-0105371. 23-OCT-1998;

22-OCT-1999;

(AMGE-) AMGEN INC.

Boone TC; Feige U, Liu C, Cheetham J,

WPI; 2000-350702/30

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re domain, pharmacologically active peptides, and linkers. Where II is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2.

(L1)c-P1-(L2)d-P2-(L3)d-P3 or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently larged that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18033 represent uncledide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                         present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autolmmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; hmmp; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 190; DB 21;
100.0%; Pred. No. 3.8e-16;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQCLAARAGGGGGGGGGGEGPTLRQCLAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                 Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17299 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
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99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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Novel composition of matter comprising an Fc domain and

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useful for treating cancer, setting, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                       FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                   the present invention describes composition of matter (I) comprising
pharmacologically active peptides, useful for treating cancer and
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclic or linear thrombopoietin mimetic peptide compound 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 190; DB 21;
100.0%; Pred. No. 3.8e-16;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLROCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96521 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9..31
/note= "optional"
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/label= linker
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/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23..36
/label= TMP_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 36; Conservative
                               autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96521
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Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                       virus associated ITP, and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARAGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:356.
                                                                                               Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17300 standard; Peptide; 36
Liu C, Feige U, Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                       WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                Matches
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õ Ω Feige U, Liu C, Cheetham J, Boone TC;

(AMGE-) AMGEN INC.

WPI; 2000-350702/30.

99WO-US25044. 98US-0105371 99US-0428082

25-OCT-1999; 23-OCT-1998; 22-OCT-1999;

04-MAY-2000

WO200024782-A2

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The present invention describes composition of matter (1) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)2-TL-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)-C-F1-(L2)d-F2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2. P3, and P4 = are each independently selected from the peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently of the tat least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaccutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAAA69526 and AAB16955 to AAB1803 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 172; DB 21;
Pred. No. 5.5e-14;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear thrombopoletin mimetic peptide compound 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQALAARAGGGGGGGGEGPTLRQALAARA 36
                                                                                                                                                       Example 1; Page 321; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96522 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15..22
/label= linker
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/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.4'
Matches 34; Conservative
                                                                                                    autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96522;
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g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCONTRACTOR SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET
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production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                            Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNR; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                             Length 36;
                                                                                                                                                                                                      Score 172; DB 21; Length JV Pred. No. 5.5e-14;
                                                                                                                                                                                  virus associated ITP, and systemic lupus erythematosus
                                                                                                                                                                                                                                                 1 IEGPTLRQALAARAGGGGGGGGGEGPTLRQALAARA 36
                                                                                                                                                                                                                                         1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                          A
                                                        Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                          AAB16963 standard; Protein; 36
                                                                                                                                                                                                              90.5%;
94.4%;
Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
                                                                                                                                                                                                                    Local Similarity 94.4
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
              WPI; 2000-365108/31.
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                                                                                                                                                                                                36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U,
                                                                                                                                                                                                                                                                                                        AAB16963;
                                                                                                                                                                                                              Query Match
 Liu C,
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                    AAB16963
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For domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from - (L1)c-P1, -(L1)d-P2-(L2)d-P2.

(L11)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides: L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
cc independently linkers; and a, b, c, d, e, and f = are each independently
cc or 1, provided that at least 1 of a and b is 1. The composition can
cartivities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
cc useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
cc half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA6943
cc banding, complement fixation, and possibly placental transfer. AAA6943
cc sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiastimmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 168; DB 21;
Pred. No. 1.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                        Disclosure; Page 190; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17293 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                       autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17293;
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The present invention describes composition of matter (I) comprising an Fe domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can bave cytostatic antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAAA69526 and AAB16955 to AAB1803 represent invention acid composition complemences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 168; DB 21; Length 36;
Pred. No. 1.6e-13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQCLAARAGGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin mimetic peptide compound 6.
                                                      Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/label= linker
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/label= TMP_1
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Best Local Similarity 94.4%;
Matches 34; Conservative
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                   autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
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                              Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                         Gaps
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5..19
//label= TMP_1
                                                                                                                                                                                                                                                        Length 36;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                      88.4%; Score 168; DB 21;
ilarity 94.4%; Pred. No. 1.6e-13;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGGGGGGGGFGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                 Claim 16; Page 62; 91pp; English
                                                                                                                                                                                                                                                                                                                                                  AAY96528 standard; peptide; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20..27
/label= linker
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/label= TMP_2
Feige U, Cheetham J;
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                WPI; 2000-365108/31.
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                       36 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                    AAY96528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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Liu C,
                                                                                                                                                                                                                                                                                                                                  RESULT 9
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Sequence
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                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4: mimetic; IL-1; TNE; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell 1 ymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                               88.4%; Score 168; DB 21; Length 41; 94.4%; Pred. No. 1.9e-13; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                     virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                            1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                     6 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                        diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                             AAB17281 standard; Peptide; 42 AA
                                                                      Claim 16; Page 65; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheetham J,
             Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044
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Best Local Similarity 94.44
Matches 34; Conservative
                           WPI; 2000-365108/31.
(AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U,
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                            AAB17281;
              Liu C,
                                                                                                                                                                                                                                                                                                RESULT 10
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 168; Db 21,
No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.96
0; Mismatches
                                                                                                                                                                                                                    Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17282 standard; Peptide; 42 AA.
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94.48;
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.4'
Matches 34; Conservative
WPI; 2000-350702/30
                                                                                                                                                 autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17282;
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A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                            ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                     88.4%; Score 168; DB 21; Length 42; 94.4%; Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
                                                      Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17308 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044
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99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                            34; Conservative
                                  autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                               42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2.
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                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17308;
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)2m-PI-(X2)b, where: Fl = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P2.

-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and s, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, c, d, e, and f = are each independently linkers; and so, e, d, e, and f = are each independently linkers; and so, e, d, e, and f = are each independently linkers of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69445 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 4%; Score 168; DB 21; 94.4%; Pred. No. 1.9e-13; Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                  Example 2; Page 327; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96530 standard; Protein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US24834
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Best Local Similarity 94.4
Matches 34; Conservative
                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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  Overlapping oligonucleotides were used to construct a synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.4%; Score 168; DB 21; Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.9e-13;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.48;
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99US-0428082.
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nes 34; Conservative
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The present invention describes composition of matter (I) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where: FI = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaccutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (tather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, complement fixation, and possibly placental transfer. AAA69443 to AAAA69526 and AAB10955 to AAB18033 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 168; DB 21; Length 60;
Pred. No. 2.7e-13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB16960 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
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ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF ACCOS NAME OF AC
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Example 2; Page 185-186; 608pp; English

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The property in the composition of matter (1) computating an ending parameter of the computation of the computation of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the present invention.
present invention describes composition of matter (I) comprising an
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269 AA; Sequence

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0; Gaps
88.4%; Score 168; DB 21; Length 269; ilarity 94.4%; Pred. No. 1.2e-12; Conservative 0; Mismatches 2; Indels C
                                                                                 1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                      2 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 37
                    Best Local Similarity
    Query Match
                                       Matches
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AAY96531 standard; Protein; 269 AA AAY96531; RESULT 16 AAY96531 

04-SEP-2000 (first entry)

Human IgGl Fc TMP fusion protein.

Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.

Homo sapiens.

WO200024770-A2.

04-MAY-2000

99WO-US24834 22-OCT-1999;

98US-0105348 23-OCT-1998;

(AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J; WPI; 2000-365108/31. N-PSDB; AAA29229 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Example 2A; Page 49-50; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP\_1-(L\_1)\_nTMP\_2], is new. TMP\_1 and TMP\_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x\_2-x\_1\_0, x\_2-x\_1\_1, x\_2-x\_1\_2, x\_2-x\_1\_3, x\_2-x\_1\_4, x\_1-x\_1-0, x\_1-x\_1-1, x\_1-x\_1-2, x\_1-x\_1-3, and

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an
is:
                                                                                                                                                                                                                                                                   aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                88.4%; Score 168; DB 21; 94.4%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB16959 standard; Protein; 268 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 94.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                               269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                  Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB16959
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently on I, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18035 to AAAB18003 represent incleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-T1-(X2)b. Where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)d-P2, -(L3)d-P2, -(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent, fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; MMP; Inbiltor; erythropotic, thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                 Ouery Match 86.3%; Score 164; DB 21; Length 268; Best Local Similarity 94.3%; Pred. No. 3.6e-12; Matches 33; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                234 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17301 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                          268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000
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                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17301;
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB180915 to AAAB18003 represent nuclectide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A compound which binds to an mpl receptor comprising a thrombopoletin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "optionally modified by bromoacetyl or PEG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                     84.2%; Score 160; DB 21; Length 36; 91.7%; Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                           1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin mimetic peptide compound 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             AAY96523 standard; peptide; 36 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..14
/label= TMP_1
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/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US24834.
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                                                                                                                                                                                                                                        Best Local Similarity 91.7
Matches 33; Conservative
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                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                             AAY96523
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10 to 14 residues in length comprising X_2^2 \cdot X_{-1}^1, X_2^2 \cdot X_{-1}^1 \cdot X_{-2}^2 \cdot X_{-1}^1, X_2^2 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot X_{-1}^1 \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 160; DB 21; Length 36; Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17303 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.2%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently loo or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes composition of matter (1) comprising an (X1)a-F1-(X2)b, where: F1 - an FC domain; X1 and X2 - are each independently selected from -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, where P1, P2, P3, and P4 - are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 - are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 - are each independently linkers; and a, b, c, d, e, and f - are each independently
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNE; antagonist; MMF; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                               Length 36;
                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                               83.7%; Score 159; DB 21; 91.7%; Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17307 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                     33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                           36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17307:
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                   Matches
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18095 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note- "optionally linked to an Fc molecule"
                                                                                                                                                                                                           DB 21; Length 36;
                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                          Score 159; DB 21
Pred. No. 2e-12;
0; Mismatches
                                                                                                                                                                                                                                                                                                     1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                          1 IEGPTLRQCLAARAGGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= linker
23..36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Cheetham J;
                                                                                                                                                                                                        83.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                            Best Local Similarity 91.7
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96524;
                                                                                                                                                                               Sequence
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                       RESULT 22
                                                                                                                                                                                                                                                                                                                                                                       AAY96524
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10 to 14 residues in length comprising X_2^2 \times_{1-0}^1, X_2^2 \times_{1-1}^1, X_2^2 \times_{1-2}^1, X_1^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2, and X_1^2 \times_{1-2}^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2 \times_{1-2}^2, X_2^2 \times_{1-2}^2 \times_{1-2}^2, X_2^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2, X_1^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2 \times_{1-2}^2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombopoletin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(11)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159; DB 21; Length 36;
Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17294 standard; Peptide; 37 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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99US-0428082.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive: EPO; TPO; CTLA4: mimetic; IL-1; TNF: antagonist; MMF; inhibitor; erythropojetin; thrombopojetin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                             21; Length 37;
                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                           Score 157.5; DB 2:
Pred. No. 3.1e-12;
                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                          1 IEGPTLRQCLAARA-GGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17295 standard; Peptide; 38
                                                                                                                                                                                                                                           82.9%;
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99US-0428082
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Best Local Similarity
                                                                                                                                                                                                               37 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(Li)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and Feige U, Liu C, Cheetham J, Boone TC; Example 1; Page 319; 608pp; English. autoimmune diseases -WPI; 2000-350702/30. (AMGE-) AMGEN INC.

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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                   AAA69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L3)d-P2,                              have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
provided that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; WBGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TRNF: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vactotoxia Teall lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.6e-12;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                     82.6%; Score 157; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQCLAARA--GGGGGGGGIEGPTLRQCLAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                               89.58;
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99US-0428082.
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Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                           38 AA;
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AAB17304
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be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 bhere P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombollytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
activities. DNAs, vectors and host cells from the present invention can
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Μ
                                                                                                                                                                                                                                                                                                                                                                                                                          82.4%; Score 156.5; DB 21; Length 39; 87.2%; Pred. No. 4.2e-12; rive 0; Mismatches 2; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQCLAARAGGG----GGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGKPEGGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:361.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000.
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                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L4)f-P4 = are each independently sequences of where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides, L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be useful for treating pharmacoutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer
                                                                                                                                                                                                                      ij
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wover composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                    ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                             DB 21; Length 39;
                                                                                                                                                                                                                      Indels
                                                                                                                                                             82.4%; Score 156.5; DB 21;
87.2%; Pred. No. 4.2e-12;
Niematiches 2;
                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGCPEGGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                                                                                           1 IEGPTLRQCLAARAGGG---GGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                  AAB17306 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                         39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999;
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                                                                                                                                                                                                                  34;
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                                                                                                                                             Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17306;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                              RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                  AAB17306
                                                                                                                                                                                                                                                                                                                                                                                                                                         555555x8
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_ITMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 - X_1 = 0, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_1 - 1, X_2 - X_2 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X_3 - 1, X
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAB469526 and AAB16095 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "optionally linked to an Fc molecule"
                                                                                                                                                                        Length 36;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                   Score 156; DB 21;
Pred. No. 4.5e-12;
0; Mismatches 4;
                                                                                                                                                                                                                                                                         1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96526 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, Feige U, Cheetham J;
                                                                                                                                                                        82.1%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000 (first entry)
                                                                                                                                                                                                                         32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365108/31.
                                                                                                                                                                                               Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                             36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96526;
                                                                                                                               Sequence
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96526
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where: FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-PI-(L2)d-P2.

-(L1)c-PI-(L2)d-P2-(L3)e-P3, or -(L1)c-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities DNAs, vectors and host cells from the present invention can be useful for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer
                                                                                                                                                                                                                   ;
0
activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The IMPS are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiastimatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietih; thrombopoietin; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                              82.1%; Score 156; DB 21;
88.9%; Pred. No. 4.5e-12;
                                                                                                                                                                                                                                                         1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               AAB17296 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J,
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                              Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
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                                                                                                                                            36 AA;
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                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17296;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                          RESULT 29
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The present invention describes composition of matter (1) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (1) is: (X1)3-F1-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of harmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention are be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP: inhibitor; erythxropietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                         9
                                                                                                                                           81.6%; Score 155; DB 21; Length 42; 81.0%; Pred. No. 6.9e-12; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                          1 IEGPTLRQCLAARA-----GGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                AAB17292 standard; Peptide; 35 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                              Best Local Similarity 81.0
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                      42 AA;
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       AAB17292;
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                          RESULT 30
                                                                                                                                                                                                                                                                                                                                                 AAB17292
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    8886666
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CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid CC sequences used in the exemplification of the present invention. XX SQ Sequence 35 AA;

Query Match 79.7%; Score 151.5; DB 21; Length 35; Best Local Similarity 91.7%; Pred. No. 1.5e-11; Matches 33; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36

δλ

Search completed: October 9, 2002, 08:58:56 Job time : 16.1874 secs

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(without alignments)
146.898 Million cell updates/sec
                                                                                                                                               October 9, 2002, 08:55:27; Search time 5.98595 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                          190
1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                  US-09-422-838C-27
                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                   OM protein
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                                                                                                                                                                                                                                                                                                    Seguence:
                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                  Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Sequence 27, Appl Sequence 31, Appl Sequence 31, Appl Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli 13, Appl 193, App 17, Appl 185, App 17, Appl 185, App 17, Appl 185, App 17, Appl App Appl Sequence 193, App Sequence 13, Appl Sequence 193, 8 Sequence 13, 8 Sequence 185, Description Sequence 1 Sequence 1 Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence SUMMARIES Query Match Length Score 64.5 64.5 64.5 64.5 Result ٠ 9

```
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Crasta, Oswald R.
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
                                                                                                                                                                                                                                                                             Sequence 27, Application US/09352159A
Patent No. 6211434
GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Malino, Jacob T.
APPLICANT: Malino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                          18, Appl
194, App
232, App
18, Appl
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232, App
16, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
        US-08-973-225-18

US-08-973-225-194

US-08-973-225-194

US-09-244-298A-194

US-09-244-298A-194

US-09-244-298A-232

US-09-516-704-194

US-09-516-704-194

US-09-516-704-132

US-09-516-704-132

US-08-451-947-57

US-08-451-947-57

US-08-451-947-57

US-08-441-447-642

US-08-238-644-57

US-08-238-644-57

US-08-238-644-57

US-08-244-941-2

US-08-236-503-2
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-05-21
NUMBER: OF SEQ ID NOS: 46
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09352168A Patent No. 6211435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 GPSIPPCADGAKAGGGGSGGG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPTLRQCL-AARAGGGGGGGGIEG 25
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NAME/KEY: SIGNAL
COCATION: (1) ... (24)
US-09-352-159-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
331.6
331.6
331.6
331.6
331.6
331.6
331.3
331.3
331.3
331.3
331.3
331.3
331.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-352-168-27
                                                                                                                                                                                                                                                          RESULT 1
US-09-352-159-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 829179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: F. CLASSIFICATION:
                                                                                                                                                         ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                             US-09-352-168-31
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-987-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-987-466-4
                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REPERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT PRILING DATE: 1998-07-12
EARLIER PRILING DATE: 1998-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 31
LENGTH: 1196
SEQ ID NO 31
LENGTH: 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polyol Amine Oxidase
TITLE OF INVENTION: Polyucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                              33.9%; Score 64.5; DB 4; Length 991; 54.2%; Pred. No. 5.1; tive 3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                          7; Indels
CURRENT APPLICATION NUMBER: US/09/352,168A CURRENT FILING DATE: 1999-07-12 EARLIER APPLICATION NUMBER: 60/092,936 EARLIER FILING DATE: 1998-07-25 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 27 LENGTH: 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-352-159-31
Squence 31, Application US/09352159A
Pattent No. 6211434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-352-168-31; Sequence 31, Application US/09352168A; Patent No. 6211435
                                                                                                                                                                                                                                                                                                                                                                                                                                           503 GPSIPPCADGAKAGGGGSGGGSGG 526
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Best Local Similarity 54.29
Matches 13; Conservative
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Best Local Similarity 54.2
Matches 13; Conservative
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; LOCATION: (1)...(24)
US-09-352-168-27
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                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Unknown
US-09-352-159-31
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                                                                                                                                                    Score 64.5; DB 4; Length 1196;
Pred. No. 6.1;
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                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Fisher, Douglas A.
APPLICANT: Gooding, Doug
APPLICANT: Streeter, Dave
TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,466
FILING DATE: Filed Herewith
                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0442 US
                                                                                                                                                                                                                                                                                         708 GPSIPPCADGAKAGGGGSGGSGG 731
                                                                                                                                                                                                                                                     3 GPTLRQCL-AARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08987466
Patent No. 5922595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AARAGGGGGGGGIEGPTLRQC 31
                                                                                                                                                                   Query Match 33.9%;
Best Local Similarity 54.2%;
Matches 13; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 584 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.99
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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TELECOMMUNICATION INFORMATION:
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-100-664A-2
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Patent No. 6057129
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: RLOSS, BRIAN
APPLICANT: PRICE, JEFFREY
TILLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEROF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.7%; Score 64; DB 4; Length 584; 61.9%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                               Sequence 4, Application US/09240359
Patent No. 6255456
GENERAL INFORMATION:
APPLICANT: Fisher, Douglas A.
APPLICANT: Fisher, Douglas A.
APPLICANT: Streeter, Dave
TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMBUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSDG for Windows Version 2.0
APPLICATION DATE:
APPLICATION NUMBER: US/09/240,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0442 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,466
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AARAGGGGGGGGIEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 61.9 Matches 13; Conservative
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CLONE: 829179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
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                                     RESULT 6
US-09-240-359-4
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APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: BRAU, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%; Score 62; DB 3; Length 440; 55.0%; Pred. No. 4.4; tive 2; Mismatches 7; Indels
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STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                            PELICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
ATORNES/AGENT INFORMATION:
NAME: JGCKSON ESQ., DAVID A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-343-1684
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.0
Matches 11; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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STATE: New Jersey
COUNTRY: USA
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403 PERRPSIRMRQGGGGGGG 422
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US-08-764-640-13
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APPLICANT: YOUNG, MICHAEL W.
APPLICANT: WICLOSK, BRIAN
APPLICANT: BLAD, JUSTIN
APPLICANT: BLAD, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: All Hackensack Avenue, 4th Floor
CITY: Hackensack
STARET: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                          32.6%; Score 62; DB 3; Length 440;
55.0%; Pred. No. 4.4;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 440; 4.4;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.6%; Score 62; DB
55.0%; Pred. No. 4.4;
tive 2; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
      TELEFAX: 2021
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
"MODILOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEO ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 440 amino acids TYPE: amino acid
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201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.69
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                               Best Local Similarity 55.0 Matches 11; Conservative
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linear
                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-100-664A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
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TELEPHONE:
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US-09-100-664A-4
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                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%; Score 60; DB 2; Length 14; 92.9%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                 APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 193, Application US/08764640
Patent No. 5869451
Patent No. 5869451
Patent No. 5869451
CENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Carrier, Ronald W.
APPLICANT: Carrier, Steven E.
Sequence 13, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                              APPLICANT: Hendren, Richard W. APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun
                         TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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LENGTH: 14 amino acids
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US-08-764-640-193
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Query Match
Best Local Similarity
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                                 ZIP: 27709
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                    COUNTRY:
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US-08-973-225-193
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Wrighton, Nicholas C.
Wrighton: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                     APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%; Score 60; DB 2; Length 14; 92.9%; Pred. No. 0.25; 1; Indels tive
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Five Moore Drive, P.O. Box 13398
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                                                                                                                                                                                                                                     ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                  Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hrubiec, Robert T.
REGISTATION UNDBER: 36.39.2
REFERENCE/DOCKET UNDBER: PK32!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 232
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                       ZIP: 27709
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                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%; Score 60; DB 3; Length 14; 92.9%; Pred. No. 0.25; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 232
CORRESSONDEWCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                         ATTORNATION:
NAME: HINDEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/POCKET NUMBER: PK3065USW
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/973,225A
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Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 193, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWILLA, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Research Triangle Park
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ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 13; Conservative
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
    0; Mismatches
                                                                                                                                                                                                                                                                               APPLICANT: Gates, curred.
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan APPLICANT: Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-1996
                                                                                                                                                                      Sequence 193, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
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Sequence 13, Application US/09516704

; Patent No. 6251864

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dower, William J. Barrett, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 193:
                                                                                                                                                                                                                             APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
  Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                        1 IEGPTLRQCLAARA 14
                                                                          1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARA 14
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FILING DATE: 11-DEC
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                        US-09-244-298A-193
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               31.6%; Score 60; DB 3; Length 14; 92.9%; Pred. No. 0.25; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 3; Length 14;
Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.O. Box 13398
                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-08-973-225-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09244298A Patent No. 6121238
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PK3281
                INFORMATION FOR SEQ ID NO: 193: SEQUENCE CHARACTERISTICS: LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/POCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Five Moore Drive, P.(CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.68;
92.98;
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                             1 IEGPTLROCLAARA 14
                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ResearCITY: NC
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-244-298A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.6%; Score 60; DB 4; Length 14; 92.9%; Pred. No. 0.25; tive 0; Mismatches 1; Indels
                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                      FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
ATTOREX/AGENT INFORMATION:
NAME: HTUDIC: Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-516-704-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schtz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQCLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLROWLAARA 14
                                         USA
                                         COUNTRY: US
ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                               Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 60; DB 4; Length 14; 92.9%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                         STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dower, William J.
Barrett, Ronald W.
CWilla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                  Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: HIDDIC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01.Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-516-704-13
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Hendren, Richard W.
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
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ADDRESSEE: Glaxo Wellcome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                 RECEPTOR
Cwirla, Steven E.
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                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 244
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Matches 13; Conservative
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ZIP: 27709
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Schatz, Peter 1.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                 Score 60; DB 2; Length 15; Pred. No. 0.27; 0; Mismatches 1; Indels
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Pred. No. 0.27;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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NAME: HTUDIC, ROBERT 1.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
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MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-973-225-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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US-08-973-225-185
; Sequence 185, Application US/08973225A
                                                                                                                                                                                                                                                                             US-08-973-225-17

Sequence 17, Application US/08973225A

Patent No. 6083913

GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 15 amino acids
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92.9%;
                                                                 31.6%; 92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 232
                                                              Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                            2 IEGPTLRQWLAARA 15
                                                                                                                                                    1 IEGPTLRQCLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                      US-08-764-640-185
                                                                                                                                                                                                                                                               RESULT 20
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CORRESPONDENCE ADDRESSE: ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                           Score 60; DB 2; Length 15; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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FILING DATE: 11-DEC-1996
CLASSIFTCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 185, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             ATTORNEY/AGENT INPORMATION:
NAME: HIUDIGC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INPORMATION FOR SEQ ID NO: 17:
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                                                                                                                                                                                                                                                                                                                                           31.6%;
92.9%;
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                           Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-17
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
CLASSIFICATION:
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US-08-764-640-185
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Dower, William J.
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 92.9
Matches 13; Conservative
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US-09-244-298A-185
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Wagstrom, Christopher R.
Wrighton, Nicholas C.
Wrighton: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK3065USW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
                                APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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Hendren, Richard W.
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GENERAL INFORMATION:
APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deprince, Randolph B. Podduturi, Surekha Yin, Qun
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                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Matches 13; Conservative
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ZIP: 27709
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TITLE OF INVENTION:
                 GENERAL INFORMATION:
Patent No. 6083913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-973-225-185
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APPLICANT:
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APPLICANT:
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NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park
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                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: Glaxo Wellcome STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park STATE: NC COUNTRY: USA 21P: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 60; DB 3; 92.9%; Pred. No. 0.27; tive 0; Mismatches
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deprince, Randolph B.
Podduturi, Surekha
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Cwirla, Steven E.
Gates, Christian
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                          Score 60; DB 4; Length 15;
Pred. No. 0.27;
0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-516-704-185
      ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
08-09-516-704-17
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                       Sequence 185, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-Mar-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                            31.6%; 92.9%;
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                                                                                       Ouery Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              RESULT 25
US-09-516-704-185
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APPLICANT DOWER, Ronald W.

Curia, Steven E.

Gates, Christian
Schatz, Peter J.

Balasubramanian, Palaniappan
Wagstrom, Christopher R.

Hendren, Richard W.

Deprince, Randolph B.

Podduturi, Surekha

TITLE OF INVENTION: PEPPIDES AND COMPOUNDS THAT BIND TO A
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

CORRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704

FILING DATE: 01-Mar-2000

CLASSIFICATION: CURROWN>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 3; Length 15;
Pred. No. 0.27;
0; Mismatches 1; Indels
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                   REGISTRATION NUMBER: 36,392
REFERENCE/POCKET NUMBER: PR3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-748-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
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92.9%;
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COMPUTER READABLE FORM:
                                                                     ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLROCLAARA 14
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TYPE: amino acid STRANDEDNESS:
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APPLICANT:
APPLICANT:
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APPLICANT:
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STATE:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%; Score 60; DB 2; 92.9%; Pred. No. 0.29;
                                                                                                                                            Expansion of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the following specific of the f
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CITY: Research Triangle Park
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; OTHER INFORMATION: /product= "Beta-ala"
US-08-764-640-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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Patent No. 5869451
Patent No. 5869451 5837683
                              Sequence 18, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                  GENERAL INFORMATION:
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US-08-764-640-18
                                                                                                                                                             APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yin, Oun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.6%; Score 60; DB 2; Length 16; 92.9%; Pred. No. 0.29; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                       Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERET
                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 232, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                         Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-764-640-194
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: Glaxo Wel
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FEATURE
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.6%; Score 60; DB 2; Length 16; 92.9%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Research Triangle Park
STATE: NC
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                            NAME: Hrubiec, Robert T.
REGISTRATION UNDHBER: 36.392
REFERENCE/DOCKET UNMBER: PK327
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA ZIP: 27709 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                   COMPUTER READABLE FORM:
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                                         USA
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                                                         27709
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                                         COUNTRY:
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Gaps
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Wrighton, Nicholas C.
TITLE OF INVENTION: PRETIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                        31.6%; Score 60; DB 3; Length 16; 92.9%; Pred. No. 0.29; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSES: Glazow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
REFERENCE/DOCKET NUMBER: PK3065USW
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 194, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
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15
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STRANDEDNESS: <Unknown>
                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.9
Matches 13; Conservative
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US-08-973-225-194
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0; 0; Gaps Query Match
Best Local Similarity 92.9%; Pred. No. 0.29;
Matches 13; Conservative 0; Mismatches 1; Indels

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Search completed: October 9, 2002, 09:06:31 Job time : 6.98595 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:54:17; Search time 8.09368 Seconds Run on:

(without alignments)
427.397 Million cell updates/sec

US-09-422-838C-27

190 1 IEGPTLRQCLAARAGGGGGGGGGEGPTLRQCLAARA 36 score: Sequence: Perfect

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR\_71:\* 1: pir1:\* 2: pir2:\*

pir3:\* pir4:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Jacobs (EC 1 10.3	EC	tical		ب		insulin precursor		probable nuclear a	hypothetical prote		1	hypothefical prote	`	hflX protein - Myc					-	protocadherin 68 -	probable Hflx - My	RNA	probable membrane	transforming prote	- 1	_		
SUMMARIES	ID	KSNCLO	KSNCLT	T48099	T20961	A53662	INSH	IPBO	JQ1094	B45344	T26807	T26808	S65543	T47772	G87033	S72938	T13690	MWAXIC	T06612	T49792	S57795	T09055	D70505	S71779	S69312	820099	S58064	T13386	64	B39490
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	Query Match Length	619	619	199	500	403	77	105	201	1733	331	333	777	434	488	518	806	1168	339	201	867	883	495	167	285	323	649	1325	443	487
ф	Query	38.4	8	L)	4	34.5	₹	34.2	4	33.9	m	m.	33.7	3	3	m	m	3	32.9	N	$\sim$	$\sim$	S	Н	П	$\vdash$	ч		31.3	
	Score	73	73	68	99	65.5	65	65	0	64.5	64	64	64	63.5	63	63	63	63	62.5	62	62	62	61	9	9	09	09	9	59.5	
	Result No.	1	7	m	4	5	9	7	Φ.	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

subtilisin-like pr subtilisin-like pr	subtilisin-like pr subtilisin-like pr	hypothetical prote	RNA-binding glycin	hypothetical prote	unknown protein F2 heterogeneous ribo	helix-Îoop-helix t	glycine-rich prote	hypothetical prote	hypothetical prote	keratin 10, type I	probable protein p
JC2191 JC5571	A39490 JC5570	H95992 S41773	859529	H85067	S35500	JC6087	T49109	B71260	F96624	KRHU0	T13926
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652 962	969 975	102 165	165	250	346	367	396	517	543	593	1428
31.3	$\frac{31.3}{31.3}$	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1
59.5 59.5	59.5 59.5	50 00 00	59	ტ ი ი	0 CO	59	υ 9 ο	ν	50	59	59
30	33	34 35	36	37	36	40	4.	7.5	43	44	45

laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)
N;Alternate names: urishiol oxidase
C;Specias: Neurospora crassa
C;Date: 30.5ep-1991 #sequence\_revision 30-Sep-1991 #text\_change 11-Jun-1999
C;Accession: A28523; A29762
C;Accession: A28523; A29762
J; Huzziker, P.E.; Lerch, K.
J; Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- a A;Reference number: A28523; MUID:88087214

A; Accession: A28523
A; Molecule type: DNA
A; Residues: 1-619 (GER>
A; Cross-references: EMBL:M14554
B; Germann, U.A.; Lerch, K.
Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
A; Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospor A; Accession: A29762; MUID:87067412

A;Molecule type: DNA A;Residues: 379-619 <GE2> A;Cross-references: GB:M14554; NID:g168823; PIDN:AAA33590.1; PID:g168824 C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquino C;Genetics:

A;Introns: 86/3
C;Superfamily: laccase
C;Superfamily: laccase
C;Superfamily: laccase
C;Superfamily: laccase
F:1-21/Domain: signal sequence #status predicted <SIG>
F;22-49/Domain: signal sequence #status predicted <PRO>
F;22-49/Domain: propeptide #status predicted <PRO>
F;30-619/Product: laccase #status predicted <ARD>
F;30-619/Product: laccase #status predicted <BB1>
F;316-372/Domain: middle beta-barrel #status predicted <BB2>
F;31-580/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F;431-280/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F;144,480/Binding site: copper (His) (type 2) #status predicted
F:145,189,191.482,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status predicted
F:477,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

38.4%; Score 73; DB 1; Length 619; 60.0%; Pred. No. 1.2; Live 0; Mismatches 10; Indels Query Match Best Local Similarity Matches 15; Conserv

10; Indels Conservative

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Gaps

0;

7 RQCLAARAGGGGGGGGIEGPTLRQC 31 δ

39 RQDSQAERYGGGGGGCNSPTNRQC 63 pp

RESULT 2

laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain TS) N;Alternate names: urishiol oxidase

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34.78;
56.58;
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Matches 16; Conservative
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:U07663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homeotic protein HB9 - human
A; Reference number: Z19351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-403 <HAR>
                                                                                                                                                                                                                                                   A; Gene: CESP:F15B9.5
                                 A; Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: HLXB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A53662
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                                                                                                                                                                                                               A; Relegates: 128523, MODE 2000/214
A; Relegate 1: 12619 of 2000/214
A; Residues: 1-619 of 2000
A; Residues: 1-619 of 2000
A; Residues: 1-619 of 2000
A; Cross-references: EMBL:M18334: NID:9168827; PIDN:AAA33592.1; PID:9168828
A; Cross-references: EMBL:M18334: NID:9168827; PIDN:AAA33592.1; PID:9168828
C; Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
C; Genetics:
A; Introns: 86/3
C; Superfamily: laccase
C; Keywords: copper; glycoprotein; oxidoreductase
C; Keywords: copper; glycoprotein; oxidoreductase
C; Keywords: copper; glycoprotein; predicted <SIG>
F; 12.7 Domain: signal sequence #status predicted <ARO>
F; 22-49,Domain: propeptide #status predicted <ARO>
F; 20-49,Domain: middle beta-barrel #status predicted <BBD>
F; 216-372,Domain: middle beta-barrel #status predicted <BBD>
F; 216-372,Domain: middle beta-barrel #status predicted <BBD>
F; 130-280,Domain: carboxyl-terminal beta-barrel #status predicted <BBD>
F; 144,480/Binding site: copper (His) (type 2) #status predicted
F; 146,189,191,482,580,Binding site: 2Cu-O cluster (His) (copper type 3) #status predicted
F; 477,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T20010.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T48099
R;Obermaler, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Ler
Submitted to the Protein Sequence Database, April 2000
A;Reference number: 224484
A;Accession: T4809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <a href="https://doi.org/10.100/bib.74">https://doi.org/10.100/bib.74</a>
A;Cross-references: EMBL:AL163816
   C;Species: Neurospora crassa
C,Date: 30-Sep-1991 #Sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: B28523
R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
B. Blod. Chem. 263, 8867-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A;Reference number: A28523; MUID:88087214
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C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20961
R;Percy, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 619;
1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.4%; Score 73; DB 1; Length 619 60.0%; Pred. No. 1.2; Live 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EGPTLRQC------LAARAGGGGGGGGTEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 EGRIRIRCPFASTICSTLVAQISLLCVDDGGGGGGGGGGVDGGVDRGC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone T20010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 RQCLAARAGGGGGGGGIEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 RODSQAERYGGGGGGGCNSPTNRQC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0%
Matches 15; Conservative
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les 16; Conserv
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A; Molecule type: protein
A; Residues: 1-30,57-77 < CBRO>
R; Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Blol. Chem. 247, 4866-4817, 1972
A; Title: Determination of the amino acid sequence of the monkey, sheep, and dog proin
A; Reference number: A92111; MUID:72258016
A; Accession: S16431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: the nucleotide sequence and conceptual translation as given are self-consiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A53662
R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A;Title: A novel human homeobox gene distantly related to proboscipedia is expressed
A;Reference number: A53662; MUID:94327547
A;Accession: A53662
                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                 A;Cross-references: EWBL:278013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5
A;Experimental source: clone F15B9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                            Score 66; DB 2; Length 500;
Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                              A;Map position: 5
A;Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1
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A;Status: principle A;Status: principle BDBJ A;Status: principle BDBJ A;Residues: 1-500 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.5%; Score 65.5; DB 57.1%; Pred. No. 5.2;
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R,Brown, H.; Sanger, F.; Kitai, R.
Biochem. J. 60, 556-565, 1955
A;Title: The structure of pig and sheep insulins.
A;Reference number: A90344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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A)Map position: 1941-1942.1
C; Superfamily: unassigned homeobox proteins;
C; Seywords: DNA bluding; homeobox; nucleus; t
F; 244-300/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 GSMLGRFLSNRGGGGGGGGGGGG 451
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A. Molecule type: protein
A. Residues: 25-30, X', 32-42, X', 44-54 < CH2>
A. Residues: 25-30, X', 32-42, X', 44-54 < CH2>
B. Ryll- A.P.; Sanger, F.; Smith, L.F.; Kitai, R.
Biochem. J. 60, 541-556, 1955
A. Title: The disulphide bonds of insulin.
A. Reference number: A90343
A. Contents: annotation; amides; disulfides
A. Contents: annotation; amides; disulfides
B. Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
R. Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
A. Title: Existence of a molecular ruler in proteasomes suggested by analysis of degra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable nuclear antigen - suid herpesvirus 1 (strain Kaplan)
C;Species: suid herpesvirus 1
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45344
E;Vicans, C.; Rozalk, Z.; Paces, V.; Schirm, S.; Schwyzer, M.
N;Vicalogy 179, 365-377, 1990
A;Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented A;Reference number: A45344; MUID:91021039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-201 <ROT>
A;Cross-references: GB:D12477; GB:D01129; NID:g222674; PIDN:BAA02044.1; PID:d1002526;
A;Experimental source: strain raspberry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: tomato ringspot virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C;Accession: JQ1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 25-54 <WEN>
A;Residues: 25-54 <WEN>
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;2-5-54,Momain: insulin chain B #status experimental <BGH>
F;25-54,85-105/Product: insulin #status experimental <MAT>
F;5-5-54,85-105/Domain: connecting peptide #status experimental <CNEP>
F;57-54/Domain: insulin chain A #status experimental <CNEP>
F;31-191,43-104,90-95/Disulfide bonds: #status experimental
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J. Gen. Virol. 72, 1505-1514, 1991
A;Title: Nucleotide sequence of tomato ringspot virus RNA-2.
A;Reference number: JQ1093; MUID:91311402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQCLAARAGGGGGGGGGIEGP----TLRQCLAA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 20.2K protein - tomato ringspot virus
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A; Status: translation not shown
A; Molecule type: genomic RNA
A; Residues: 1-201 <RQT>
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Best Local Similarity 61.59
Matches 16; Conservative
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nes 16; Conserva
A; Molecule type: protein
A; Residues: 85-105 <CHE>
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A; Status: preliminary
                                                                                                       A; Status: preliminary
                                                                 A; Accession: S48185
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(Species: Bos primigenius taurus (cattle)

(Species: Bos primigenius taurus (cattle)

(Species: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999

(SAccession: A40809; A92080; A92074; A91185; A90341; S48184; S48184; S46258; A01

(S.D'Agostino, J.; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L.

(A) Endocrinol. J, 327, 331, 1987

(A) Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid

A; Reference number: A40909; MUID: 88288209

A; Accession: A40909.
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Blochem. J. 53, 366-374, 1953
A;Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of A;Reference number: A90342
A;Accession: A90342
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A.Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigat
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A; Residues: 57-82 <STE>
R; Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
Eur. J. Blochem. 20, 183-189, 1971
A; Title: Bovine proinsulin: amino acid sequence of the C-peptide isolated from pancreas.
A; Reference number: A91185; MUID:71257721
A; Accession: A91185
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A; Residues: 25-105 A0012-
A; Residues: 25-105 A0012-
J. Biol. Chem. 246, 1365-1374, 1971
A; Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
A; Reference number: A92074; MUID:71116409
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                                                                                                                                                                                                                                                                                                                                                                        9
                                                          C.Keywords: hormone; pancreas
F;1-30/Domain: insulin chain B #status experimental <BCH>
F;1-30/57-77/Product: insulin *status experimental <MAT>
F;31-56/Domain: connecting peptide *status experimental <CPEP>
F;37-77/Domain: insulin chain A *status experimental <ACH>
F;7-63,19-76,62-67/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                34.2%; Score 65; DB 1; Length 77; 44.4%; Pred. No. 1.4;
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Eur. J. Biochem. 223, 759-764, 1994
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 44.4
Matches 15; Conservative
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A; Residues: 57-82 <SAL>
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A; Residues: 25-54 <SA2>
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A; Residues: 85-105 <SAN>
R; Sanger, F.; Tuppy, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-105 <DAA>
A;Residues: 31-56 <PET>
C;Superfamily: insulin
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A; Accession: S65543
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 16-Feb-2001
C;Accession: T26808
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26807
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                                                                             A; Residues: 1-1733 <VLC>
A; Cross-references: GB:M34651; NID:g334070; PIDN:AAA47471.1; PID:g334072
C; Superfamily: pseudorabies virus 1 nuclear antigen
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R; Steward, C
submitted to the EMBL Data Library, October 1998
A; Reference number: Z20269
A; Accession: T26808
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Rsteatimental type: DNA
A; Residues: 1-333 «WIL>
A; Rxperimental source: Glone Y41C4A
C; Genetics: A; Constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the constrained to the cons
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A:Accession: T26807
A:Status: 126807
A:Accession: T26807
A:Accession: T26807
A:Accession: T26807
A:Accession: T26807
A:Accession: T26807
A:Accession: T26807
A:Accession: T26807
A:Residues: 1-331 CMIL>
A:Residues: 1-331 CMIL>
A:Residues: 1-331 CMIL>
A:Residues: 1-331 CMIL>
A:Residues: 1-331 CMIL>
C:Genetics: Source: clone Y41C4A
A:Acene: CSEP:Y41C4A.4a
A:Access: CSEP:Y41C4A.4a
A:Access: T2871: 22871: 22873
C:Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                  Length 1733;
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2; Mismatches 13; Indels
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                                                                                                                                                                                                                                              Query Match

33.9%; Score 64.5; DB 1;
Best Local Similarity 42.9%; Pred. No. 23;
Matches 18; Conservative 2; Mismatches 13;
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R, Steward, C
submitted to the EMBL Data Library, October 1998
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A;Status: translation not shown A;Molecule type: DNA
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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Cydecession: T47772
R;Nyskatura, G; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M submitted to the Protein Sequence Database, February 2000
A;Reference number: 224475
A;Accession: T47772
A;Accession: T47772
A;Molecule type: DNA
A;Residues: 1-434 <NYA>
A;Residues: 1-434 <NYA>
A;Residues: Lembininary
A;Molecule type: DNA
A;Residues: Cultivar Columbia; BAC clone F2413
C;Genetics:
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific, splice form I N; Contains: 3',5'-cyclic-nucleotide phosphodiesterase, cAMP-specific, splice form III C; Specials: Drosophila melanogaster C; Date: 28-oct-1995 #sequence_revision 19-Jul-1996 #text_change 17-Nov-2000 C; Accession: 865543; 819662; 865542; 865544; A26651 R;Quiv, Y:, Chen, C.N.; Mallon, T.; Richter, L.; Beckendorf, S.K.; Davis, R.L. A;Title: Characterization of the memory gene dunce of Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 'MVCSFCCCTNFRN',4,'P',6,'S',94-777 <Q14>
A; Residues: 'MVCSFCCTNFRN',4,'P',6,'S',94-777 <Q14>
A; Cross-references: EMBL:X55174
A; Cross-references: EMBL:X55174
B; Chen, C.M.; Denome, S.; Davis, R.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 9313-9317, 1986
A; Title: Molecular analysis of cDNA clones and the corresponding genomic coding seque
A; Reference number: A26651; MUID:87092243
A; Accession: A26651
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A;Gene: Flybase:dnc; dunce
A;Cross-references: FlyBase:FBgn0000479
A;Cross-references: FlyBase:FBgn0000479
A;Introns: 93/2: 125/3: 152/2: 165/2: 200/2: 262/3: 294/1: 407/3: 496/2: 534/2: 588/3
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'
C;Keywords: alternative splicing; phosphoric diester hydrolase
F;137-77/Product: CAMP-dependent 3',5'-cyclic-nucleotide phosphodiesterase, splice f
F;439-667/Pomain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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A;Residues: 416-777 <CHE>
A;Cross-references: GB:MI4982; NID:g157278; PIDN:AAC34201.1; PID:g157280
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S65542
A;Molecule type: DNA
A;Residues: 'WobEQ',86-87,'IG',90-91,'QKYHSRYLKNRRHTLANVR',94-777 <Q13>
A;Cross references: EMBL:X55174
A;Accession: S65544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X55174
A;Accession: S19662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X55174
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A; Residues: 137-777 <Q12>
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A; Residues: 1-777 <QIU>
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A;Cross-references: FlyBase:FBgn0025833
A;Introns: 37/3; 448/3; 611/2; 690/3
A;Note: EG:EG0003.2
                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                  100 GGGGGGGGPGGASITQAIAQAA 121
                                                                                                                                                                                                                                                                                                                                                                                                            15 GGGGGGGIEGPTLRQCLAARA 36
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Best Local Similarity
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                                                                                                                                                                                   -806 <MUR>
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A; Molecule type: DNA
                                                                                                                 A; Accession: T13690
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                                                                                                                                                                                                                                                   C; Species: Mycobacterium leprae
C; Date: 20-Apr-2001
Sccession: G87031
R; Cole, S.T.; Etglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Cole, S.T.; Etglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
R.; Davies, R.M.; Dutherford, K.M.
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A; Title: Massive gene decay in the leprosy bacillus
A; Reference number: A66909; MUID: 21128732; PMID: 11234002
A; Accession: G87033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hflx protein - Mycobacterium leprae
N;Alternate names: B2235_C2_202 protein
C;Species: Mycobacterium leprae
C;Dapecies: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72938
R;Smith, D.R.; Roblson, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2235.
A;Reference number: S72587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross references: EMBL:U00019; NID:9467079; PIDN:AAA17274.1; PID:9467091
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C;Species: Drosophila melanogaster
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                                                                                                                                                                                                                               probable ATP/GTP-binding protein [imported] - Mycobacterium leprae
DB 2; Length 434;
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Pred. No. 12;
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                                          Indels
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Pred. No. 11;
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5; Mismatches
                                            2; Mismatches
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  Score 63.5;
Pred. No. 9;
                                                                                                            13 RAGGGGGGGG-----IEGPTLRQCL 32
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    33.4%;
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nes 11; Conservative
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                                              13; Conservative
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Matches 11; Conserv
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A; Residues: 1-518 <SMI>
        Query Match
Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-488 <STO>
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                                              Matches
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A; Accession: C3448
A; Molecule type: protein
A; Residues: 308-314, X', 316-329 cBRZ>
A; Residues: 308-314, X', 316-329 cBRZ>
A; Residues: 308-314, X', 316-329 cBRZ>
C; Comment: In this protein, the coiled-coil rod-like region found in many myosin heaven protein is globular and does not self-associate into filaments.
C; Genetics:
A; Genetics:
A; Introns: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 371/3; 4
A; Introns: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 371/3; 4
C; Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 hom C; Keywords: actin binding; APP; hydrolase; nucleotide binding; P-loop; phosphoprotein F; 10-653/Domain: myosin motor domain homology cAMOT>
F; 10-653/Domain: myosin motor domain promology cAMOT>
F; 101-108/Region: actin binding #status predicted
F; 671-1168/Domain: carboxyl-terminal cTD>
F; 671-1168/Region: alanine/glycine/proline-rich
F; 983-1030/Domain: SH3 homology cSH3>
F; 1034-1168/Region: alanine/glycine/proline-rich
F; 1017/Alinding site: APP (Lys) #status predicted
F; 311/Binding site: Phosphate (Ser) (covalent) #status experimental
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C;Species: Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Species: 30-59p-1990 #sequence_revision 30-5p-1990 #text_change 19-Jan-2001
C;Accession: A33891; C34446; A24146
R;Jung, G; Korn, E.D.; Hammer III, J.A.
Proc. Natl. Acad. SCI. U.S.A. 84, 6720-6724, 1987
A;Title: The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like and non A;Reference number: A33891; MUID:88016163
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A.Cross-references: GB:J02974; NID:g155624; PIDN:AAA27707.1; PID:g155625
A.Cross-references: GB:J02974; NID:g155624; PIDN:AAA27707.1; PID:g155625
A.Note: this gene and protein are called MIB in this paper
R.Brzeska, H. Lynch, T.J.; Martin, B.; Korn, E.D.
J. Biol. Chem. 264, 19340-19348, 1989
A.Title: The localization and sequence of the phosphorylation sites of Acanthamoeba A.Reference number: A34448; MUID:90037074
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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C;Accession: T13690 B;Rurphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, November 1998 A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: 217699
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Pred. No. 17;
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388 QCRVLGGGGTGGGGLGGP 406
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                                                                                                                                                                                                                                                                                                                     11; Conservative
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A; Accession: S66368
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                                                                                                                                         A; Gene: CPH1
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                                                                                                           C; Genetics:
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                                                                                  hypothetical protein F16J13.120 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000 (C.Saccession: T06612 (B.Sevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A.Reference number: 215789 (A.Reference number: 215789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Accession: T49792
Submitted to the Protein Sequence Database, May 2000
A. Reference number: 225022
A. Reference number: 225022
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Residues: 1-201 < CCH>
A. Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
A. Cross-references: BAC clone B9J10; strain OR74A
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S25795
probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Chlamydomonas reinhardtii
N:Alternate names: DNA photolyase homolog; probable blue light photoreceptor
C:Species: Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Accession: S57795; S66368
C:Accession: S57795; S66368
C:Accession: S57795; S66368
C:Accession: S57795; Mulp. B.: Lefebvre P.A.
Plant Mol. Biol. 28, 443-454, 1995
A:Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the Accession: S57795
A:Accession: S57795
A:Accession: S57795
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C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
C;Superfamily: Arabldopsis thaliana hypothetical protein T12H17.200
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A; Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:P16J13.120
A; Experimental source: cultivar Columbia; BAC clone F16J13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 52.0%; Pred. No. 9.3;
Matches 13; Conservative 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.6
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 RAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 RGGGGGGGGVNG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: ATSP:F16J13.120
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                                 RESULT 18
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Ricole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A.Recression: D70505
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A;Coss.references: GB:Z98209; GB:AL123456; NID:93261838; PIDN:CAB10901.1; PID:e33228 A;Experimental source: strain H37Rv
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C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protocadherin 68 - human
C:Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
C;Accession: D70505
A; MOLECULE type: mRNA
A; Residues: 1-867 <SMW>
A; Cross-references: EMBL:L07561; NID:9945420; PIDN:AAC37438.1; PID:9945421
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                                                                                                                                                                                                                                                                      Length 867;
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                                                                                                                                                                                                                                                                                                                             9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-889 <JIN>
A;Cross-references: EMBL:AF029343; NID:92599501; PID:92599502
                                                                                                                                                             A;Introns: 34/3; 159/2; 210/3; 265/3; 329/3; 406/1; 837/3
C;Keywords: carbon-carbon lyase; photoreceptor
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                                                                                                                                                                                                                                                               DB 2;
24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T09055 Transport R; Jin F. Xu, H.; Israel, D. Submitted to the EMBL Data Library, October 1997 A; Reference number: 216540
                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                        32.6%; Score 62; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                            3 GPTLRQCLAARAGGGGGGGGGIEGP 26
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1325 (CAT>
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A; Residues: 1-1325 (CAT>
A; Gibson, W.; Graves, J.P.; Sterling, J.F.; Eisenberg, M.T.
B; Voelker, R.A.; Gibson, W.; Graves, J.P.; Sterling, J.F.; Eisenberg, M.T.
Mol. Cell. Biol. 11, 894-905, 1991
A; Title: The Drosophila suppressor of sable gene encodes a polypeptide with regions s A; Reference number: A39612; MUID:91117256
A; Accession: A39612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Weaver, T.A.; White, R.A.
R;Weaver, T.A.; White, R.A.
A;Description: hdc, an imaginal specific gene required for adult morphogenesis in Dro
A;Reference number: S58064
A;Accession: S58064
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C:Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13386, A39612
C;Accession: T13386, A39612
S;Balles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover, D. submitted to the EMBL Data Library, May 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17665
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                                                                                            A;Cross-references: EMBL:X60063; NID:g62927; PIDN:CAA42665.1; PID:g62928 C;Superfamily: jun transforming protein; fos/jun DNA-binding domain homology C;Keywords: DNA binding; nucleus; transcription regulation F;237-277/Domain: fos/jun DNA-binding domain homology <FUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hdc protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1998
C;Accession: S58064
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                                                                                                                                                                                                                                                ; DB 2; Length 323; .16;
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A;Cross-references: FlyBase:FBgn0003575; FlyBase:FBgn0020381
                                                                                                                                                                                                                                                                                                           5; Indels
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                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                      31.6%; Score 60; 72.2%; Pred. No.
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A; Residues: 1-719,723-1325 <VOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AAAAGGGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                         11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                    13; Conservative
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A; Residues: 1-649 <WEA>
                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                       A; Molecule type: DNA
A; Residues: 1-323 <HAR>
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                                     A;Status: preliminary
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A; Accession: S20099
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Rydiltinan, M.J. Niu, X.
Plant Mol. Biol. 30, 1301-1306, 1996
A.Fithe: CDNA encoding a wheat (Triticum aestivum cv. Chinese spring) glycine-rich RNA-b A:Reference number: S71779; MUID:96311016
A;Accession: S71779
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c.species: Gallus gallus (chicken)
c.species: Gallus gallus (chicken)
c.spate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
c.shate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
c.shate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
R.Hartl, M.; Hutchins, J.T.; Vogt, P.K.
Oncogene 6, 1623-1831, 1991
A;Title: The chicken junb gene and its product.
A;Reference number: S20099; MUID:92019832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein YLR338w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein L8300.13-a
C;Species: Saccharomyces cerevisiae
C;Bate: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 05-Nov-1999
C;Accession: S69312
R;Du, Z.
                                                                                                                                                       glycine-rich RNA-binding protein GRP1 - wheat
c:Species: Triticum aestivum (common wheat)
C:Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-167 <GUI>
A;Cross-references: EMBL:U32310; NID:9974604; PIDN:AAA75104.1; PID:9974605
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Pred. No. 9.3;
4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;142-150/Domain: transmembrane #status predicted <TMl>F;201-217/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, January 1994
                  205 GESMSRQAGGRAGGSGGGVGLRGP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 12R
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 LPPNAGGGGGGGGAGAPAI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 55.68;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LAARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 57.9% hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 TLRQCLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 TVNEAQSRRSGGGGGG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-285 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: MIPS:YLR338w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S69312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
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                                                                                                            RESULT 23
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Best Local Similarity
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                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dypothetical protein F8D11.2 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C; Accession: E96495
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C; Accession: E9649
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A;Residues: 1-487 <KIE>
A;Note: the lack of a domain necessary for correct folding and activity of other serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form B - hum. Nylternate names: subtilisin homolog precursor, short splice form C:Species: Homo sapiens (man) (Species: Homo sapiens (man) (C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 31-Mar-2000 R:Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J. DNA Cell Biol. 10, 757-769, 1991 A:Title Identification of a second human subtilisin-like protease gene in the fes/fps. M:Reference number: A39490; MUID:92075167
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C; Genetics:
                                                                                                                                                                                                                                                                                                 Gaps
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C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: alternative splicing; hydrolase; serine proteinase
F;196-434/Domain: subtilisin homology <SBT>
F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.3%; Score 59.5; DB 2; Length 443; 92.3%; Pred. No. 24; tive 0; Mismatches 0; Indels 1
                                                                                                                                                                                      31.6%; Score 60; DB 2; Length 1325; 68.8%; Pred. No. 56;
                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: barley pathogen resistance protein Mlo
                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GDB:131390; OMIM:167405
A;Map position: X
A;Introns: 92/1; 170/3; 603/2; 645/1
A;Note: EG:115C2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1162 GGGGGGGVVLPNLSQ 1177
                                                                                                                                                                    Ouery Match 31.69
Best Local Similarity 68.89
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                      15 GGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-443 <STO>
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NAlternate names: kexin-like protease isoform
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C; Accession: JC2191
R; TSU11, A.; Hine, C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y.
Biochem: Biophys. Res. Commun. 200, 943-950, 1994
A; Title: Identification of novel conNas encoding human kexin-like protease, PACE4 isof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA
A; Residues: 1-652 <TSU>
C; Comment: This protein consists of a signal peptide, a propeptide, a substilisin-lik
C; Comment: This protein cleaves precursor proteins at dibasic amino acid residues.
                                                                                                                                                                                                                                                                                                                                   subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Gross references: GDB:131390; OMIM:167405
A.Map position: 15q26-15q26
C.Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C.S.Reywords: alternative splicing; hydrolase; serine proteinase
F:196-434/Domain: subtilisin homology <SBT>
F:205.246,420/Active site: Asp, His, Ser #status predicted
            DB 2; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.3%; Score 59.5; DB 1; Length 652; 60.0%; Pred. No. 34; tive 0; Mismatches 9; Indels
                                                                          Indels
                                                                0; Mismatches
         Score 59.5;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: October 9, 2002, 09:05:06 Job time: 9.09368 secs
                                                                                                                       11 AARAGGGGGGGGIEGPTLRQCLAAR 35
                                                                                                                                                                              24 AAGAGGAGGAGGPGFRP-LAPR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AARAGGGGGGGGIEGPTLRQCLAAR 35
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31.3%;
                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.09
Matches 15; Conservative
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Gaps

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Compugen Ltd.
GenCore version 5.1.3
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OM protein - protein search, using sw model

October 9, 2002, 08:51:41; Search time 4.29977 Seconds Run on:

(without alignments) 324.181 Million cell updates/sec

US-09-422-838C-27 190

1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched: 105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					SUMMARIES	
Result		& Ouerv				
NO.	Score	Match	Match Length	DB	QI	Description
-	73	38.4		Н	LAC1_NEUCR	P06811 neurospora
7	73	œ		Н	LAC2_NEUCR	P10574 neurospora
m	65	ಶ		Н	INS_BOVIN	_
4	65	4		<del></del>	YR21_TRSVR	
Ŋ	65	4		~	HB9_HUMAN	
9	65	34.2		1	SYV2_MOUSE	_
7	64.5	33.9	٦	П	VNUA_PRVKA	
æ	64	33.7		-	INS_SHEEP	-
σ	64	33.7	584		CNA1_DROME	
10	63	33.2	394	Н	FXD3_CHICK	
11	63	33.2	1168	Н	MYSC_ACACA	P10569 acanthamoeb
12	62	32.6	440	Н	DCO_DROME	
13	61.5	C	4499	<b>,</b>	DYHA_CHLRE	
14	61	32.1	1178	Н	PHYB_SORBI	
15	09		323	Н	JUND_CHICK	
16	9		348	٦	SXL_CERCA	
17	9		1322	Н	SUS_DROME	P22293 drosophila
18	59.5		391	П	SOX1_MOUSE	
19	59.5		696	Н	PAC4_HUMAN	
20	59		367	_	BET3_MESAU	
21	59		497	_	FXD2_HUMAN	O60548 homo sapien
22	59		517	-	Y967_TREPA	trepc
23	59		593	П	K1CJ_HUMAN	P13645 homo sapien
24	59		753	Н	ZIN_HUMAN	
25	59			-	ECR_LUCCU	luci
26	58.5	30			SSB_MYCLE	mycob
27		30			HH3R_HUMAN	Q9y5nl homo sapien
28	58	30			EVX2_HUMAN	homo
29	58	30			ONC2_HUMAN	homo
30	58	30			BRN1_MOUSE	mus n
31	58	(-,	497	Н	BRN1_RAT	Q63262 rattus norv
32	58	30			BRN1_HUMAN	homc
33	28	30		1	K1CJ_MOUSE	P02535 mus musculu

P54865 cellulomona	O54839 mus musculu	O55165 rattus norv	P25764 oryza sativ	Q15911 homo sapien	P49842 homo sapien	Q64537 rattus norv	088456 mus musculu	P17656 caenorhabdi	P23091 avian muscu	P91705 drosophila	
XYND_CELFI	EOMD_MOUSE	KF3C_RAT	PHYB_ORYSA	ABF1_HUMAN	ST19_HUMAN	CANS_RAT	CANS_MOUSE	CC02_CAEEL	TMAF AVIS4	PER_DROSC	FXGA_CHICK
~	_	Ч	٦	Н	,	-	Н	Н	Н	Н	П
644	688	196	1171	3703	368	266	269	301	369	375	440
30.5	30.5	30.5	30.5	30.5	30.3	30.0	30.0	30.0	30.0	30.0	30.0
58	58	28	8	58	57.5	57	57	57	57	57	57
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## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88087214; PubMed-2961749;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
"Characterization of two allelic forms of Neurospora crassa laccase.
Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:885-896(1988).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 379-619 FROM N.A.
MEDLINE=87067412; PubMed=2947240;
Germann U.A., Lerch K.;
Isolation and partrial nucleotide sequence of the laccase gene from Neurospora crassa: amino acid sequence homology of the protein to human ceruloplasmin.";
                                                                  01-JUL-1989 (Rel. 11, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: BINDS 4 CU-10NS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELULAR LOCATION: Secreted (Potential).
SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                   Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M14554; AAA33590.1; -.
EMBL; M18333; AAA33591.1; -.
PIR; A28623; KSNCLO.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR00255; Multicu_oxidse2.
InterPro; IPR002955; Multicu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
                 619 AA
                                                      01-JAN-1988 (Rel. 06, Created)
                   STANDARD;
                                                                                                                                                                                                                       NCBI_TaxID-5141;
                 LAC1_NEUCR
LAC1_NEUCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:885-896(1988)
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                       COPPER (TYPE I) (PROBABLE).

N-LINKED (GLCNAC...) (POTENTIAL).

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01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Germann U.A., Mueller G., Hunziker P.E., Lerch K.; "Characterization of two allelic forms of Neurospora crassa laccase
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: 4 benzenediol + 0(2) = 4 benzosemiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
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Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Serreted (Potential).
-!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 619;
                                                                                                                                                    R (TYPE 3) (PROBABLE).
R (TYPE 3) (PROBABLE).
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PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
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0; Mismatches
                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 73;
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                                                                               LACCASE.
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MEDLINE=88087214; PubMed=2961749;
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Best Local Similarity 60.0
Matches 15; Conservative
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                               Glycoprotein; Repeat.
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619 AA;
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ID LAC2_NEUCR
AC P10574;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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  There are no restrictions on
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                                                                                                                                                                              Pfens, PF00394; Cu-oxidase, 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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MEDLINE-88288209; Pubmed=2456452;
D'Agostino J., Younes M.A., White J.W., Besch P.K., Field J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.4%; Score 73; DB 1; Length 619; 60.0%; Pred. No. 0.64;
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PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                        or send an email to license@isb-sib.ch).
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                            PIR; B28523; KSNCLT.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; Multicu_oxidse2.
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                                                                                                            EMBL; M18334; AAA33592.1; -.
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NCBI_TaxID=9913;
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619 AA;
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nes 15; Conserv
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P01317;
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                                                                                                                                          Sanger F., Tuppy H.;
"The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.";
Biochem. J. 49:481-490(1951).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brange J., Dodson G.G., Edwards D.J., Holden P.H., Whittingham J.L., "A model of insulin fibrils derived from the X-ray crystal structure of a monomeric insulin (despentapeptide insulin)."; Proteins 27:507-516(1997).
                                                                                                                                                                                                                                                                                                          "Isolation and characterization of proinsulin C-peptide from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND
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                                                                                                                                                                                                                                                                                                                                                                                                                    Salokangas A., Smyth D.G., Markussen J., Sundby F.; "Bovine proinsulin: amino acid sequence of the C-peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY.
Saith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
Reynolds C.D.;
"The structure of des-Phe bl bovine insulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AN FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWW="http://www.expasy.org/spotlight/articles/spt1t009.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger F., Thompson E.O.P.;
"The amino-acid sequence in the glycyl chain of insulin. 2. The
investigation of peptides from enzymic hydrolysates.";
Biochem. J. 53:366-374(1953).
                                                                                                                                                                                                                                                      MEDLINE=71116409; PubMed=5545080;
Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D.,
Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDES, SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS. Ryle A.P., Sanger F., Smith L.F., Kitai R.; "The disulphide bonds of insulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DATABASE: NAME-Protein Spotlight;
[2]
SEQUENCE OF 25-105.
MEDLINE=71166442; PubMed=4928892;
Molan C., Margoliash E., Peterson J.D., Steiner D.F.;
"The structure of bovine proinsulin.";
J. Biol. Chem. 246:2780-2795(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acta Crystallogr. B 38:3028-3032(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS).

    Biol. Chem. 246:1365-1374(1971).

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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 57-82.
MEDLINE=71257721; PubMed=5105368;
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                                                                                                                                                                                                                                     SEQUENCE OF 57-82.
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PIR; A01585; IPBO

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                                                                                                                                                                                                                                                                                                                                                                                      SMARY; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal; 3D-structure.
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 20.2 kDa protein in RNAZ.
Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
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"Nucleotide sequence of tomato ringspot virus RNA-2.";
J. Gen. Virol. 72:1505-1514(1991).
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                                                                                                 PDB; 1BPH; 31-OCT-93.
PDB; 1CPH; 31-OCT-93.
PDB; 1DPH; 31-OCT-93.
PDB; 1PID; 07-DEC-96.
InterPro; 1PR000739; Insulin_IGF_relaxin.
Pf00049; Insulin; 1.
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POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11393 MW;
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                                                                                                                                                                                                                                                                                                                   PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
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                             2INS; 31-MAY-84.
1APH; 31-OCT-93.
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105 AA;
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hes 16; Conserv
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A40909;
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P25245;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3;
1; Mismatches 10; Indels
                                                                  34.2%; Score 65; DB 1; Length 201; 61.5%; Pred. No. 1.7;
                                                                                                                     5; Indels
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0006AEAD71D594FE CRC64;
                    201 AA; 20194 MW; 9038506E18D7B450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Homeobox protein HB9.
                                                                                                                                                                                                                                                                                                                                               PRT; 401 AA
                                                                                                                     1; Mismatches
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POLY-ALA.
HOMEOBOX.
POLY-GLY
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MEDLINE-94327547; PubMed-7914194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U07664; AAB60647.1; -. EMBL; U07663; AAB60647.1; JOINED. HSSP; P14653; 1B72.
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242 301 HOM
316 325 POL
401 AA; 40932 MW; 0
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Best Local Similarity 54.2%;
Matches 13; Conservative
                                                                                              Best Local Similarity 61.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
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135
177
301
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                               HB9_HUMAN
P50219;
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                                                                     Query Match
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HB9_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence and organization of the mouse valy1-tRNA synthetase gene G7a/Bat6 located in the MHC class III region.";
Immunogenetics 49:468-470(1999).
-:- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valy1-tRNA(Val).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00986; TRNASYNTHVAL.
PROSITE; PS00178; AA_TRNA_LICASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- ENZYME REGULATION: CAN BE REGULATED BY PROTEIN KINASE C-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FACTOR 1 (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-!- SIMILARITY: THE N-TERMINAL DOMAIN IS SIMILAR TO ELONGATION
                        SYV2_MOUSE STANDARD; PRT; 1263 AA.
092109; 09QUN2;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Valyl-tRNA synthetase 2 (EC 6.1.1.9) (Valine--tRNA ligase 2) (VALRS
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen L., Madan A., Qin S., Shaffer T., Ratcliffe A., Abbasi N., Dickhoff R., James R., Loretz C., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
A -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BALBAC, AND C57BL/RIJ; TISSUE-Brain; MEDLINE-99216447; PubMed=10199925; Snoek M., van Vügt H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001412; tRNA-synt_I.
Interpro; IPR002303; tRNA-synt_val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002300; tRNA-synt_la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF109905; AAC84151.1; EMBL, AF109906; AAC84172.1; EMBL, AF087680; AAD26532.1; EMBL, AF087141; AAD26531.1; HSSP, P96142; IGAX. MGD; MGI:90675; Vars2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
Pfam; PF00133; tRNA-synt_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004046; GST_C.
InterPro; IPR004045; GST_N.
                                                                                                                                                                                                                                                                     VARS2 OR G7A OR BAT6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FACTOR 1-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
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SYV2_MOUSE
                                                                 PDDT TARKEN TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE PLANT TO THE
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Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                               procedure.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNA1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
    PT PT
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                      Gaps
                                                                                                                                                                                                                                                                      MEDLINE=91021039; PubMed=2171211;
Vlock C., Kozmik Z., Paces V., Schirm S., Schwyzer M.;
"Pseudorabies virus immediate-early gene overlaps with an oppositely
oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1733;
                             DB 1; Length 1263; 7.9;
1219 1219 E -> K (IN REF. 2).
1263 AA; 140214 MW; B510E73284FCE26D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OC8CD8BE475BB5E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                          Pseudorabies virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPTLRQCL-AARAGGGGGG-----GGIEGPTLRQCLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                               PRT; 1733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 AA
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64.5;
                               Score 65;
                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-THR.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-ARG.
POLY-GLY.
                                                                      4 PTLRQCLAARAGGGGGGGGGIEGPTLRQCL 32
                                                                                           14 PSLRALIAARYGEAGDGPGWGGPHPRICL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                  2;
                              34.2%;
51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1733 AA; 172166
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M34651; AAA47471.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%;
                                                                                                                                                                                                                                                                                                                enhancer regions.";
Virology 179:365-377(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.98;
                                                                                                                                                                                               Probable nuclear antigen.
                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308
889
1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin precursor.
                                                                                                                                                                                                                                         NCBI_TaxID=33703;
                                                                                                                                                                                                                                                                                                                                                                                                                                        B45344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouer, Best Local Similar
                                                                                                                                              VNUA_PRVKA P33485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INS_SHEEP
P01318;
CONFLICT
                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                           Ohlsen S.M., Lugenbeel K.A., Wong E.A.; "Characterization of the linked ovine insulin and insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.; "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F. Biol. Chem. 247:4866-4871(1972).

-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AN PATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1. SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 1; Length 105; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 INSULIN B CHAIN.
82 C PEPTIDE.
105 INSULIN A CHAIN.
91 INTERCHAIN.
104 INTERCHAIN.
915
1, 11235 MW; 8B277C7FB9922BC7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQCLAARAGGGGGGGGGIEGP----TLRQCLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 VEGP---QVGALELAGGPGAGGLEGPPOKRGIVEOCCA 92
                                                                                                                                                                                                           SEQUENCE OF 25-54 AND 85-105.
Brown H., Sanger F., Kitai R.;
"The structure of pig and sheep insulins.";
Blochem. J. 60:565-565(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S16430; INSH.
HSSP; P01315; 91NS.
InterPro; IPR000739; Insulin_IGF_relaxin.
PRINTS; PR0049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
SEQUENCE FROM N.A.
MEDLINE=94280618; PubMed=8011164;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=72258016; PubMed=4626369;
                                                                                                                       factor-II genes.";
DNA Cell Biol. 13:377-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U00659; AAB60625.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMA:RT; SM00078; IlGF; 1
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 57-82
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; FRUCT.
SMART; SMO0471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
Hydrolase; cAMP; Alternative splicing.
Hydrolase; cAMP; Alternative splicing.
TO MAMMALIAN REGULATORY SUBUNIT OF TYPE 2
CAMP DEPENDENT PROTEIN KINASE).
15-JUL-1998 (Rel. 36, Last annotation update)
cAMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Learning/
                                                                                                                                                                                                                                                                                                                                                                                                            -i- ALTENNATIVE PRODUCTS: DIFFERENT FORMS ARE GENERATED BY THE USE OF DIFFERENT TRANSCRIPTION START SITES AND SPLICE PATTERNS.
-i- DISEASE: MUTATION OF DUNCE PRODUCES FEMALE FLIES THAT ARE STERILE.
-i- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Edopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                        Chen C.-N., Denome S., Davis R.L.;
"Molecular analysis of CDNA clones and the corresponding genomic coding sequences of the Drosophila dunce+ gene, the structural gene for cAMP phosphodiesterse.",
Proc. Natl. Acad. Sci. U.S.A. 83:9313-9317(1986).
-!- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)0 = ADENOSINE 5'-PHOSPHATE.
                                                                                                                                                      MEDLINE-92085274; PubMed-1660926;
Qiu Y.H., Chen C.-N., Malone T., Richter L., Beckendorf S.K.,
Davis R.L.;
                                                                                                                                                                                                          "Characterization of the memory gene dunce of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLY-RICH.
99239BE33C620501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
-!- SUBUNIT: MONOMER.
                                                      Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWBL, X55168, CAA38960.13 JOINED.
EWBL, X551709, CAA38960.13 JOINED.
EWBL, X55171; CAA38960.13 JOINED.
EWBL, X55171; CAA38960.13 JOINED.
EWBL, X55171; CAA38960.13 JOINED.
EWBL, X55173; CAA38960.13 JOINED.
EWBL, X55174; CAA38960.13 JOINED.
EWBL, X55177; CAA38960.13 JOINED.
EWBL, X55177; CAA38960.13 JOINED.
EWBL, M14922; AAC34201.13 JOINED.
                                                                                                                                     SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                               SEQUENCE OF 223-584 FROM N.A. MEDLINE-87092243; Pubmed-3025834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M14979; AAC34201.1; JOINED.
EMBL; M14980; AAC34201.1; JOINED.
EMBL; M14981; AAC34201.1; JOINED.
                                                                                                                                                                                                                       melanogaster.";
J. Mol. Biol. 222:553-565(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00471; HDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003607; HDc.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X55167; CAA38960.1; -.
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                     unemory process protein).
DUNCE OR DNC.
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559 5
584 AA;
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAXY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D3 (HNF3/FH transcription factor genesis) (Winged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.; "Aberrant caell growth induced by avian winged heltx proteins."; Cancer Res. 57:123-129(1997).
-i. FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
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  Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.2%; Score 63; DB 1; Length 394; 58.3%; Pred. No. 4.7;
                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PROCOSS: FORKHEAD.
SMART: SM00339; FH; 1.
PROSITE: PS00657; FORK HEAD.1; 1.
PROSITE: PS00658; FORK HEAD.2; 1.
PROSITE: PS50039; FORK HEAD.3; 1.
DNA-binding: Nuclear protein; Transcription regulation.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324A4B36B9E31899 CRC64;
33.7%; Score 64; DB 1;
61.9%; Pred. No. 5.2;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i - SUBCELLULAR LOCATION: Nuclear.
-i - SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLY.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORK-HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97141794; PubMed-8988052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 RAGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T02495; -. InterPro; IPR001766; Fork_head.
                                                                                                                                  394 AA; 40995 MW;
                                                                                                     11 AARAGGGGGGGGIEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U37274; AAC60066.1; -. HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                            Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                    helix protein CWH-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYSC_ACACA
ID MYSC_ACACA
                                                                                                                                                                                                                                                                            FXD3_CHICK
P79772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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**REDLINE=90037074; Pubmed=2530230;

**REDLINE=90037074; Pubmed=2530230;

**REDLINE=90037074; Pubmed=2530230;

**REDLINE=90037074; Pubmed=2530230;

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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-88015463; Pubmed-3477803;
Jung G., Korn E.D., Hammer J.A. III;
"The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; Pr00Lus; Das, ...
PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000355; myosin_head; 1.
SMART; SM00324; MYSc; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Myosin; ATP-binding; Phosphorylation; Multigene family; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A. MEDILINE-66259656; PubMed-3104500; Hammer J.A. III, Jung G., Korn E.D.; "Genetic evidence that Acanthamoeba myosin I is a true myosin."; Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAIL HOMOLOGY REGION 1 (TH.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLY/PRO/ALA-RICH (TH.2).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLY/PRO/ALA-RICH (TH.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 84:6720-6724(1987).
                                01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                               Acanthamoeba castellanii (Amoeba).
Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P08799; ILVK.
InterPro; IPR001452; SH3.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and non-myosin-like sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J02974; AAA27707.1; -.
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1168
108
                                                                                                                                                      Myosin IC heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A33891; MWAXIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGENESIS, AND FUNCTION.
MEDLINE-98337187; PubMed-9674430;
Price J.L., Blau J., Rothenfluh A., Abodeely M., Kloss B., Young M.W.;
"Double-time is a novel Drosophila clock gene that regulates PERIOD protein accumulation.";
Cell 94:83-95(1998).
                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CASEIN KINASE I SUBFAMILY. COULD BE THE ORTHOLOG OF CKI-EPSILON.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98337188; PubMed=9674431;
MIDSS B., Price J.L., Saez L., Blau J., Rothenfluh A., Wesley C.S.,
Young M.W.;
                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
Last sequence update)
16-DCT-2001 (Rel. 40, Last annotation update)
Discs overgrown protein Kinase (EC 2.7.1.-) (Double-time protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biological rhythms; Transferase; Serine/threonine-protein kinase; ATP-binding. 9 277 PROFETM FINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Drosophila clock gene double-time encodes a protein closely related to human casein kinase I epsilon."; cell 94:97-107(1998).
                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                             Score 63; DB 1; Length 1168;
Pred. No. 12;
2; Mismatches 6; Indels
311 311 PHOSPHORYLATION.
1168 AA; 127309 MW; D07084B373A37A32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; Fggn0002413; dco.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002280; Ser_thr_pkinase.
Pfam; PF00069; pkinase.
PROSITE; PS00107; PROPEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                            920 OILGAKGGGGGGGGRGRGGPS 939
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                                             33.2%;
                                                                                                              8 QCLAARAGGGGGGGGIEGPT 27
                                           Query Match 33.27
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P40233; 1CSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CENTRAL BRAIN
                                                                                                                                                                                                                          DCO_DROME
076324;
                                                                                                                                                                                                                                                                                                                           DCO OR DBT
MOD_RES
SEQUENCE
                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                             DCO_DROME
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                         M->I: IN DBTL; LENGTHENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain genes.;
J. 621 Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
DYNEIN HAS ATPASE ACTIVITY.
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                          P->S: IN DBTS; SHORTENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas reinhardtil flagellar alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                 32.6%; Score 62; DB 1; Length 440; 55.0%; Pred. No. 6.6;
                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                      B875891D5747391D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dynein alpha chain, flagellar outer arm (DHC alpha).
ODA11 OR ODA-11.
                ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                           PRT; 4499 AA.
                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Motil. Cytoskeleton 37:120-126(1997).
                                                                                          POLY-GLY.
POLY-GLY.
                                                             POLY-GLN
                                                                             POLY-GLY
                                                                                                                                          PERIOD.
                                                                                                                                                                       PERIOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND REVISIONS. STRAIN-21GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94274778; PubMed-8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97329535; Pubmed-9186009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1142-4499 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001298; Filamin.
InterPro; IPR002909; IPT_TIG.
InterPro; IPR001798; Kelch.
                                                                                                                                                                                        440 AA; 48073 MW;
                                                                                                                                                                                                                                                                                                               403 PERRPSIRMRQGGGGGGG 422
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InterPro; IPR003593; AAA.
                                                                                                                                                                                                                                                                                  4 PTLRQCLAARAGGGGGGGI 23
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
   23
38
128
332
332
351
426
437
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InterPro; IPR001736;
                                                                                                                                                                                                                                   Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dynein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-21GR;
                                                                                                                                                                                                                                                                                                                                                                                         DYHA_CHLRE
NP_BIND
BINDING
ACT_SITE
DOMAIN
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                     Query Match
                                                                                                                          MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                         039610;
                                                                                                                                                         MUTAGEN
                                                              DOMAIN
                                                                               DOMAIN
                                                                                            DOMAIN
                                                                                                             DOMAIN
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Sorghum bicolor (Sorghum) (Sorghum vulgare).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.; The phytochrome gene family in tomato and the rapid differential evolution of this family in anglosperms."; Moi. Biol. Evol. 17:362-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                   .
.
                                                                                                                                                                                                                              DB 1; Length 4499;
                                                                                   COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
                                                    Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                               (POTENTIAL).
319AC7FD30F1591A CRC64;
                                                                                                                           COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                     COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                               ATP (POTENTIAL)
                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                       4194 GETLFKTVVEVAGGGGGGGGGGGGGGNAVRQAL 4226
                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                         Pred. No. 54;
                                                                                                                                                                                                                                                                         3 GPTLRQCLAARAGGGGGGGGGIEG---PTLRQCL 32
                                                                                                                                                                                                                                32.4%; Score 61.5;
                                                                          FILAMIN
                                          PROSITE; PS50194; FILAMIN_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. 58M;
MEDLINE=20188796; PubMed=10723737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. 58M;
MEDLINE=97198556; PubMed=9046599;
                                                                                                                                                                         ATP
                                                                                                                                                                                                ATP
                                                                                                                                                                                                          503606 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE OF 208-1178 FROM N.A.
                                                                                                                                                                                                                                          48.5%;
Pfam; PF00630; Filamin; 1.
                                                                                                                                                                                                                                                      16; Conservative
          Pfam; PF01344; Kelch; 3.
SMART; SM00382; AAA; 3.
SMART; SM00429; IPT; 1.
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                    2688
3023
3262
3262
3515
1723
2026
2376
2754
                                                                                                                                                                                                        4499 AA;
                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4558;
                                                                                                                   2655
3003
3170
3486
1716
2019
2369
2717
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                                                                                                                                                                                                                                                                                                                                                                                                          Phytochrome B.
                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
01-MAR-2002
                                                                Coiled coil
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                                                                                                                                                                                                                                                                                                                                                     PHYB_SORBI
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                      NP_BIND
NP_BIND
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DOMAIN
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                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                               RESULT 14
PHYB_SORBI
                                                                                                                                                                                                                                                      Matches
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Oncogene 6:1623-1631(1991).
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242
270
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061374;
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DOMAIN
SEQUENCE
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      SETTING DRANGE SOLUTION OF STREET OF STREET STREET STREET STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET STREET SOLUTION OF STREET STREET SOLUTION OF STREET STREET STREET SOLUTION OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                           PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE. SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY. SIMILARITY: CONTAINS 2 PAS (PER-ARMT-SIM) DIMERIZATION DOMAINS. SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50112; PAS; 2. PHYTOCHROME 1: 1. PROSITE; PS00245; PHYTOCHROME 1: 1. PROSITE; PS50046; PHYTOCHROME 2: 1. Transcription regulation Photoreceptor; Phytochrome; Chromophore; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 1; Length 1178;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 CHROMOPHORE (BY SIMILARITY).
129136 MW; C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AGG-1992 (Rel. 23, Created)
01-AGG-1992 (Rel. 23, Last sequence update)
01-AGZ-2000 (Rel. 39, Last annotation update)
Transcription factor jur-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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MEDILINE-92010832, Pubmed-1923529;
Hartl M., Hutchins J.T., Vogt P.K.;
"The chicken junD gene and its product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-HIS.
POLY-GLY.
      SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; AFB001018; GAR.
InterPro; IPR004594; HATPase_c.
InterPro; IPR004594; HATPase_c.
InterPro; IPR004599; HIS_KIN_sig.
InterPro; IPR004561; His_KinA.
InterPro; IPR001014; PAS.
InterPro; IPR001014; PAS.
InterPro; IPR001014; PAS.
InterPro; IPR001024; Phytochrome.
Pfam; PF01500; GAR; 1.
Pfam; PF00518; HATPase_c; 1.
Pfam; PF00518; HATPase_c; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01031; PHYTOCHROME.
SMART; SM00065; GAR; 1.
SMART; SM00068; HISTA; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS501109; HIS_KIN; 1.
PROSITE; PS501109; HIS_KIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF182394; AAB41398.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ARAGGGGGGGGGIEGPT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ceratitis capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropoda: Tracheata: Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccone G., Peluso I., Artiaco D., Giordano E., Bopp D., Polito L.C., "The Ceratitis capitata homologue of the Drosophila sex-determining gene Sex-lethal is structurally conserved, but not sex-specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS A1, A2, A3, A4, AND EMBRYO-SPECIFIC ISOFORMS E1, E2 AND E3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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-!- FUNCTION: UNKNOWN; APPARENTLY NOT INVOLVED IN SOMATIC SEX DETERMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB 1; Length 323;
Pred. No. 8.2;
                                                             -i - SIMILARITY: BELONGS TO THE B2IP FAMILY. JUN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUCINE-ZIPPER.
A7F6D21A97DBB676 CRC64;
-!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY - ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sex-lethal protein homolog (CCSXL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P05412; 1FOS.
TRANSFAC; 702196; .
InterPro; IPR00112; Leuzip_Jun.
InterPro; IPR001871; bZIP.
Pfam; PP00170; bZIP; 1.
PRINTS; PR00043; LEUZIPPRJUN.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98171464; PubMed=9502730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 AA; 33205 MW;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X60063; CAA42665.1; -. PIR; S20099; S20099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AAAAGGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota: Neotera: Endopterygota; Diptera: Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91117256; PubMed-1703632; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T.; "The Drosophila suppressor of sable gene encodes a polypeptide with regions similar to those of RNA-binding proteins."; Mol. Cell. Biol. 11:894-905(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voelker R.A., Graves J.P., Gibson W., Eisenberg M.T.;
"Mobile element insertions causing mutations in the Drosophila suppressor of sable locus occur in DNase I hypersensitive subregions of 5'-transcribed nontranslated sequences.";
Genetics 126:1071-1082(1990).
--- FUNCTION: AFFECTS THE TRANSCRIPT LEVELS OF THOSE ALLELES THAT IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- DEVELOPMENTAL STAGE: AT ALL STAGES.
-i- SIMILARITY: HAS REGIONS SIMILAR TO THOSE OF RNA-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                            PRINTS; ..., SW0360; RRW; 2. SWART; SW00360; RRW; 2. PROSITE; PS00030; RRW_RNP_1; 1. PROSITE; PS00030; RRW_RNP_1; 1. GIVZASN FICH DOMAIN.

TO GIVZASN FICH DOMAIN.

110 188 RNA-BINDING (RRM) 1. RNA-BINDING (RRM) 2. COMPANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 1; Length 348; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO.
MISSING (IN ISOFORM A1).
CABA3DA5C2C8874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUPPRESSES. MAY BE INVOLVED IN RNA METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AGG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 188 RN
196 276 RN
68 276 PO
95 99 PO
293 311 PO
312 316 PO
37 44 MA; 1
                                                                                                                                                                                                                 EMBL; AF026145; AAC38968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suppressor of sable protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%;
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00961; HUDSXLRNA.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                             InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-9 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                         Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGGGGGGGMGGP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GGGGGGGGIEGP 26
                                                                                                                                                                                                                                                   P19339; 1SXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A comparison of the properties of Sox-3 with Sry and two related genes, Sox-1 and Sox-2.";
Development 122:509-520(1996).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M., Norris D., Rastan S., Stevanovic M., Goodfellow P.N.,
                                                                                                                                                                                                                                                                                                                              Score 60; DB 1; Length 1322;
                                                                                                                                                                                                                                                       446 474 GLN-RICH (OPA-REPEAT).
1087 1162 RNA-BINDING (BY SIMILARITY).
1322 AA; 143555 MW; D5F534EB5702EA08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                      HIGHLY CHARGED DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 AA.
                                                                                                                                                                                                                                                                                                                                                  Pred. No. 27;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96189340; PubMed=8625802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:98357; SOX1.
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
                                                                                                                                            PIR; A39612, A39612.
FlyBase; FBgn0003575; su(s).
InterPro; IPR000571; Zf-CCCH.
Pfam; PF00642; Zf-CCCH, 2.
RNA-binding; Nuclear protein.
DOMAIN 138 327 HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00398; HMG; 1.
DNA-binding; Nuclear protein.
                                                                                                      EMBL; M57889; AAA28920.1; -. EMBL; X59364; CAA42010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X94126; CAA63846.1; -. HSSP; Q05066; 1HRY.
                                                                                                                                                                                                                                                                                                                                 31.6%;
                                                                                                                                                                                                                                                                                                                                                  68.88;
                                                                                                                                                                                                                                                                                                                                                                                                                             1159 GGGGGGCVLPNLSQ 1174
                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      15 GGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lovell-Badge R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOX-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOX1 OR SOX-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOX1_MOUSE
P53783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129;
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DOMAIN
                                                                                                                                                                                                                                                                                             SEQUENCE
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DOMAIN
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"A novel human PACE4 isoform, PACE4E is an active processing protease containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a second human subtilisin-like protease gene in
the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paired basic amino acid cleaving enzyme 4 précursor (EC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of novel cDNAs encoding human kexin-like protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAC4_HUMAN STANDARD; PRT; 969 AA. P29122; Q15099; Q15100; Q9UEJ1; Q9UEJ7; Q9UEJ7; Q9UEJ9; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEG7; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UEJ9; Q9UE
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                                                                                                                                                                                                                                                    DB 1; Length 391;
                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  9F81ED667F947C05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 204:1381-1382(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 200:943-950(1994)
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                                                                                                                                                                                                                                               Score 59.5; DB Pred. No. 11; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                     POLY-ALA
                                               POLY - ALA
                                                                                                                       POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97335942; PubMed=9192737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; Pubmed=1741956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94235049; PubMed=8179631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95071480; PubMed=7980617;
204 PC
288 PC
306 PC
364 PC
39237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 LSGPA----GARGGGGGGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLROCLAARAGGGGGGG 22
                                                                                                                                                                                                                                               31.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      convertase 4) (SPC4).
197
280
296
357
391 AA;
                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barr P.J.;
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SEQUENCE
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TSUJI A., Matsuda Y.;

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TSUJI A., Matsuda Y., MITH UNIQUE RESTRICTED

DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES

TO CONSTITUTIVE SECRETORY PATHER XY(K/K) R CONSENSUS MOTIF.

TO CAPABLE OF CLEAVAGE OF ARG-XAA-ARA-ARG-I-ZAA BONDS,

WHERE XAA CAH NE ANY MANNO ACID AND YAA IS ARG OR LYS.

TO CAPALLY AMANNO ACID AND YAA IS ARG OR LYS.

TO CORACTOR: PACRAA-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE

RETICULUM WINDOPLASMIC AS BOTH A MONOMER AND A DIRER-SIZED COMPLEX

WHERE AND ALTURE PACEAA-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT

TRETICULUM WINDOPLASMIC AS BOTH A MONOMER, SUGGESTING THAT

TRETICULUM RODELASMIC PRECURS ITS TERTIARY OR QUATERNARY STRUCTURE.

C. - SUBCHILLY. PACEAA-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT

C. - SUBCHILLY. PACEAA-I EXISTS ONLY AS A MONOMER,

TRETICULUM RODELASMIC PACEAA-I EXISTS ONLY AS A MONOMER,

C. - SUBCHILLY. PACEABLED AND REMAIN PROBABLY IN ZYMOGEN FORM

IN ENDOPLASMIC RETICULUM. PACEAE-II AND PACEAE-II ARE RETAINED

C. INTRACELLULAR LEVER PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-

TENANTARIC PACABA MICHT RE SECRETED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC KIDBY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE EXPRESSED IN PLACENRA. PACE4E-I IS EXPRESSED IN CRREBELUM, PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
                                                                   Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), W. Extn-1ke processing endoprotease."; J. Biochem. 122:438-452(1997).
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-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERMINUS. PACE4B MIGHT BE SECRETED.

ALTERNATIVE PRODUCTS: 8 ISOFORMS; PACE4A-I/PACE4 (SHOWN HERE),
PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Biochem. J. 339:639-647(1999).
                      SEQUENCE FROM N.A. (ISOFORMS PACE4A-1; A-II; CS; D; E-I; E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,
                                                                                                                                                                                                                                                                                  Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G., "Punctional analysis of human PACE4-A and PACE4-C isoforms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                             identification of a new PACE4-CS isoform.";
FEBS Lett. 396:31-36(1996).
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                                                                                                                                                                                                                                 ALTERNATIVE SPLICING (ISOFORM PACE4CS).
MEDLINE-97064242; PubMed-8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99233559; PubMed=10215603;
                                                MEDLINE=98021085; PubMed=9378725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moehring T.J.;
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DB 1; Length 969;

Score 59.5;

31.3%;

Query Match

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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                      Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                                                         Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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0
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                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
Nuclear protein; Transcription regulation; Repressor.
DOMAIN 11 14 POLY-ALA.
                6
                                                                                                                                          30 MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                      367 AA.
              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLY.
POLY-GLY.
POLY-GLY.
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                                      11 AARAGGGGGGGGIEGPTLRQCLAAR 35
                                                            24 AAGAGGAGGAGGAGFRP-LAPR 47
                                                                                                                                                                                                                                                                           MEDLINE=96140430; PubMed=8552091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35905 MW;
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InterPro; IPR001092; HLH_dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S80870; AAB50691.1;
              15; Conservative
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99
179
217
240
282
319
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SMART; SM00353; HLH; 1
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=10036;
                                                                                                                                                                               BETA3 protein.
                                                                                                                                                                                                                               Mesocricetus.
                                                                                                                     BET3_MESAU
009029;
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DOMAIN
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BET3_MESAU
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                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORKhead box protein D2 (Forkhead-related protein FKHL17) (Forkhead-related transcription factor 9) (FREAC-9).
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                                                                                                                                                                                                                         MEDLINE-98066765; PubMed=9403061;
MEDLINE-98066765; PubMed=9403061;
MEDLINE-98066765; PubMed=9403061;
Cederberg A., Carlsson P., Encrbaeck S.,
"Cloning and characterization of freac-9 (FKHLI7), a novel kidney-expressed human forkhead gene that maps to chromosome 1p32-p34.";
                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                        -- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
-- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                Enerbaeck S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Nuclear protein; Transcription regulation.
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Pred. No. 15;
                               497 AA.
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FORK-HEAD.
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                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
                                                          30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last anno
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                                                                                                                                     FOXD2 OR FKHL17 OR FREAC9
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                                 STANDARD;
                                                                                                                                                                                                                                                                                                                      Genomics 46:78-85(1997).
                                                                                                                                                        Homo sapiens (Human).
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                               FXD2_HUMAN
O60548;
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DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Y967_TREPA
               FXD2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NICHOLS;
MEDILINE-99332770; PubMed-9665876;
MEDILINE-99332770; PubMed-9665876;
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
Hatch B., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SEQUENCE FROM N.A.
MEDLINE-89125611; PubMed-2464696;
Rieger M., Franke W.W.;
"Identification of an orthologous mammalian cytokeratin gene. High degree of intron sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution of human degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution degree of intro sequence conservation during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution during evolution evolution during evolution evolution during evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolution evolu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.; "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.1%; Score 59; DB 1; Length 517; 60.0%; Pred. No. 16; 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.

DOMAIN 152 161 POLY-GLY.

SEQUENCE 517 AA; 56597 MW; E224976333989DF6 CRC64;
                                                                                                                                                                                                                                                                                    Treponema pallidum.
Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 281:375-388(1998).
                                                                                                                             Last sequence update)
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                                                                       16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequ
16-00T-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001264; AAC65925.1; -. TIGR; IP0967; -.
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                                                                                                                                                                                                                 Hypothetical protein TP0967.
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Best Local Similarity 60.0°
Matches 12; Conservative
    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-160;
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P13645;
Y967_TREPA
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                                            083933;
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Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.; "Extensive size polymorphism of the human keratin 10 chain resides in the C-terminal V2 subdomain due to variable numbers and sizes of glycine loops.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92376531; PubMed=1380725; Rothnagel J.A., Dominey A., Dominey A., Dempsey L.D., Longley M.A., Greenhaldh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.; Mutations in the rod domains of keratins 1 and 10 in epidermolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94216497; PubMed-7512983; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; Genetic mutations in the K1 and K10 genes of patients with epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARTANTS EHK PRO-156 AND SER-156.
MEDLINE-94117870; PubMed=7507123;
MCLean W.H.I., Eady R.A.J., Dopping Hepenstal P.J.C., McMillan J.R.,
Lelgh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
Darmon M.Y., Semat A., Darmon M.C., Vasseur M.; "Sequence of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                              "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compton J.G., Bale S.J.; "Preferential sites in keratin 10 that are mutated in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJNE-94117868; PubMed-7507150;
Rothnagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.;
"Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng J., Syder A.J., Yu Q.-C., Letai A., Paller A.S., Fuchs E.; "The genetic basis of epidermolytic hyperkeratosis: a disorder of differentiation-specific epidermal keratin genes."; cell 70:811-819(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126
                                                                                                                                                                                                           'Exons I and VII of the gene (Ker10) encoding human keratin 10
                                                                                                                                                                                                                                                                                                                                                       Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
                                                                                                                                                                  Tkachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
                                                                                                                                                                                                                                undergo structural rearrangements within repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 89:910-914(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Hum. Genet. 54:179-190(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease severity.";
J. Clin. Invest. 93:1533-1542(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Invest. Dermatol. 102:13-16(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS EHK HIS-156 AND SER-161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92141228; PubMed-1371013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92386600; PubMed-1381287;
                                                                                                                                                                                                                                                                                                              TISSUE=Keratinocytes;
MEDLINE=93162043; Pubmed=1286667;
                                                                               Biol. Rep. 12:277-283(1987).
                                                                                                                                              MEDLINE-92339897; PubMed-1378806;
                                                                                                                                                                                                                                                                                             SEQUENCE OF 180-184 AND 577-589.
                                                                                                                      SEQUENCE OF 197-593 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 257:1128-1130(1992).
                                                                                                                                                                                                                                                    Gene 116:245-251(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperkeratosis.
                                                                                                                                                                                         Kisselev L.L.;
                                                                expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE GIVE-RICH REGION (1905TIONS 490-560).

-1- DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF EPIDEBHOLYTIC
HYPPERKERATOSIS (EMR) (ALSO KNOWN AS BULLOUS CONGENITAL
ICHTHVOSIPORM ERYTHRODERA (BCIE)); A HEREDITARY SKIN DISORDER
CHARACTERIZED BY BLISTERING AND A MARKED THICKENING OF THE STRATUM
CORNEDM. AT BIRTH, AFFECTED INDIVIDUALS USDALLY PRESENT WITH
REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS.
WITHIN A FEW WEEKS, THE ERYTHRODERMA AND BLISTER FORMATION
DIMINISH AND HYPERERATOSES DEVELOD. TRANSMISSION IS AUTOSOWAL
                                                                                                                                                                                                                             Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRATUM CORNEUM.
-!- POLYMORPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMINANT, BUT MOST CASES ARE SPORADIC.
DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF ANNULAR EPIDERMOLYTIC
ICHTHVOSIS (AEI), A DISTINCT PHENOTYPIC VARIANT OF EPIDERMOLYTIC
HYPERKERATOSIS. IT RESEMBLES CLINICAL AND HISTOLOGIC FEATURES OF
BOTH EPIDERMOLYTIC HYPERKERATOSIS AND ICHTHYOSIS BULLOSA OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-70 kDa) [K1 TO K8].
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
-!- CAUTION: REF: 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN POSITIONS 513 TO 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: SEEN IN ALL SUPRABASAL CELL LAYERS INCLUDING
Morley S.M.;
"Mutations in the rod 1A domain of keratins 1 and 10 in bullous
congenital ichthyosiform erythroderma (BCIE).";
J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                            "Genetic and clinical mosaicism in a type of epidermal nevus."; New Engl. J. Med. 331:1408-1415(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT AEI THR-446.
MEDLINE-99072665; PubMed-9856845;
Suga Y., Duncan K.O., Heald P.W., Roop D.R.;
"A novel helix termination mutation in keratin 10 in annular epidermolytic ichthyosis, a variant of bullous congenital ichthyosiform erythroderma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Invest. Dermatol. 111:1220-1223(1998).
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                                                                                                                                                                                         MEDLINE=95059228; PubMed=7526210;
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InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
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Aarhus/Ghent-2DPAGE; 7405; IEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X14487; CAA32649.1; -. EMBL; M19156; AAA59468.1; -. EMBL; M77663; AAA59199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L20218; AAB59438.1; -. L20219; AAB59439.1; -.
                                                                                                                                                                 VARIANT EHK THR-150.
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                                                                                                                                                                                                                                                                Fuchs E.;
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   NEW TOOLS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
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WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                           EMBL; AF212940; AAF29527.1; -. EMBL; BC004910; AAH04910.1; -. InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7. PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                                                                                                                    80581 MW;
                                                                                                                                                                                                                                                                                           78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                      (20E receptor).
                                                                                                                                                                                                                                                                                                   Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                       581
628
674
716
752
79
                                                                                                                                                                                                                                                                                                                  14 AGGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                    753 AA;
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_TaxID=7375;
                                                                                                                                                                                       436
489
542
587
635
677
                                                                                                                                                                                                                                                             402
                                                                                                                                                                                                                                                                                                                                                                                                                             ECR OR NRIH1
                                                                                                                                                                                                                                                                                                                                                                       ECR_LUCCU
                                                                                                                                                                                                                                                                                                                                                                                                                      receptor)
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                        RESULT 25
ECR_LUCCU
                                                                                                                                                                                                                                              SITE
   οy
                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY: BELONGS TO THE STRIATIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat proteins principally expressed in the brain."; J. Biol. Chem. 275:19970-19977(2000).
       PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                                                                                                                                                                                                    Y -> D (IN EHK; SEVERE PHENOTYPE)
/FTId=VAR_003831.
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20347911; PubMed=10748158; Castets F., Rakitina T., Gaillard S., Mogrich A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BINDS CALMODULIN IN A CALCIUM DEPENDENT MANNER. FUNCTION AS SCAFFOLDING OR SIGNALING PROTEIN. SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-BOUND (BY
                                                                                                                                                                                                                                                            Length 593
                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                         M -> T (IN EHK). /FTId=VAR_010507.
                                                                                                                                                                              /FTId=VAR_003827.
R -> C (IN EHK).
                                                                                                                                                                                                                                                            DB 1;
                                                                                           GLY/PHE/SER-RICH.
                                                                                                                  FTIG=VAR_010505.
                                                                                                                         M -> R (IN EHK). / FTId=VAR_010506
                                                                                                                                                        N -> H (IN EHK).
/FTId=VAR_003826
                                                                                                                                                                                               FTIG=VAR 003828
                                                                                                                                                                                                       R -> P (IN EHK).
                                                                                                                                                                                                                              /FTIG=VAR 003830
                                                                                                                                                                                                                                                                                                                                                            01-WAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                         R -> H (IN EHK)
                                                                                                                                                                                                                      -> S (IN EHK)
                                                                                                                                                                                                                                                                                                                                                753 AA
                                                                                                    GLY/SER-RICH.
                                                                                                                                                                                                                                                                          3; Mismatches
                                                                           LINKER 12.
                                                                                                                                                                                                                                                            Score 59;
                                                             LINKER 1.
                                                                                                                                                                                                                                                                   Š
                                                                     COIL 1B.
                                                     COIL 1A.
                                                                                    COIL 2
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                   Pred.
PRINTS; PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 402-753 FROM N.A.
                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                 11 AARAGGGGGGGGIEG 25
                                     456
593
181
202
202
294
317
456
144
126
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                                                                                                                                         150
                                                                                                                                                                       156
                                                                                                                                                                                                      156
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                                                                                                                                                                                      156
                                                                                                                                                        154
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                     146
457
146
182
203
295
318
                                                                                                 451
126
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                                                                                                                        150
                                                                                                                                        150
                                                                                                                                                                       156
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                                                                                                                                                                                                                     156
                                                                                                                                                                                                                                    160
                                                                                                                                                        154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Muscle;
                       Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monneron A.;
                                                                                                                                                                                                                                                                                                                                              ZIN_HUMAN
Q9NRL3;
                                                                                                                                                                                                                                                                                                                                                                                      Zinedin.
                                                                                                           VARIANT
                                                                                                                        /ARIANT
                                                                                                                                        ARIANT
                                                                                                                                                        /ARIANT
                                                                                                                                                                       VARIANT
                                                                                                                                                                                      /ARIANT
                                                                                                                                                                                                      /ARIANT
                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                    VARIANT
                                     DOMAIN
                                             DOMAIN
                                                            DOMAIN
                                                                    DOMAIN
                                                     DOMAIN
                                                                           DOMAIN
                                                                                    OMAIN
                                                                                           DOMAIN
                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                        ZIN_HUMAN
                                                                                                                                                                                                                                                                                                                                RESULT
Dp
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Eukaryota, Medazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pherygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS). CAUTION: The name "Zinedin" probably originates from the name of the famous soccer player from Marseille (Zinedine Zidane)!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDILINE=97449774; Pubmed=9304790;

Hannan G.N., Hill R.J.; Hill R.J.; Hill R.J.; Hannan G.N., Hill R.J.; Hill R.J.; Hill R.J.; Hill R.J.; Hill R.J.; Hill R.J.; Hill R.J.; Hill R.J.; R.J.; Hill R.J.; R.J.; Hill R.J.; R.J.; Hill R.J.; R.J.; Hill R.J.; R.J.; Hill R.J.; R.J.; Hill R.J.; R.G. R.J.; R.G. R.J.; R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.G. R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.J.; R.
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0
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15-DEC-1999 (Rel. 37, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAVEOLIN-BINDING (POTENTIAL). POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.1%; Score 59; DB 1; Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4DA016A8FF7EDB5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 757 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 21;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherford K.M., Rutherfors, Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fsihi H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G., Takiff H.E., Eiglmeier K., Bergh S., Cole S.T.; "Gene arrangement and organization in a approximately 76 kb fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSB_MYCLE STANDARD, PRT, 168 AA.
P46390; O53126;
D1-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein).
SSB OR ML2684 OR MLCB1913.20C.
                                                                                                                                                                                                                                                                                                                                                     Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encompassing the oric region of the chromosome of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.1%; Score 59; DB 1; Length 757; 76.9%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HORMONE-BINDING (POTENTIAL).
C1511452ED37D359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       MODULATING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR RECEPTOR-TYPE, C4-TYPE.
                                                                                                                                                                        InterPro: IPR001536; Hormone_rec_lig.
InterPro: IPR001733; Strdhormone_receptor.
InterPro: IPR001628; Zf-C4.
Pfam: PF00104; hormone_rec; 1.
Pfam: PF00105; Zf-C4; 1.
PRINTS: PR00198; STRDHORMONER.
PRINTS: PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00430; LRF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97124199; PubMed-8969512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiology 142:3147-3161(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83075 MW;
                                                                                                                                           EMBL; U75355; AAB81130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 76.9
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       300
366
321
361
674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 GGGGGGGGVPGMT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 GGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                      301 3
301 3
337 3
454 6
757 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1769;
                                                                                                                                                             HSSP; P20393;
                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                        -i- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR REPLICATION OF THE CHROMOSOME. IT IS ALSO INVOLVED IN DNA RECOMBINATION AND REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Thalamus;
MEDLINE-21181559; PubMed=11284713;
Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; "Molecular cloning and characterization of a new human histamine receptor, HH4R.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
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                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE SSB FAMILY.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9YSNI, 09H4K8; Q9GZX2; 01-MRR-2002 (Rel. 41, Created) 01-MRR-2002 (Rel. 41, Last sequence update) 01-MRR-2002 (Rel. 41, Last annotation update) Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 30.8%; Score 58.5; DB 1; Length 168; Local Similarity 52.0%; Pred. No. 6.7; hes 13; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN 124 133 POLY-GLY.
SEQUENCE 168 AA; 17700 MW; 077C62E430623658 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7)
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"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L39923; AAB53120.1; ALT_FRAME.
EMBL; AL022118; CAA17953.1; -.
EMBL; AL583926; CAC32216.1; -.
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MEDLINE=99278519; PubMed=10347254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 GPSLRYATAKVNKASRSGGGGGFG 131
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HSSP; P02339; 1EYG.
InterPro; IPR000424; SSB.
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                                                                                                                                             (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 414.865-871(2001).

-!- FUNCTION: THE H3 SUBCLASS OF HISTAMINE RECEPTORS COULD MEDIATE THE HISTAMINE SIGNALS IN CNS AND PERIPHERAL NERVOUS SYSTEM. SIGNALS THROUGH THE INHIBITION OF ADENYLATE CYCLASE AND DISPLAYS HIGH CONSTITUTIVE ACTIVITY (SPONTAMENUS ACTIVITY IN THE ABSENCE OF AGONIST). AGONIST STIMULATION OF ISOFORM 3 NIETHER MODIFIED ADENYLATE CYCLASE ACTIVITY NOR INDUCED INTRACELLULAR CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANBOUS: Does not bind to cimetidine and tripolidine. Shows modest affinity for thioperamide, imetit, N-alpha-methylhistamine and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to iodoproxyfan while isoforms 1 and 3 bind it with high affinity. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.; "Genomic organization and characterization of splice variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; 1 (SHOWN HERE), 2; 3/H35; 4; 5; 6 AND 7; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED PREDOMINANTY IN THE CINS, WITH THE GREATEST EXPRESSION IN THE THALAMUS AND CAUDATE NUCLEUS. THE VARIOUS ISOFORMS ARE MAINLY CORRERESED IN BRAIN, BUT THEIR RELATIVE EXPRESSION LEVEL VARIES IN A REGION-SPECIFIC MANNER. ISOFORMS 3 AND 7 ARE HIGHLY EXPRESSED IN THE THALAMUS, CAUDATE NUCLEUS AND CEREBELLUM WHILE ISOFORMS 5 AND 6 SHOW A POOR EXPRESSION. ISOFORMS 5 AND 6 SHOW A HIGH EXPRESSION IN THE ANGEDALA, SUBSTAMTIA NIGRA. ISOFORM 7 IS NOT FOUND IN HYPOTHALAMUS, OR SUBSTAMTIA NIGRA.
                                                                                                                                                                                                   An amino acid variation in the human histamine h3 receptor from a
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3).
Ullmer C., Zirwes E., Lubbert H.;
"Cloning and functional expression of the human histamine H3S
                                                                                                                                                                                                                              patient suffering from orthostatic dysregulation.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT VAL-280
                                                                                                                                                                         Wiedemann P., Bonisch H., Bruss M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                       Biochem. J. 355:279-288(2001).
                                                    receptor
                                               human histamine H3
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A -> V (IN ORTHOSTATIC DYSREGULATION).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MISSING (IN ISOFORM 5).
MISSING (IN ISOFORM 5).
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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2ACF7440FBE95B6C CRC64;
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MISSING (IN ISOFORM 7)
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16-OCT-2001 (Rel. 40, Last annotation update)
Homeobox even-skipped homolog protein 2 (EVX-2).
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DOMAIN 1 39 EXTRACELLU
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                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                         AB019000; BAB17030.1; -..., AL0296652; CAC51025.1; -..., AL78250; CAC39434.1; -..., AL078633; CAC34014.1; -..., AF363791; AAKS0040.1; -...
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16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                              EMBL; AF140538; AAD38151.1; -. EMBL; AB045369; BAB20090.1; -.
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62.5%;
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nes 10; Conserv
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EMBL; AJ278250;
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Q03828;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
One cut domain family member 2 (ONECUT-2 transcription factor) (OC-2).
ONECUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                              Genomics 10:43-50(1991).
-!- SUBCELULAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY EMBRYOGENESIS AND NEUROGENESIS IN A BIPHASIC MANNER.
-!- SIMILARITY: BELONGS TO THE EVEN-SKIPPED FAMILY OF HOMEOBOX
                                                                          D'Esposito M., Morelli F., Acampora D., Migliaccio E., Simeone A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental protein; Homeobox; Nuclear protein.
                                                                                              "EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, is localized at the 5' end of HOX4 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 1; Length 476; Pred. No. 18;
        SEQUENCE FROM N.A.
Birren B., Linton L., Nusbaum C., Lander E.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6AA99041BA151C3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ALA.
POLY-ALA.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA.
POLY-ALA.
POLY-ALA.
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                                                                                                                                                                                                                                                                                                   EMBL; AC009336; -; NOT_ANNOTATED_CDS.
EMBL; MS983; AAA52414.1; -.
EMBL; AS9982; AAA52414.1; JOINED.
HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 2.
                                                  SEQUENCE OF 144-300 FROM N.A. MEDLINE-91257849; PubMed-1675198;
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1. DNA-binding; Developmental prote.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47799 MW;
                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.5%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308
351
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 LGSRGGGGGGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413
476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                       Boncinelli E.;
                                                                                                                                                                                       PROTEINS.
                                                                                                                                                                                                                                                                                                                                                MIM; 142991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONC2_HUMAN
095948;
                                                                                                                        chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ONC2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                     MEDLINE=99115605; PubMed=9915796; Jacquenin P. D., Lannoy V., Rousseau G.G., Lemaigre F.P.; Jacquenin P., Lannoy V., Rousseau G.G., Lemaigre F.P.; an ovel mammalian member of the ONECUT class of homeodomain transcription factors whose function in liver partially overlaps with that of hepatocyte nuclear factor-6."; J. Biol. Chem. 274.2665-2671(1999).
-i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. ACTIVATES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=92228768; PubMed=1565620; Hara Y., Rovescalli C., Kim Y., Nirenberg M.; Structure and evolution of four POU domain genes expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                      OF A NUMBER OF LIVER GENES SUCH AS HNF3B.
--- SUBCELLUTAR LOCATION: Nuclear.
--- SIMILARITY: CONTAINS 1 CUT DOMAIN.
--- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
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15-JUL-1998 (Rel. 36, Last annotation update)
Brain-specific homeobox/FOU domain protein 1 (BRN-1 protein).
POUJF3 OR OTF8 OR BRN1 OR BRN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.5%; Score 58; DB 1; Length 485; 65.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 POLY-SER.
52482 MW; AF21E052EFBE5DA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 89:3280-3284(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-HIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y18198; CAB38253.1; -. TRANSFAC; T03259; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 GGGGGGGGGGPEDELLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 GGGGGGGIEGPTLRQCLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02376; CUT; 1.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003350; CUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391
466
37
66
82
82
165
303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
75
152
298
485 AA;
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Hes 13; Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 604894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRN1_MOUSE
P31361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%; Score 58; DB 1; Length 495; ilarity 91.7%; Pred. No. 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOU.
HOMEOBOX.
AM; 77B802E890C9A014 CRC64;
                                                                                                                                                                                                           PIR; S31223; S31223.
HSSP; P14859; 10CT.
HGD; MGI:102564; Pou3f3.
InterPro; IPR001356; Homeobox.
InterPro; IPR001357; POU.
Ffam; PF00046; homeobox; 1.
PRINTS; PR00157; POU.
PRINTS; PR00158; POUDOMAIN.
PROBOM: PS000058; POU; 1.
SMART; SM00382; POU; 1.
SMART; SM00382; POU; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00017; HOMEOBOX_2; 1.
PROSITE; PS00017; HOMEOBOX_2; 1.
PROSITE; PS00017; HOMEOBOX_2; 1.
PROSITE; PS00045; POU_2; 1.
PROSITE; PS00045; POU_2; 1.
PROSITE; PS00045; POU_2; 1.
PROSITE; PS00045; POU_2; 1.
PROSITE; PS00045; POU_2; 1.
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POLY-ALA.
POLY-ALA.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 383 PC
401 460 HC
495 AA; 50012 MW;
                                                                                                                                                                                                EMBL; M88299; AAA39960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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Matches 11; Conserv
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SEQUENCE
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